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Adt05028 Haemophil Ads49042 Bacterial Aca48331 Prokaryot

Aca26583 Prokaryot Aaz97180 Human pro Abl14243 Drosophil Aac39924 Arabidops

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Breast cancer differentially expressed gene product #47.
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ds; cytostatic; gene therapy; DKFZp5661133 activity inhibitor; breast cancer; differential expression.

A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene. Disclosure, Page, 111pp, English Trepicchio WL, Strahs A, Trepicchio WI Immerman F, Dorner AJ; WPI; 2004-804779/79. (AMHP ) WYETH. (STRA/) STRAHS A. 

The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKZP5661133 activity. The methods are useful for treating cancer, e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention. Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for inhibition of DKFZp5661133 activity. Claim 30; SEQ ID NO 47; 257pp; English. WPI; 2003-577534/54. CHIR ) CHIRON CORP. Hansen 

Achise475 Cotton gy Adj40364 Plant cDN Adj40364 Plant cDN Ads48153 Bacterial Abq43783 Oligonucl Abv12580 Human pro Adv12680 Human pro

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Solid tumour prognosis gene seqid 2116. BP ADU11677 standard; DNA; 475 27-JAN-2005 (first entry) ADU11677; RESULT

cytostatic, gene therapy, expression profile, solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds. WO2004097052-A2 Unidentified

29-APR-2003; 2003US-0466067P. 23-JAN-2004; 2004US-0538246P. 29-APR-2004; 2004WO-US013587.

11-NOV-2004.

Slonim DK; Burczynski ME, Twine NC, /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids"

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unaupervised clustering aecond classes is a subcluster formed by an unaupervised clustering about a second classes is a subcluster formed by an apoulation of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, and the majority of the second class of patients as a second clinical outcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at the teat another storage medium including data that represent at least one reference expression profile of the gene. (iii) a program capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the captesion profile, and (iv) a processor capable of executing the compourlear cells of patients who have the solid tumour correlate with clinical outcomes of the patients and a nucleic acid or protein array comprising concentrated probes for solid tumour prognosis genes, where cap patients of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients has a second class of the invention. Note: The sequence represents a solid tumour prognosis gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format

controlly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                        profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood mononuclear calls (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an
                                    invention describes a method comprising comparing an expression
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## Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other; 475 00 00 00 Length: Matches: Conservative: Mismatches: Indels: 2.97 45.00 100.0% 100.0% Alignment Scores:

## 396 GTTTTGTATTTGAACCGCAAGGGGATA 422 Gaps: 1 ValleuTyrLeuAsnArgLysGlyIle 9 US-10-774-176-14 (1-9) x ADU11677 (1-475) Best Local Similarity: Query Match: Percent Similarity: Š

Canine 5T4 tumour-associated antigen gene. AAA27060 standard; DNA; 901 BP 22-AUG-2000 (first entry) AAA27060; RESULT 3 AAA27060 

Canine; TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;

Location/Qualifiers
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Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
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                                                       The present sequence encodes the canine 5T4 tumour-associated antigen carcinomas but has a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the human or murine 5T4 gene sequence. The 5T4 antigen was shown to be the nucleic acid encoding the antigen and the antigen tresponse. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
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                    Disclosure, Page 78-79; 79pp; English.
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N-PSDB; ABJ05564.
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnostis or prognosis of breast cancer cells of or detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lung cancer-associated polynucleotide #197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ValLeuTyrLeuAsnArgLysGlyIle 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-774-176-14 (1-9) x ABT07721 (1-927)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0399245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2002; 2002WO-US012476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.33
45.00
100.0%
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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transcript in a cell from a patient, comprising a range cancer transcript in a cell from a patient, comprising a contacting a blological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for thibiting proliferation of a lung cancer-associated polypeptide, for thibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell corrections to other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences harviet and pulmo cancer, such as antibodies. Sequences harviet.
                                                                                                                                                  cancer-associated
patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                            The invention relates to a method for detecting a lung
                                                                                    Claim 22; Page 336; 453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nvention
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Length: Alignment Scores:

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

927 0 0 0 Matches: Conservative: Mismatches: Indels: Gaps: 6.33 45.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match:

1 ValLeuTyrLeuAsnArgLysGlyIle 9 US-10-774-176-14 (1-9) x ABX76333 (1-927)

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775 Gririgiarricaaccecaaeceara 801 ADB80503 RESULT

ADB80503 standard; DNA; 927 BP

04-DEC-2003 (first entry)

Ovarian cancer-associated transcript #34.

cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.

Homo sapiens

Location/Qualifiers 1. .927 /\*tag=

WO2002102235-A2

27-DEC-2002

18-JUN-2002; 2002WO-US019297

2001US-0299234P. 2001US-0315287P. 2001US-0317544P. 2001US-0350666P. 2002US-0372246P. 05-SEP-2001; 18-JUN-2001; 27-AUG-2001; 12-APR-2002; 

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The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The mucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, detecting and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                           Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used for the detection method of the invention.
                                                                                                                                                                                                                                                         Claim 10; Page 297; 332pp; English
EOS BIOTECHNOLOGY INC.
                                               Mack DH, Gish KC;
                                                                                                                P-PSDB; ADB80504.
(EOSB-)
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

927 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 6.33 45.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match Best Local

GTTTTGTATTTGAACCGCAAGGGGATA 801 1 ValLeuTyrLeuAsnArgLysGlyIle 9 US-10-774-176-14 (1-9) x ADB80503 (1-927) 775 셤 Š

RESULT 7 ADN38723

ADN38723 standard; cDNA; 927 BP

ADN38723;

17-JUN-2004 (first entry)

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.

Human; differential expression; cancer; anglogenic disorder; fibrotic disorder; psortiasis; isofinemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; ulnerary; gene therapy; vaccine; gene; ss.

Homo sapiens.

WO2003042661-A2.

22-MAY-2003

13-NOV-2002; 2002WO-US036810

13-NOV-2001; 2001US-035066F. 21-NOV-2001; 2001US-0332464P. 29-NOV-2001; 2001US-0334393P.

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
               p53 pathway; Leucine rich repeat capricious related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for diagnosing or treating cancer. The invention is gene therapy. The present sequence is human LRRCAPS related DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 74-75; 99pp; English.
                                   cancer; gene therapy; ds
                                                                                                                                                                                                                        22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                         21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                                          Belvin M, Schleithoff L, P. Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                        (EXEL-) EXELIXIS INC.
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                                                                                                               WO2003035831-A2
                                                                           Homo sapiens.
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                                                                                                                                                     01-MAY-2003
                                     LRRCAPS;
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The invention relates to mucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and mucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosling and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, infilammatory diseases, autoimmune diseases, ratinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                              Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a nucleic acid sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                               08-JAN-2002; 2002US-03472IIP.

10-JAN-2002; 2002US-0347349P.

08-FEB-2002; 2002US-0355250P.

13-FEB-2002; 2002US-0355714P.

20-FEB-2002; 2002US-0356714P.

20-MAR-2002; 2002US-0356809P.

04-AFR-2002; 2002US-03701I0P.
                                                                                                                                                                                                                                                                                                          (ROSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                Ginsburg WM,
                                                                                                                                                                                         05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
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09-SEP-2002; 2002US-0409450P.
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45.00
100.0%
100.0%
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P-PSDB; ADN38724.
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Mack DH,
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Lioubin MN,

Funke RP,

Plowman GD,

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Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; ancertic; nocropic; immunosupressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; antibolic disorder; diabetes; obesity; infectious disease; ancrexia; neurodegenerative disease; Altheimer's disease; parkinson's disease; immune disorder; haematopoictic disorder; cardiovascular disorder;
 Length:
Matches:
Conservative:
Mismatches:
                                                           Indels:
Gaps:
                                                                                                                                                                      790 GITTTGTATTTGAACCGCAAGGGGATA 816
                                                                                                                                          ValleuTyrLeuAsnArgLysGlyIle
                                                                                                            US-10-774-176-14 (1-9) x AAD56198 (1-973)
                                                                                                                                                                                                                                     ABV99349 standard; DNA; 1156 BP
                                                                                                                                                                                                                                                                                                                                 Human NOV8a coding sequence.
 6.69
45.00
100.0%
100.0%
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                                Percent Similarity:
Best Local Similarity:
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AAD56198 standard; DNA; 973

RESULT 8 AAD56198 Human LRRCAPS related DNA #5.

(first entry)

07-AUG-2003

AAD56198;

ValleuTyrLeuAsnArgLysGlylle 9

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US-10-774-176-14 (1-9) x ADN38723 (1-927)

Percent Similarity: Best Local Similarity:

Query Match:

**Gaps**:

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99127-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX poteins and coding sequences are useful in the manufacture of a andicament for treating sequences are useful in the manufacture of a andicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disquences and proteins are useful for treating.

The NOVX coding sequences and proteins are useful for treating, concer, neurodegenerative diseases, ancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, fertility, bronchial asthma, AlDS, dyslipidemia, metabolic disorders, fertility, bronchial asthma, AlDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or disanostic methods
                                                                    Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Pena CEA, Burgess CE, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                 New NOVX polypeptides and polymucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feline; cat; oncofoetal leucine-rich glycoprotein; 574; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                                                                            Claim 16; Page 114-115; 619pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ValLeuTyrLeuAsnArgLysGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK87175 standard; cDNA; 1260 BP
03-JAN-2002; 2002US-0345705P.
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45.00
100.0%
100.0%
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                                                                                                                                                                                                                                                                 disorders, and asthma.
                                            (CURA-) CURAGEN CORP
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Best Local Similarity:
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DB:
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2001US-0294465P.
2001US-0294465P.
2001US-029489P.
2001US-029489P.
2001US-0299310P.
2001US-0299310P.
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20010S-0304398P.
20010S-0312903P.
20010S-0318462P.
20010S-0318770P.
20010S-0325430P.
20010S-0325681P.
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2001US-0283675P.
2001US-028366F.
2001US-0288066P.
2001US-0288342P.
2001US-0288348P.
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2001US-0277321P.
2001US-0277327P.
2001US-0277338P.
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2001US-0277833P.
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2001US-0279344P.
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2001US-0280233P.
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2001US-0338092P.
2001US-0337185P.
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                                                                                                                                               38-MAR-2002; 2002WO-US007288
                                                                                                                                                                                                                                     2001US-0274849P
                                                                                      WO200272771-A2
                                                                                                                                                                                                                                               12-MAR-2001; 2
13-MAR-2001; 2
13-MAR-2001; 2
14-MAR-2001; 2
16-MAR-2001; 2
16-MAR-2001; 2
20-MAR-2001; 2
20-MAR-2001; 2
20-MAR-2001; 2
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30-MAR-2001; 2
30-MAR-2001; 2
02-APR-2001; 2
02-APR-2001; 2
04-APR-2001; 2
30-APR-2001; 2
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22-MAR-2001;
23-MAR-2001;
26-MAR-2001;
27-MAR-2001;
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03-MAY-2001; 2
15-MAY-2001; 2
16-MAY-2001; 3
16-MAY-2001; 3
30-MAY-2001; 3
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18-JUN-2001;
                                                             Homo sapiens
                                                                                                                                                                                                                                   09-MAR-2001;
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10-SEP-2001;
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1156 9 0 0 0

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The present invention relates to the isolation of canine and feline oncofectal leucine-rich glycoproteins known as 574, and the concofectal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are treatment of tumours or other diseases associated with cell and/or treatment of tumours or other diseases associated with cell and/or proliferation, infections, and inflammatory conditions in animals, proliferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating focetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foctal cells may then be subject to biochemical or genetic sampling used for testing foctal abnormalities, or to determine the sex of the foctus (ss). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                              Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                    /*tag= a
/product= "5T4 protein"
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                               Location/Qualifiers
                                                                                                                                                                                                                                                                   (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 68; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB97513 standard; DNA; 1260 BP
                                                                                                                                                                                                                                                                                                        Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                  13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                               L3-NOV-2001; 2001WO-GB005004
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P-PSDB; AAU98694.
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                                                                                                                        WO200238612-A2.
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Pred. No.:
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Felis sp
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ò 셤 Major Histocompatibility Complex class I peptide epitope; MHC; Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other; 1260 9 0 0 (first entry) Feline 5T4 antigen DNA 04-DEC-2003 ADB97513;

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The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope of the 5T4 antigen. The invention further provides a polyepitope string of the 5T4 epitope; a nucleic acid centuring the 5T4 epitope string of the 5T4 epitope; a vector system capable of acid to a cell, a cell pulsed with the 5T4 epitope, a polyepitope of the 5T4 epitope, a polyepitope of the 5T4 epitope, a polyepitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid in a subject; and a T cell line or clone capable of comprising the 5T4 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 5T4 epitope in conjunction with an MHC class in molecule. The 5T4 epitope or its encoding nucleic acid and the vector system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for diagnosting or monitoring the 5T4 epitope or its ancel acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or is useful in the manufacture of a medicament for treating and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New major histocompatibility complex class I peptide epitopes from human
5T4 tumor-associated antigen, useful for preventing and/or treating a
disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing a disease. This polynucleotide sequence represents the feline
5T4 antigen, 5T4 epitope, polyepitope string, vaccine, T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                             /*tag= a
/product= "Feline 5T4 antigen protein"
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                                                                                                     Location/Qualifiers
1. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 67; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                         (OXFO-) OXFORD BIOMEDICA UK LTD.
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                                                                                                                                                                                                                                                                                                                                 13-FEB-2002; 2002GB-00003419.
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P-PSDB; ADB97520.
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Best Local Similarity:
                                                                                                                                                                                                          WO2003068816-A1.
                                                               Unidentified
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ADB97452
ID ADB97
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Human
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                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a Major Histocompatibility Complex (WHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polymucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                                           gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                          New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
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                                                                                                                                             1. .1260
/*tag= a
/product= "Peline 5T4 antigen protein"
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                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 49; 63pp; English
                                                       DNA encoding feline 5T4 protein.
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                                                                                                                                                                                                                                                          13-FBB-2002; 2002GB-00003420.
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                                 (first entry)
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45.00
100.0%
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P-PSDB; ADB97455.
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                                                                                                                                                                                          WO2003068815-A2
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                                                                                                             Unidentified
                                 04-DEC-2003
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           ADB97452;
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22-AUG-2000 (first entry)

AAA27058;

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The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour fagnosis, targetling and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                             cancer;
                                           Human, TAA, tumour-associated antigen, anti-tumour; cytostatic; immunostimulant, vaccine; carcinoma; colorectal cancer; gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1117 GTTTTGTATTTGAACCGCAAGGGGATA 1143
5T4 tumour-associated antigen gene
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                                                                                                                                                                                                                                                                                                                                                                         99GB-00001739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll MW, Myers KA;
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Best Local Similarity:
                                                                                                                                                                                                    WO200029428-A2.
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                 18-NOV-1999;
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Key
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                                                                                                                                                                                                                                                                                                                                                                            which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The Scrw antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The Scrw antibody is also useful for treating inflammatory disease including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system diseases, cancers, central nervous system diseases, cardiovascular diseases, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacterelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce Scrv of the invention
                                                                                                                                                                                                                                                                                                  Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                     The specification describes the use of a single chain antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
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                                  Location/Qualifiers
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                                           1. .1263
/*tag= a
/product= "5T4"
                                                                                                                                                                                                         (OXFO-) OXFORD BIOMEDICA UK LTD.
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                                                                                                                                                          18-NOV-1999; 99WO-GB003859.
15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                                                                                    13-NOV-2000; 2000WO-GB004317.
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                                                                                                                                                                                                                                                                            P-PSDB; AAB83839.
                                                                                           WO200136486-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity
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                                                                                                                25-MAY-2001.
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                                                                                                                                                                                                                                          Myers KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK87174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1117
           Canis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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                                  Key
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 514, and the concofoetal leucine-rich glycoproteins known as 514, and the proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell profit profit profit in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 514 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 514 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The called may then be subject to biochemical or genetic sampling used for cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                               Location/Qualifiers
1. .1263
/*tag= a
/product= "5T4 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 67; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2000; 2000WO-GB004317.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                      WO200238612-A2
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25-FEB-2002; 2002US-00084817
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                                                                              01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                  Belvin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ56299;
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$X $\frac{1}{2}$ \frac{1}{2}$ \
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes the mouse 5T4 tumour-associated antigen (TPA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor associated antigen, 5T4 capable of eliciting cytotoxic T\text{-lymphocyte} response useful in vaccinating against and in treating tumors.
                                                                                    Mouse, TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; ds.
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Matches:
Conservative:
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                               Mouse 5T4 tumour-associated antigen gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD BIOMEDICA UK LTD.
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                                                                                                                                                                                                                                                                                                                                                                        99WO-GB003859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99GB-00001739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carroll MW, Myers KA;
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                                                                                                                                                                                                     Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1999;
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DB:
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway—modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                            Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-76; 99pp; English.
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                                                                                                           21-OCT-2002; 2002WO-US033540.
                                                                                                                                                           22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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                                                                                                                                                                                                                                                                                                                            Schleithoff L, 19 H, Friedman
                                                                                                                                                                                                                                                                            (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-421410/39.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                              Francis-Lang H,
WO2003035831-A2.
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                                                                                                                                                                                                This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymocleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protoconcepuse that is amplified in neuroblastoms cells and is common in small cell lung cancers. The present invention describes these CDNA molecules as useful for in hybridisation assays to detect expression of mucleic acids (or complementary nucleic acids) in a present in a given sample, as useful for in hybridisations as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymocleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the US Patent Office at
                                                                                                                      New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bladder cancer associated cDNA sequence SEQ ID NO:192
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
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                                                                                                                                                                               Claim 1; SEQ ID NO 105; 27pp; English.
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                                                                             Plon SE,
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23-PEB-2001; 2001US-0270784P.
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                                                                             SG, Nuchtern JG,
                     (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S B.
(SHOH/) SHOHET J M.
                                                                                                   WPI; 2003-635698/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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DB:
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                                                                              Stuart
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with a polymucleotide to that selectively hybridises to a sequence that is 80 % identical to a concertance of sequences that is 80 % identical to a concertable of sequences (see ACC50951 to ACC50951 to ACC50951 to ACC51059 concertable of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 concertable of sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in disgnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnosic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                  (ROSB-) EOS BIOTECHNOLOGY INC
03-AUG-2001; 2001US-0310099P.
08-NOY-2001; 2001US-0343705P.
13-NOY-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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Best Local Similarity:
Query Match:
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WO2003035831-A2
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                                                                                                                                                                                                                                                                                       The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated cell to treat lung cancer in a patient and for treating a memmal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell ung cancer or other benign or precancerous lestons, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                  Claim 22; Page 335; 453pp; English
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                                                                                                        (EOSB-) EOS BIOTECHNOLOGY INC
                        2001US-0290492P.
2001US-0339245P.
2001US-0350666P.
                                                                 29-NOV-2001; 2001US-0334370P.
              2001US-0284770P
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                                                                                                                                                            2003-093161/08
                                                                                                                                  Aziz N, Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
          18-APR-2001;
                        10-MAY-2001;
                                       09-NOV-2001;
                                                     13-NOV-2001;
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                       Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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LRRCAPS; cancer; gene therapy; ds.
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                                                                                                                                                                                                        Funke RP, Lioubin MN,
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                                                                             22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                         21-OCT-2002; 2002WO-US033540
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15-PBB-2002; 2002US-0357600P.
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                                                                                                                                                                 (EXEL-) EXELIXIS INC.
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01-MAY-2003
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                                                                                                                                                                The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified leudine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
inflammatory disease, autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
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                                            Lioubin MN,
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Matches:
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                                            Plowman GD,
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                                                                                                                                               Disclosure; Page 76-77; 99pp; English
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2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
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 01-MAR-2002; 2002US-0361196P
                                                        Francis-Lang H, Friedman L;
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                                           Schleithoff L,
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                      (EXEL-) EXELIXIS INC.
                                                                            WPI; 2003-421410/39.
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Best Local Similarity:
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29-NOV-2001; 2
03-DEC-2001; 2
14-DEC-2001; 2
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Pred. No.:
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DB:
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention or by detecting a polypeptide of the invention. The comprision of the invention, antibodies which specifically bind a nucleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides.

Contibodies and methods are useful for disgnosting, prognosting and treating cancer and other conditions such as psoriasis, is chaemad, heart disease, the convenient of the provenient of the content of the content of the content of the conditions and nucleic acids. According the content of the content of the conditions and nucleic acids and uterating including they may are according to the content of the conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; tumour-associated antigenic target; TAT; cell death; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumour-associated antigenic target (TAT) cDNA sequence #53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a nucleic acid sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2053
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 39; 1385pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aziz N, Ginsburg WM,
Murray R, Watson SR,
                                2002US-0359077P.
2002US-0368809P.
2002US-0370110P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                       2002US-0396839P
                                                                                                                                                                                                                                                                            2002US-0397775P
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                                                                                                                                                          2002US-0372246P
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                                                                         29-MAR-2002;
04-APR-2002;
12-APR-2002;
05-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                         09-SEP-2002;
13-FEB-2002;
20-FEB-2002;
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Wood WI;

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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of
                                                                                                                                                                                                                                 New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                 Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; breast cancer; prognosis; gene expression; diagnosis.
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                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 355; 3069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                 Jackman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR25444 standard; DNA; 2053 BP
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                                   25-SEP-2003; 2003WO-US030907
                                                                  25-SEP-2002; 2002US-0414006P
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                                                                                                 (GETH ) GENENTECH INC
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                                                                                                                                 Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-593473/57.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004065545-A2
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 08-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                   Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                   Hillan KJ, Polakis P, Polson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 53; 319pp; English.
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                                                                                                                                                              19-AUG-2002; 2002US-0404809P.
21-AUG-2002; 2002US-0405645P.
23-SEP-2002; 2002US-0413192P.
15-NOV-2002; 2002US-0419008P.
15-NOV-2003; 2003US-0426847P.
02-JUL-2003; 2003US-0484959P.
                                                                                                                                                                                                                                                                                                               Frantz G, Hil
u TD, Zhang Z;
                                                                                                                                 19-AUG-2003; 2003WO-US025892
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cancer; cytostatic; gene;
                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                            a FJ, Fr.
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                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-257144/
P-PSDB; ADL06552.
                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide, use
treating cancer.
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                                                               WO2004016225-A2
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                                   Homo sapiens.
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Spencer SD,
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Query Match: DB:

ADN0396

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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ 1D NO:2070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
to control levels.
                                                                                                                                                                                                                                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Mismatches:
five genes in a cell sample taken from patient,
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Matches:
                                 Disclosure, SEQ ID NO 1305, 226pp; English
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                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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DB:
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ACN38510
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CC The invention relates to human tumour-associated antigenic target (TAT) colypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide colypeptides, expression vectors and host cells comprising and TAT nucleic acids and colypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptides, a peptide or organic cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antegonists, binding molecules and compositions are useful cantibodies, antegonists, binding molecules and compositions are useful increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, badder cancer, pancreatic cancer, cervical cancer, cancers of the central colorectal cancer, melanoma and leukaemia. TAT nucleic acids may further be cused as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; ss; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klimczak LJ, Laeng P;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA of an exemplary efficacy gene for BAD SeqID174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PSYC-) PSYCHIATRIC GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADV35098 standard; cDNA; 2053 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2001; 2001US-0299151P.
07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-0325150P.
14-NOV-2001; 2001US-0333047P.
18-JAN-2002; 2002US-0349936P.
04-MAR-2002; 2002US-0361834P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-2002; 2002US-00175523.
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45.00
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Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-118903/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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P-PSDB; ABG22988.

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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as well as Parkinson's and Alzheimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, nootropic, antimanic and antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polymucleotide is a human cDNA sequence of a gene that is differentially expressed in the presence of a peraperic compound and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene for bipolar affective disorder,
               Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contacted with the test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
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                                                                                                            Example 6; SEQ ID NO 174; 39pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents an exemplary efficacy
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2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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23-AUG-2000;
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Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed carriers. (I) is useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and cannot or produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this contract of the printed specification, but was obtained in
                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
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                                                                                                                              Claim 1; SEQ ID NO 22979; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Kawai Y; T, Koga H;

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The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length cDnts were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this specent din not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                               830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                      Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki
                                                                         WPI; 2001-524255/58
                                                                                                  P-PSDB; AAM93333
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Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;

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2359
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-10-774-176-14 (1-9) x AAK94253 (1-2359)

1540 GITTIGIATITIGAACCGCAAGGGGAIA 1566 1 ValLeuTyrLeuAsnArgLysGlylle 9 ઠે 셤

ADL30831 standard; cDNA; 2359 BP RESULT 31 

ADL30831;

(first entry) 20-MAY-2004 Full length human cDNA clone SeqID 2864.

human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene

Homo sapiens

EP1396543-A2

10-MAR-2004.

07-JUL-2000; 2003EP-00025638 08-JUL-1999;

08-JUL-1999; 99JP-00194486. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183865. 07-JUL-2000; 2000RP-001140895.

(REAS-) RES ASSOC BIOTECHNOLOGY

Hayashi K, Ishii S, Kawai Y; K, Kojima S, Otsuki T, Koga H; Ota T, Nishikawa T, Isogai T, Wakamatsu A, Sugiyama T, Nagai Ota T,

WPI; 2004-204755/20. P-PSDB; ADL30832.

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA from both the 5' and 3' full length human cDNA clone of the invention.
                 full
New oligonucleotide primers (830 cDNAs) useful for synthesizing
length human cDNAs.
                                                                                                                                                                                         Example 1; SEQ ID NO 2864; 1340pp; English
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X44X8X000000000X8

Length: Matches: Conservative: Mismatches: Indels: Gaps: 18.3 45.00 100.0% 100.0% 120.0% Best Local Similarity: Query Match: DB:

Percent Similarity: Alignment Scores: Pred. No.:

US-10-774-176-14 (1-9) x ADL30831 (1-2359)

2359 0 0 0 0

Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;

1540 GTTTGTATTTGAACCGCAAGGGGATA 1566 ValleuTyrLeuAsnArgLysGlyile 9

RESULT 32

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ВР AAK94254 standard; cDNA; 2361

AAK94254;

(first entry) 06-NOV-2001 Human full-length cDNA, SEQ ID NO: 2866

Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

Homo sapiens

EP1130094-A2

05-SEP-2001.

07-JUL-2000; 2000EP-00114089

99JP-00194486. 2000JP-00118774. 2000JP-00183765. 08-JUL-1999; 11-JAN-2000; 02-MAY-2000;

(HELI-) HELIX RES INST.

Ξ Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga

WPI; 2001-524255/58. P-PSDB; AAM93334.

830 Primers useful for synthesizing full length cDNA clones and in genetic manipulation.

their use

Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful

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88; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetee; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoathritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
            length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
clarifying the function of the protein encoded by the cDNA. The full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding protein that promotes STAT6 activation #64.
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                                                                                                                                     Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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2002JP-00377326.
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                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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26-DEC-2002;
27-DEC-2002;
15-MAY-2003;
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protein or its epitope-bearing fragments to a non-human animal as an antipody antipose. The protein or its epitope-bearing fragments to a non-human animal as an antipose. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATE activation such as allegic diseases, inflammation, autoimmune diseases, diabetes, also the for treating disease associated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthitis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemotrhage, viral hepatitis and AIDS. The protein has efficient promoting STATE activity. The protein or mucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a human cDNA encoding a protein which promotes STATE activation.
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T, Koga
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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K, Kojima S, Otsuki
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Conservative:
Mismatches:
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na T, Nagai
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02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000BP-00114089.
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Best Local Similarity:
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmuno disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
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Matches:
Conservative:
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Indels:
               Example 1; SEQ ID NO 2866; 1340pp; English
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2002JP-00377326.
2002US-0436467P.
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Best Local Similarity:
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15-MAY-2003;
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diabetes and cancer.

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cuseful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antibody. Which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or canceptability to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATS activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful cor to the treating disease associated with STATS activation such as allergic diseases, inflammation, autoimmune disease, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STATS activation and/or prevention of Thi hyperactive diseases associated with STATS activation and/or prevention of Thi hyperactive diseases. Subarachonid hasmoring allergic rhintis, ischaemic heart diseases, subarachonid hasmorings, viral hepatitis and AIDS. The protein has efficient promoting STATS activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with axessaive compounds for treating and preventing disease associated with axessaive activation or inhibition of STATS. The present associated with axessaive activation or inhibition of STATS. The present management of activation or inhibition of STATS. The present managements are activated with axessaive managements.
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                                          transducer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
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                                          invention relates to a purified protein promoting signal
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Claim 4; SEQ ID NO 125; 1368pp; English.
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2002JP-00377326.
2002US-0436467P.
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26-DEC-2002;
27-DEC-2002;
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16-MAY-2003;
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11-MAY-2000; 2000US-0203336P. 25-MAY-2000; 2000US-0207087P.

26-MAY-2000; 2000US-0207546P

26-APR-2001; 2001WO-US013360 27-APR-2000; 2000US-0199963P

WO200181363-A1.

01-NOV-2001

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein for its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression a activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharaccutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, inflammation, autoimmune diseases, diabetes, compositions disease associated with STAT6 activation and/or prevention of treating disease associated with STAT6 activation and/or prevention of thin hyperactive diseases. Compositions are also useful in rheumatoid arthitis, osteoarthitis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid hemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                                           New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                           Muramatsu S, Ishizawa K;
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                                                                                                      Honda G,
                                                                                                           Sugahara T, Matsuda A,
(ASAH ) ASAHI KASEI KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes and cancer.
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2557 9 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 20 45.00 100.0% 100.0% 12 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: 

1690 GTTTTGTATTTGAACCGTAAAGGCATA 1716 1 ValLeuTyrLeuAsnArgLysGlyIle 9 US-10-774-176-14 (1-9) x ADI26158 (1-2557)

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ABA90338 standard; cDNA; 1149 ABA90338

ABA90338;

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Indele:

Gaps:

973 GTGCTCTACCTAAACCGCCGGCGTC 999

ADU01816 standard; cDNA; 3993 BP

RESULT 38 ADU01816 ADU01816;

1 ValLeuTyrLeuAsnArgLysGlylle

US-10-774-176-14 (1-9) x ABA90338 (1-1149)

Length: Matches: Conservative: Mismatches:

42.00 100.0% 88.9% 93.3%

Percent Similarity: Best Local Similarity:

Query Match:

(first entry) Human polynucleotide #13. 12-FEB-2002

Human; nootropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquillaer; antiarthmic; cardiant; antiaethmatic; antiinflammatcry; antilipaemic; hepatotropic; virucide; antidiabetic; nephrotropic; anorectic; cytostatic; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; respiratory disease; liver disease; renal disease; skeletal muscle disease; gastrointestinal disease; placental disease; esticular cancer; male fertility; pancreatic disease;

Homo sapiens

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583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026, 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255, 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as given in the specification. The polypeptides amino acid sequence as given in the specification. The polypeptides are useful for treating diseases and antibodies against the polypeptides are useful for treating diseases uncloading the polypeptides are useful for congestive heart failure, Hodgkin's disease and myocardial infarction; congestive heart failure, Hodgkin's disease and myocardial infarction; respiratory diseases including asthma, chronic obstructive pulmonary diseases including asthma, chronic obstructive pulmonary chearists, Type II diabetes mellitis, and impaired glucose tolerance; congestivitis; skeletal muscle diseases including cenal failure, acute tubular necrosis and constitute, and impaired glucose tolerance; congestivities; skeletal muscle diseases including conditions and intestinal obstruction; lymph diseases including myotonia congenita and intestinal obstruction; lymph diseases including confinence including confinence including confinence including chartering characterial diseases including diseases including diseases including diseases including characterial diseases including characterial d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of testes including testicular cancer, male reproductive diseases including low testosterone and male infertility; and disease of pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence encodes a polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polypeptide comprising a 277, 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith RF, Xiang Z, Kabnick KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1149 BP; 120 A; 468 C; 417 G; 144 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 51-52; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murdock PR, Rizvi SK,
                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-041392/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABB53273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xie Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agarwal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lai Y,
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27-JAN-2005 (first entry)

Novel human polynucleotide segid 283.

cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc; proliferative disorder; inflammatory disorder; immune disorder; metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis; ulcerative colitis; human; gene; ss.

Homo sapiens.

WO2004093804-A2.

04-NOV-2004.

19-APR-2004; 2004WO-US012047. 2003US-0463732P

02-MAY-2003; 2003US-0467199P. 02-MAY-2003; 2003US-0467230P. 19-MAY-2003; 2003US-0471306P. 19-MAY-2003; 2003US-0471336P. 08-JUL-2003; 2003US-0485223P. 08-JUL-2003; 2003US-0485224P. 14-JUL-2003; 2003US-0486446P. 14-JUL-2003; 2003US-0486480P. 08-AUG-2003; 2003US-0493573P. 2003US-0493577P 08-AUG-2003;

(FIVE-) FIVE PRIME THERAPEUTICS INC.

08-SEP-2003; 2003US-0505059P

Lee E, Hestir K, Chu K, Masuoka L, Williams LT;

WPI; 2004-775861/76. P-PSDB; ADU02548.

New first nucleic acid molecule comprising a polynucleotide sequence given in the specification, useful in preparing a composition for diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.

Claim 1; SEQ ID NO 283; 291pp; English.

The invention describes a new first nucleic acid molecule comprising a polynucleotide sequence given in the specification. Also described are: an animal injected with the nucleic acid molecule; a second nucleic acid molecule about 70, 80, 90 or 95\* homologous to the first nucleic acid molecule or that hybridises to the first polynucleotide sequence that is at least a pringency conditions; a vector comprising the nucleic acid molecule or a promoter that drives the expression of the nucleic acid molecule and a promoter that drives the expression of the nucleic acid molecule and ucleic acid molecule; a nucleic acid molecule; a nucleic acid molecule; a nucleic acid molecule; a nucleic acid molecule and a carrier or a buffer and one or more compositions comprising the nucleic acid molecule and animal injected with the polypeptide; a polypeptide composition comprising the notypeptide; a nucleic acid molecule molecule and a carrier or buffer; a cell animal injected with the polypeptide and acarrier or buffer; a cell culture medium comprising the polypeptide or transfected cells transfected with the polypeptide or transfected cells transfected with the polypeptide; and acrivitor or infected host cell; synthesising Nanodiscs simultaneously and for synthesising a series of simultaneously-synthesised Nanodiscs and for synthesising a derivatal structure; immunising a non-human animal; cordetermination of crystal structure; immunising a non-human animal; screening for modulators of the processor of the polypeptide in a sample, an antibody specifically recognising, binding to or modulating a child complement; determining the presence of an antibody to the polypeptide in a sample. An antibody specifically recognising, binding to or modulating and molecule or the biological activity of at least one polypeptide. acid molecule or its biologically active fragment; an antibody composition comprising the antibody and a carrier; a bacteriophage, where the antibody is displayed on the bacteriophage; a bacterial cell comprising the bacteriophage; a non-human animal injected with the

antibody composition; a host cell that secretes the antibody; making an antibody; diagnosing a disease, disorder, syndrome, or condition comprising cancer, or proliferative, inflammatory, immune, metabolic, bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or conditions in a patient; a modulator composition comprising a modulator and a carrier; gene therapy; prophylactic or therapeutic treatment of a subject; an isolated modified cell comprising at least one first heterologous nucleic acid molecule, where the first heterologous nucleic that polypeptide; a non-human animal deficient in the polypeptide or first hon-human animal; and one or more cells derived from the non-human animal; and one or more cells derived from the non-human animal; and one or more cells derived from the non-human animal; and one or more cells derived from the non-human animal; and one or more cells derived from the non-human animal. diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis. This sequence encodes a novel human polypeptide of the invention. \$

Sequence 3993 BP; 719 A; 1298 C; 1224 G; 752 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 42.00 100.0% 88.9% 93.3% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-10-774-176-14 (1-9) x ADU01816 (1-3993)

RESULT 39

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ABL11890 standard; cDNA; 4289 BP

ABL11890;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 30152.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US009231.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE ) PE CORP NY.

Myers EW; Li PWD, Venter JC, Adams M,

WPI; 2001-656860/75. P-PSDB; ABB67787 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Claim 1; SEQ ID NO 30152; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of

Matches:

8888888

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The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The nucleic acid can also be used to detect mutations in GPCR genes and gene expression products such as mRNA. AASS7072-AASS7203 represent D. melanogaster G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR), useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coupled protein receptor genomic and coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; G-protein coupled receptor; GCPR; insecticide; diagnostic; mutation detection; ds.
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                     Sequence 4289 BP; 1219 A; 962 C; 967 G; 1141 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding Drosophila G-protein coupled receptor, GCPR #22.
                                                                                                                                                                                                                                                                                           4289
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Conservative:
Mismatches:
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18-JUL-2000; 2000US-00618893.
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Best Local Similarity:
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DB:
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Sequence 4289 BP; 1219 A; 962 C; 967 G; 1141 T; 0 U; 0 Other;

4289

Length:

160

Alignment Scores: Pred. No.:

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The invention describes an isolated protein (I) consisting or comprising an amino acid sequences (SI), as given in the specification, an allelic variant of (SI), an orthologue of (SI) or fragment of (SI). (I) allelic variant of (SI), an orthologue of (SI) or fragment of (SI). (I) is useful for identifying an agent that binds to (I) which comprises contacting the protein with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the protein. (I) is useful for identifying modulators as potential or insecticides, to determine the biological activity of the protein of insecticides, to determine for high-throughput screening), as targets for insecticides, to determine for high-throughput screening), as targets contacting agents for use in human drugs and for identifying compounds that receptor activity. An antibody (II) that selectively binds to (I) is useful for assessing normal and aberrant subcellular compounds that modulate G-protein coupled receptor (GPCR) nucleic acid expression, diagnostic assays for qualitative changes in GPCR nucleic acid that lead to insecticidal activity/tolerance, to detect mutations in GPCR may and as an agent and activity and as an amand an amand and an expression of nucleic acid expression. A host cell comprising a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated G-protein coupled receptor useful for identifying modulators as potential insecticides, to determine the biological activity of the protein and for identifying compounds that modulate receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor; GPCR; insecticide; drug screening; insecticide screening; insecticidal activity; insecticidal tolerance;
                                                                                                                                                                                                                                                                                                                                                                                 Drosophila G protein coupled receptor genomic DNA seq id 22.
C4000
                   Conservative:
Mismatches:
                                                          Indels:
                                                                                                                                                                         3275 ATCATATATCTTAACCGTAAAGGCATC 3301
                                                                                                                                                    ValLeuTyrLeuAsnArgLysGlylle 9
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                                                                                                                 US-10-774-176-14 (1-9) x AAS57114 (1-4289)
                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-DEC-1999; 99US-0168677P.
12-JAN-2000; 2000US-0175691P.
23-MAR-2000; 2000US-0191638P.
18-JUL-2000; 2000US-00618893.
                                                                                                                                                                                                                                                                     ADC35812 standard; DNA; 4289
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42.00
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly; gene; ds.
                     Percent Similarity:
Best Local Similarity:
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us-10-774-176-14.p2n.rng

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containing (III) is useful for conducting cell-based assays involving the GPCR protein or its fragments, and identifying GPCR protein mutants. This sequence encodes a fruit fly G-protein coupled receptor (GPCR).
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Sequence 4289 BP; 1219 A; 962 C; 967 G; 1141 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                           Gaps:
      160
42.00
100.0%
77.8%
93.3%
                             Best Local Similarity:
                     Percent Similarity
Alignment Scores:
                                     Query Match:
DB:
       Pred. No.:
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US-10-774-176-14 (1-9) x ADC35812 (1-4289)

3275 ATCATATATCTTAACCGTAAAGGCATC 3301 1 ValleuTyrLeuAsnArgLysGlyIle 9 ::::::||||||||||||| ઠ

ADX27916 standard; cDNA; 874 BP 용

(first entry) 21-APR-2005 ADX27916;

Plant full length insert polynucleotide segid 10736.

recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lighin production; plant growth regulator; yield; plant growth, plant development; seed oil; protein yield; protein content; gene; ss. plant protectant; plant growth regulant; gene therapy; plant; 

Unidentified.

US2004034888-A1.

19-FEB-2004.

28-APR-2003; 2003US-00425114.

06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.

LIU J. ZHOU Y. (/min/) (ZHOU/)

KOVALIC D K. SCREEN S E. TABASKA J E. (KOVA/) (SCRE/) (TABA/) (CAOY/)

CAO Y.

Zhou Y, Kovalic DK, WPI; 2004-180133/17. Liu J,

× Cao

Screen SE, Tabaska JE,

New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

Claim 1; SEQ ID NO 10736; 15pp; English

The invention describes a recombinant DNA construct comprising a polymuclectide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office a to fitp, sequence then 17boc1D:2004034888. The polymuclectide of the invention are also useful in physical arrays of molecules and as

15-JUL-2004

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om base 200001 (Human cancer-associated genomic DNA LOCUS ABD32791 Accession Abd32791
             improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
breeding markers. The recombinant DNA construct is useful for
                                                                                                                                                                                                 Sequence 874 BP; 250 A; 160 C; 179 G; 285 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments
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Continuation (3 of 4) of
WP Sequence split into 4
WP Fragment Name
WP ABD32791_0
WP ABD32791_1
WP ABD32791_2
WP ABD32791_3
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Best Local Similarity:
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DB:
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ABD32791 0
ABD32791 1
ABD32791 2
ABD32791 3
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                                                                                                                                                                                                                                                                        Percent Similarity:
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Pred. No.:
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Bigwood D;

Pauloski NR,

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Taylor I,
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                                                                                                                                                                                           The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                 Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor marker; 88; gene; lung tumor; cytostatic; neoplasm; expression;
DNA microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99291 BP; 26458 A; 20539 C; 22297 G; 29997 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99291
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                       Claim 16; SEQ ID NO 744; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30721 ATATATCTAAACAGAAAAGGTATA 30744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-10-774-176-14 (1-9) x ABD33549 (1-99291)
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ID ADZ70593/C

XX

AC ADZ70593;

XX

C ADZ70593;

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BE Human cDNA from lung cancer marker gei

XX

W Tumor marker; 88; gene; lung tumor; C; XX

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W DNA microarray.

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CS Homo sapiens.

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W W02005032495-A2.

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PD 14-APR-2005.

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PD 14-APR-2005.

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PR 01-OCT-2004; 2004WO-US034163.

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RAB D BAYER PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LeuTyrLeuAsnArglysGlyile 9
15-DEC-2003; 2003WO-US040081
                        17-DEC-2002; 2002US-00322281
                                                   (SAGR-) SAGRES DISCOVERY INC
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                                                                             Morris DW, Malandro MS;
                                                                                                       WPI; 2004-499109/47.
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The invention relates to providing a patient diagnosis for lung cancer comprising comparing the level of expression of genes or gene products in a biological sample from a normal level of expression of genes or gene products in a biological sample from a normal individual.

Also included are distinguishing between normal and disease tissues, conditionable of a patient being treated for lung cancer by administering an anti-cancer agent, identifying a compound useful for the treatment of lung cancer and an array for distinguishing between normal conditions and disease tissues (comprising 2 or more probes corresponding to 2 or more genes selected from any of the 200 nucleotide sequences given in the specification). In providing a patient diagnosis for lung cancer, one or more genes are selected from any of the 200 nucleotide sequences as mentioned in the specification, or one or more genes products are polypeptides selected from any of the 200 nucleotide sequences as mentioned in the specification, or one or more genes products are polypeptides selected from any of the 200 nucleotide sequences are polypeptides selected from any of the 200 nucleotide sequence are polypeptides selected from any of the 200 nucleotide sequence are polypeptides selected from any of the 200 nucleotide sequence act polypeptides selected from any of the 200 nucleotide sequence data for this patent did not form part of the present sequence represent a cDNA from one of the 200 und concer marker genes. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did nelectronic format directly from WIPO
                                                                                                                      Providing a patient diagnosis for lung cancer comprises comparing the level of expression of genes or gene products in a biological sample from the patient with that from a normal individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ds; gene; neuropsychiarric disorder; attention deficit disorder; ADD; schizoaffective disorder; inpolar disorder; unipolar affective disorder; schizophrenia; adolescent conduct disorder; pharmacogenomics; fingerprinting; paternity testing; antidepressant; neuroleptic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 114596 BP; 33213 A; 26849 C; 24628 G; 29906 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 278; 60pp; English.
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2005-285325/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                          P-PSDB; ADZ70594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BXBXBXBXBXBXBXBXB
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                                                                                                                                                                                                The invention relates to a nucleic acid comprising a polymorphic region of a Calcium/Calmodulin-dependent protein kinase-like gene (CADPKL) allelic variant, and the polypeptide it encodes. CADPKL allelic variants are useful in determining whether a subject has or is at risk of developing a neuropsychiatric disorder, such as schizophrenia, attention deficit disorder (ADD), schizoaffective disorder, bipolar disorder, unipolar affective disorder and adolescent conduct disorder. The polypeptides, polymucleotides, antibodies and modulators of the CADPKL allelic variants are useful for disquosing or treating these antibodies to a CADPKL polypeptides may be used to raise antibodies to a CADPKL polypeptide. The nucleic acids may be used as probes or primers, in pharmacogenomics for designing therapies for the disorders, and in fingerprinting for detection of different individuals
                                                                                                                 New variants of calcium/calmodulin-dependent protein kinase-like nucleic acids and polypeptides, useful for diagnosing and treating neuropsychiatric disorders, e.g. schizophrenia, schizoaffective disorder, and bipolar disorder.
                                                                                                                                                                                                                                                                                                                                                       with the same species (e.g. paternity testing). This sequence represents human CADPKL genomic DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 157875 BP; 44403 A; 35734 C; 34322 G; 43416 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus licheniformis genomic sequence tag (GST) #2800.
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                                                                                                                                                                           Claim 1; Page 119-200; 223pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LeuTyrLeuAsnArgLysGlylle
                                                                     Barrington-Martin R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK75509 standard; DNA; 1209 BP.
            09-JAN-2001; 2001US-00757300.
23-AUG-2001; 2001US-00935464.
                                              (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
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                                                                                           WPI; 2002-590643/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                     Meyer JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK75509;
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The invention describes a method of monitoring differential expression of the genes in a first Bacillus cells relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells, examining the array, and determining array of Bacillus comprision by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells. The method is useful for monitoring control argumental argumental serveral genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and controling gene copy number variation and stability. Monitoring changes in which Bacillus cells adapt to changes in culture conditions, conversion of genes may be used to provide a representation of the way controling streams of pens may be used to provide a representation of the way controling streams or other physiological provocation. Extensive follow conformental stress or other physiological provocation. Extensive follow controling frame, since sequence information is available.

This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence tag (GST) used in the method cof the invention. Note: The sequence tag for this patent did not form to part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                             Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytosine methylation, 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide for detecting cytosine methylation SEQ ID NO 20421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1209 BP; 376 A; 289 C; 295 G; 249 T; 0 U; 0 Other;
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NOVOZYMES BIOTECH INC. NOVOZYMES AS.
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100.0%
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                                                                                                                   Clausen IG;
                                                                                                                                                                                                  WPI; 2002-416684/44.
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(NOVO)
                                                                                                                   Berka R,
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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated c, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-
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for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                      Guetig D;
                                                                                                                                                                                                                                                                                                                                                                      Berlin K,
01-SEP-2001; 2001WO-EP010074
                                                                                                01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.
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                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                           (BPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                      Olek A,
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Sequence 1859 BP; 243 A; 251 C; 648 G; 717 T; 0 U; 0 Other;

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ABQ33831 standard; DNA; 1859 BP. ABQ33831; BXSXXXXXXXXXXXXXXXX

Oligonucleotide for detecting cytosine methylation SEQ ID NO 20422.

(first entry)

12-JUL-2002

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Antibacterial; Listeria; food contamination; mutational analysis;

Listeria monocytogenes ATCC 19115.

infection; ds

Homo sapiens.

WO200218632-A2

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomaclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of clipomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervolus, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation investigating cell differentiation. The method allows the methylation are spirally represent genomic DNA sequences used to illustrate the method in the for the contained the contained of the contained of a wide respiratory squences used to illustrate the method in the contained the contained the contained of the contained the contained of the contained the contained of the co
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05-SEP-2000; 2000DE-01044543.
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WPI; 2002-332479/37.

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WPI; 2002-332479/37.

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New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, XX

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The present invention relates to nucleic acid sequences (ABQ67188-

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Claim 14; SEQ ID NO 3815; 180pp; French.

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Contaminants in foods, or mutational analysis and for analysis of gene contaminants in foods, or mutational analysis) and for analysis of gene corression. Proteins encoded by the nucleic acid sequences can be used to contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins and code of sequences can be used to contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins and sequence cat sequence and in alectronic format part of the printed specification, but was obtained in alectronic format part of the printed specification, but was obtained in alectronic format can be printed specification, but was obtained in alectronic format can be printed specification, but was obtained in alectronic format part of them NIPO at ftp, wipo.int/pub/published_pct_sequences. (Updated XX

Sequence 3617 BP; 1098 A; 635 C; 837 G; 1043 T; 0 U; 4 Other;
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Search completed: April 25, 2006, 12:36:46 Job time : 336.3 secs

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BX511225 Zebrafish

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67711CV9	14 AC137180 14 AC126287 14 AC126477 14 AC098339 2 AB003574 14 AC151080 14 AC113658	14 AC15/302 2 AE003503 14 AC119117 1 CNSPAX05 14 AC122070 14 AC123485 14 AC098394 1 BX571874 6 AX041921 10 G44076	10 BV256819 115 HFU296484 115 HFU296486 115 AJ748787 6 AX410480 2 AXE544853 2 AXE544853 2 AXE544853 6 CQ136997 6 CQ258668 6 CQ258668 6 CQ258668 6 CQ258668 6 CQ258668 6 CQ258668 10 BV296508	BV32 BV25 BV23 BV23 BV39 AY227 AY227 AX644 AR644 AR644	ens (human)  i Metazoa; Chordata; Cran; Eutheria; Euarchontoglir; Homo.  i Marshall, W. B. and Zhang ons and methods relating on and methods relating ne Inc. (CA) Location/Qualifiers  1290 //organism="Homo sapiens" //organism="Homo sapiens"
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FEATURES SOURCE

REFERENCE AUTHORS TITLE JOURNAL

RESULT 1 CQ687716 LOCUS DBFINTTON ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PAT 15-SEP-2000
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BIOMEDICA LTD (GB)
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Homo sapiens (human)
Homo sapiens
Eukaryota; hetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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C12N15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065,
C07K19/00,
C12N15/00
                                                                                                      Burczynski, M.B., Twine, N.C., Slonim, D.K., Trepicchio, W.L., Strahs, A., Immerman, P. and Dorner, A.J.
Methods for prognosis and treatment of solid tumors
Patent: WO 2004097052-A 2116 11-NOY-2004;
Wyeth (US); Burczynski, Michael B. (US)
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Carroll, M. W. and Myers, K.A.

Carroll, M. W. and Myers, K.A.

Patent: JP 202530060-A 3 17-SEP-2002;

OXFORD BIOMEDICA LTD

OS Canis sp. (dog)

PN 17-SEP-2002

PN 18-NOV-1999 GB 9825303.2, 27-JAN-1

SO-JUL-1999 GB 9917995.4

PI MILES WILLIAM CARROLL, KEVIN ALAN MYE

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PC C12N15/00,

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    /organism="Homo sapiens"
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JP 2002530060-A/3.
Canis sp.
Canis sp.
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Polypeptide.
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AX821548
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
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Methods of diagnosis of breast cancer, compositions and methods of screening for medulators of breast cancer
Parent: WO 02059377-A 57 01-AUG-2002;
BOS Biotechnology, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                            tumour immunotherapy
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                                             Carroll, M.W. and Myers, K.A.
5t4 tumour-associated antigen for use in
Patent: 8P 1160323-A 3 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 57 from Patent WO02059377.
AX829164.1 GI:39838931
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Sequence 3 from Patent W00238612.
AX467373 GI:21900603
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lauraslatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
Felis sp.
Felis sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
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MHC class I peptide epitopes from the human 5t4 tumor-associated
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Polypeptide
Patent: WO 0238612-A 3 16-MAY-2002;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1260
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Patent: WO 03068816-A 1 21-AUG-2003;
Oxford Biomedica (UK) Limited (GB)
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Sequence 1 from Patent WO03068816.
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Homo sapiens (human)
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AX025011
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Datemary 200230060-A 1 17-SEP-2002;
CXFORD BIOMEDICA LTD
OS Homo sapiens (human)
OS Homo sapiens (human)
PD 17-SEP-2002
PD 17-SEP-2002
PP 18-NOV-1999 GB 9901739.4 PR 18-NOV-1999 GB 9901739.4 PR 30-JUL-1999 GB 9917995.4
PP 18-NOV-1998 GB 9825303.2,27-JAN-1999 GB 9901739.4 PR 18-NOV-1998 GB 9917995.4
PP 18-NOV-1998 GB 9917995.4
PP C12N15/00,
PC C12N15/00,
PC C12N15/00,
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PC POlypeptide
PH Rey 1..1263
PT SOURCE 1..1263
PT SOURCE 1..1263
                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
   PAT 10-DEC-2003
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JP 2002530060-A/1.
Mono sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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   linear
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                                                                                                                                                                 Carroll, M.O., Harrop, R.O. and Kingsman, S.O. MHC class II peptide epitope of 5t4 antigen Patent: WO 03068815-A 1 21-AUG-2003; Oxford Biomedica (UK) Limited (GB)
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Matches:
Conservative:
Mismatches:
Indels:
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AX821548 1260 bp
Sequence 1 from Patent W003068815.
AX821548.1 GI:39724930
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1 (bases 1 to 1263)
Carroll,M.W. and Myers,K.A.
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45.00
100.0%
                                                                         Felis catus (cat)
Felis catus
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Polypeptide.
BD249731
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BD249731
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PAT 15-SEP-2000
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W., Bllard, F.M. and Myers, K.A. Antibodies Antibodies Oxford Blomedica (UK) Limited (GB) Location/Qualifiers 1.1263 /organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                               Callott,....
Polypeptide
Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOWEDICA LTD (GB)
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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Matches:

    1263
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/db_xref="taxon:9606"

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Sequence 14 from Patent W00136486.
AXI49553
AXI49553.1 GI:14347991
                                                                                                                                                               1117 GTTTTGTATTTGAACCGCAAGGGGATA 1143
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Sequence 1 from Patent W00029428.
AX025011 GI:10184932
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(GB)

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1135 GTTTTGTATTTGAACCGTAAAGGCATA 1161
Oxford Blomedica (UK) Limited Location/Qualifiers
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 1 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Patent: WO 0238612-A 1 16-MAY-2002;
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AX467371 GI:21900602
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AX316086
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Homo sapiens
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AX316086
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BD24973.1
BD24973.1
BD24973.2
BD24973.1
BD24973.1
BD24973.1
BD24973.2
JP 2002530060-A/2.
Mus musculus (house mouse)
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Carroll, M. W. and Myers, K.A.
BCarroll, M.W. and Myers, K.A.
Carroll, M.W. and Myers, K.A.
BO179ptide
LOSPED BIOMEDICA LTD
OXFORD BIOMEDICA LTD
OX Mus musculus (mouse)
PN JP 2002530060-A/2
PP 18-NOV-1999 GB 99217995.4
PI MILES WILLIAM CARROLL, KEVIN ALAN MYERS
PC CILVIS/09, AGIK39/00, AGIK48/00, AGIP35/00, CO7K1/06, CO7K14/065, PC CILVIS/09
CC CO7K19/00,
CC POlypeptide
FT Source
FT Source
FT Source

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                                                                                                                                               PRI 18-APR-2005
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Direct Submission
Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer
Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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I (bases I to 2053)

Myers, K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.

Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains leucine-rich repeats
J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="placenta"
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62. .372
                                                                                                                                               linear
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Homo sapiens 5T4 gene for 5T4 oncofoetal antigen.
Z29083
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    6
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2 (bases 1 to 2053)
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                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 2 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Polypeptide
Patent: WO 0029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB)
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                                         Sequence 2 from Patent WO0029428.
AX025012
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AX316087
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                                                                                                                                                                Mus musculus (house mouse)
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                                                                                                                    AX025012.1 GI:10184933
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RESULT 17
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BD127282.1 GI:23222277
GI:6650211
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1.363
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364.1644
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Homo sapiens (human)
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/gene="5T4"
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/gene="5T4"
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                                           Rattus norvegicus
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Burneted (03-NOV-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST/CDNA project.
This sequence is from a Xenopus Gene Collection (XGC) library, from
a library constructed by Aaron M. Zorn. CDNA was prepared from RNA
extracted from gastrula embryos. EcoRI-NotI cut CDNA was then
ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA, complete cds. AF063939
                                                                                                                                                                                                                                                                                                                                     Senopus tropicalis (Structure Craniata, Vertebrata; Buteleostomi; Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; 1 (bases 1 to 2183)

Amaya, B., Ashurst, J.L., Bonfield, J.K., Croning, M.D.R., Davies, R.M., Francis, M.D., Garrett, N., Gilchrist, M.J., Grafham, D.V., Voigt, J. and Zorn, A.M.
                                                                                                                                                                                                                                                     VRT 03-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="TGas020h08"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stage 10.5-13 mixed)"
                                                                                                                                                                                                                                   Z183 bp mRNA linear Xenopus tropicalis finished cDNA, clone TGas020h08. CR855786. GI:55295318
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Host: Escherichia coIi XL1-blue.
Location/Qualifiers
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Mismatches:
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Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 GTTTTATATTTAAACAGGAAAGGGATT 818
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/trailation="MPCAGSRQPSAGDCRLRIARLALVILGWVSASAPSSSLPSSST8
PAAFLASGSAQPPAERCESBAARTVKCWNRNILEVPADLPPYVRNIFILIGNO
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TPAGSNYSVSTPSPLLLSLILAHI VPPEDQRQNGSFBGHVAFEGAVAAALRSGHLRGF
HHLELASNHFLYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHILSSLHLRBUALRGF
KRUMSTLAGAGGAHYRFLDNLRNSLVSCLTYASFRNLTHILSSLHLBDNAL
KRNBGLLDLTSSDLDCDATLPGSLOTSYTPGINVPWTSTLIVALIGAFFLVVPDKARLTCAFPEK
NRRGLLDLTSSDLDCDATLPGSLOTSYTPGINVLALIGAFFLLVLYLNRKGIKKWHH
NIRDACRDHMEGYHYRYEINADPSLTNLSSNSDV"
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                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
                                        Eukaryotan Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Rattus.

1 (Jases 1 to 2333)
Ninkina,N.N. and Buchman,V.L.

Structure and expression of the rat 574 gene
Unpublished

2 (bases 1 to 2333)
Buchman,V.L.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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'product="5T4 oncofetal_antigen homolog"
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Mismatches:
Indels:
Gaps:
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/dev_stage="newborn"
1. .2333
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/db_xref="GI:6650212"
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Rattus norvegicus (Norway rat)
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db_xref="GI:45502668"
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Best Local Similarity:
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                              PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
                                                                                                                                                                                                                                                                                                                             C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualiflers
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                              Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                    PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KBIICHI NAGAI, PI
SHINICHI KOJIMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota, T., Nighikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
                                                              Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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/db_xref="taxon:9606"
424. .1575
/note="unnamed protein product"
/codom_start=1
/protein_id="CAP85958.1"
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Mismatches:
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Location/Qualifiers
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/organism="Homo sapiens"
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JP 2002017375-A/2713
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1 (Jases 1 to 2359)

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                                                                                                                                                     APSGSNASVGAPSPLVELILMHIVPPEDERONRSFEGMVVAALLAGRALOGIERILELA
SNHFLSTLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRLTHLESLHLEDNALKVLHNG
TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPERONRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRGIKK"
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/trānslation="MPGGCSRGPAAGDGRLRLARLALVILGWVSSSSPTSSASSFSSS
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LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPF
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3
mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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/mol_type="mRNA"
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TLABLOGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPBRMRNVL
LBLNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYBINADPRLTNLSSNSDV"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Patent: WO 03104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                                                                                                                                                                                              Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2866 10-MAR-2004; Research Association for Biotechnology (JP)
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/note="unnamed protein product"
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Sequence 2866 from Patent EP1396543.
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2714 22-JAN-2002;
HELLAR RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2714
PD 22-JAN-2002
PP 07-JUL-2000 JP 200253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Primer for synthesizing full-length CDNA and use thereof FH Key
Location/Qualifiers
T CDS (426). (1685).
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Ota,T., Nishlkawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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/mol_type="genomic DNA"
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JP 2002017375-A/2714.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                     /trainlation="MPGGCSRCPAAGDGRLRLARLALVILGWVSSSPTSSASSFSSS
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AFGGSRASVGAPSPLVELILMHIVPEEDERQRRSFEGHVVAALLAGGALGRLELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTVVSFRNLTHLESLHLEDNALKVLHG
TLAELGGLPHRVFLDNNWCDCHAADMVTWLKETFVVQGKORLTCAYPEKNRVL
TELNSADLDCDPLIPPSLQTSSVYFGIVLALIGAIFLUVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
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highly similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Otsuki, T., Ota, T., Nishikawa, T., Hayashi, K., Suzuki, Y., Yamamoto, J., Wakamatsu, A., Kimura, K., Sakamoto, K., Hatano, N., Kawai, Y., Ishii, S., Saito, K., Kojima, S., Sugiyama, T., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Nagai, K., Sugano, S. and Isogai, T. Signal Sequence and Keyword Trap in silico for Selection of Full-Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped cDNA Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK074790 2361 bp mRNA linear PRI 09-J
Homo sapiens CDNA FLJ90309 fis, clone NT2RP2000903, highly s
to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
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AK074790.1 GI:22760466
AK074790.1 GI:22760466
Homo sapiens (full insert sequence).
Homo sapiens (human)
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Matches:
Conservative:
Mismatches:
Indels:
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                                            /proteIn_id="CAF06467.1"
/db_xref="GI:40881327"
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Isogai, T. and Otsuki, T.
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Best Local Similarity:
Query Match:
DB:
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Rattus norvegicus (NOTMEN) tark)

Rattus norvegicus (NOTMEN) tark)

Rattus norvegicus

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rukaryota; Muroidea; Muridae; Murimae; Rattus.

(Lases 1 to 2361)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlausner, R.D., Colling, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Guastrane, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sakwinski, M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samailus, D.E.,

Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROD 13-DEC-2004
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Submitted (02-DEC-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                      /clone_11b="NT2RP2"
/note="cloning vector: pMB188FL3
mRNA from NT2 neuronal precursor cells after 2-weeks
retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2361 bp mRNA linear ROD 13-DE RALtus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2361
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Conservative:
Mismatches:
Indels:
                                                                                                                                            /clone="NT2RP2000903"
/cell_line="NT2"
/cell_type="teratocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1542 GTTTTGTATTTGAACCGCAAGGGGATA 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
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                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-774-176-14 (1-9) x AK074790 (1-2361)
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Location/Qualifiers
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Director MGC Project.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                 (bases 1 to 2379)
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                                               Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Whe site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.79 bp mRNA linear PRI 29-JUN-2004 Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317 BC031161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHLELASNHFLYLPRDILDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KYLHRYTLERMQGLAHVRPLDNNPWYDCYMADMVSWLKETEVVPDKARLTCARPEK
WRNGGLDLTSSDLDCDATLPGSLOTSYVFGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MPGAGSRQPSAGDGRLRLARLALVILGWVSASAPSSSLPSSSTS
APPTAGSAGAPPPARRCPAAGRCSBARTWWRNRLLEWPDALPPVYNLFTTGNQ
MTVL.PAGARRQPPLATULATULGGHILKEVGAGAFBILPGILRLDLGHNPLTNLSAF
TFAGSNVSVSTPSPLLELIIMHIVPPEDQRQNGSFEGHVAFEGHVAAALRSGLALRGL
                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="MGC:9332 IMAGE:7193411"
/tissue type="Heart, rat (Brown Norway)"
/clone_lib="NHH MGC_234"
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Conservative:
Mismatches:
Indels:
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/note="Vector: pExpress1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="Tpbg protein"
protein_id="AAH87011.1"
db_xref="GI:56268820"
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db_xref="RGD:621453"
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BC037161.2 GI:33872201
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gene="Tpbg"
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Homo sapiens
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Best Local Similarity:
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:22713382.
On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help desk
Email: cgapbe.remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov
Contact: nisc.mgc@nhgri.nih.gov
Contact: nisc.mgc@nhgri.nih.gov
Contact: N. Ayele.K., Becketrom-Sternberg, S.M., Benjamin, B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Guita,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
TBurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H.F., Moore, T., Max, S.L., Wang, J., Hasieh, F., Diatchenko, L., Marusina, K., Barmara, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scherkin, G.J., Uscquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, An., Gay, L.J., Hulyk, S.Y., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Banches, R.M., Madan, A., Young, A.C., Schevon, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Radden, S.C., Mall, Length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 26 Row: m Column: 15 This clone was selected for for ill length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="Muscle, rhabdomyosarcoma"
/clone lib="NIH MGC 17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonyms: M6P1, ST4-AG, ST4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pOTB7"
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/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating dectal descrinoma. 5 month old virgin mouse." /clone lib="MCI CGAP_Mam6" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskelllo,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCLELASNHFLPLPRDLIAQLPSLRYLDLRNSLVSLTYASFRNLTHLBSLHLBDNAL
KVILNSTLARWGGLAHVKVFLDNNPWYCDCYMADMYMLKETBYVPDKARLTCAPPBK
MRNRGLLDLNSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKMMH
NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAAFLASGSAQPPPAERCPAACECSEAARTVKCVNRNILLEVPADLPPYVRNLFITGNQ
MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGIRRLDLSHNPLTNLSAF
AFAGSNASVSAPSPLEELILMHIVPPEDQRQNGSFEGMVAFEGMVAFALRSGLALRGL
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protein [Punction unknown]"
                       nstitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Gene Collection (MGC), Cancer Genomics Office, National Cancer
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/gene="Tpbg"
/note="LRRCT; Region: Leucine rich repeat C-terminal
                                                                                                         Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="synonym: 5T4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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                                                                                    REMARK
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Sciurophathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 2423)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausmer, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Bosak, S.A., McEwant, T.L.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Bouffard, G.G., Blakesley, R.W., Toung, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 IMAGE:5353871), complete cds.
                                                                                                                                                                                                                                                                                                                                       AFSGSNASVSAPSPLVELILMHIVPPEDERQNRSFEGMVVAALLAGGALRELELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRALTHLESLHIEDNALKVLHNG
TLAELQGLPHIRVPLDNNPWVCDCHMADMVTMLKETEVVQGKDRLTCAYPEKMRNYL
LEINSADLDCDPILDPSZYPYGIVYALIGAIFLLGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLIYLSSNSDV"
                                                                                                                                                                                                                                                                                  APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
LAVLPAGAFARRPPLAKLAALNLSGSRLDEVRAGAFKHLPSLRQLDLSHNPLADLSPF
                                                                                                                                                                                                                                                           translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
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Submitted (15-SEP-2003) National Institutes of Health, Mammalian
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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'db_xref="MIM:190920"
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                                                       /gene="TPBG"
/codon_start=1
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BC058198.1 GI:34849573
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Best Local Similarity:
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KEYWORDS
SOURCE
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AUTHORS
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Paarlasgsaoppparcpaacesraattwickurniletvpadlepytvruletigog
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Krnbglldlassblodvlpglonytpgliyvlgiylaligaifilvylinrkgikkmhi
Nirdacrdhmegyhyryeinadprlinissblotva
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                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                               Sugahara,T., Mateuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene Patent: WO 03104277-A 123 18-DEC-2003; Asahi Kasei Kabushiki Kaisha (JP) Location/Qualifiers
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/note="unnamed protein product"
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Sequence 125 from Patent WO03104277.
AX961914
                                                                                                                                                                                                                           AX961912 2557 bp DN Sequence 123 from Patent WO03104277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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                                                                                                                                                            1536 GTTTTGTATTTGAACCGTAAAGGCATA 1562
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International consortium for macaque cDNA sequencing and analysis.

DNA sequences of macaque genes expressed in brain or testis and its
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WTVLPAGAFRAQPPLADLEALNILGSMILIKEVCAGAFEHLPGERRLDLEHRELTRISAF
WFAGSNASVSAPSPFLEKI LINHI VPPEDQRONGSFEGAVVAFEGAVAAALRSGILLRGI
TRLELASNHFILFLERLI LINHI VPPEDQRONGSFEGAVAFEGAVAAALRSGILLRGI
TRLELASNHFILFLERDLIAQLPSIRYLDLRNNSLVSLTYASFRNITHLESLHIEDNAL
KVLHNSTLASKGILATVYFLDNNPWVCDCYMADMYAMLKETEVVPDKARLTCAFPEK
MRNRGILDLASSDLOCHVLPGSLQTYSYVFLGILDLASSGILVYLNRKGIKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNOV"
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J. (Dasea I to 2714)

Hashimoto, K., Kusuda, J. and Sugano, S.

Direct Submission

Direct Gla-MR-2004) Katsuyuki Hashimoto, National Institute of

Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo capping; fis (full insert sequence).
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                     Sugahara, T., Matsuda, A., Honda, G., Muramatsu, S. and Ishizawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis testis cDNA clone: QtsA-11109, similar trophoblast glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3. AB168308.1 GI:67967899
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                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product"
                                                                                                                                                State activation gene
Patent: WO 03104277-A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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556. :1836
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COMMENT

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/db_xref="InterPro:IPR00
                                                                                                 nsAV12159 5551 bp DNA linear PRI 15-APR-2005
Homo sapiens 574 oncofetal trophoblast glycoprotein gene.
AJ012159
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SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRULTHLESLHLEDNALKYLHNG
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LELNSADLDCDPILDPPSLQTSYYPLGIYLALIGAIPLLGAIPLLYLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson Institute for Cancer Research, Christie Hospital, Wilmslow Road, Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                  King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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5331. .5336
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5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
HOmo sapiens (human)
HOmo sapiens
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Biochim. Biophys. Acta 1445 (3), 257-270 (1999)
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2716. .5400
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2716. .2800
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                                                                                                                               SCOS
                                                                                                                                                                                                                                                                                                                                                                                                 (B-mail:khashi@mih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
The International consortium for macaque cDNA sequencing and analysis consists of: Department of Virology and Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan, Division of Genetic Resources, National Institute of Infectious Diseases of Japan, Tokyo, Japan, National Institute of Infectious Diseases of Japan, Tokyo, Japan, National Health Research Institute, Taipei, Taiwan; Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan; Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA, Center for Information Biology, National Institute of Genetics of Japan, Mishima, Japan. Clone distribution: clone distribution information can be found at: http://www.nih.go.jp/yoken/genebank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Custom primers were used for 5' and 3'-end sequencing. The full-insert sequencing was done by primer-walking method using ABI DNA sequencer.
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glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3"
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ValLeuTyrLeuAsnArgLysGlyIle 9

US-10-774-176-14 (1-9) x AB168308 (1-2714)

Pred. No.:

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Submitted (13-MMY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Dec 15, 2000 this sequence version replaced gi:11558491.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm:, EMBL, Sw:, SWISSPROT, Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP3-492P14 is from the library RPCI-3 constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence from clone RP3-492P14 on chromosome 6q13-15 Contains a single stranded DNA binding protein pseudogene, the TPBG gene for trophoblast glycoprotein (5T4-AG) and a CpG island, A1121977
                                                                                                 MTVLPAGAFARQPPLADLEALMLSGRHIKEVCAGAFEHLPGIRRLDISHNPLTNLSAF
VFAGSNASVSAPSPLEELILNHIVPPEDQRQNGSFEGWVAFEGWVAALRSGIALRGL
TRIELASNHFLFLPRDLLAGLPSLKTLDLRNBSLVSLTYASTENLTHLSASHLEDDNAL
KVLHSTLAGROGLAHVKAFLDLNNPWVCDCYMADWYAMLKSTENUTHESHLEDNAL
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         /product="5T4 oncofetal trophoblast glycoprotein"
5713. 5718
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5759. 5764
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HTG; CpG island; TPBG.
Homo sapiens (human)
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Best Local Similarity:
Query Match:
DB:
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HSJ492P14
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Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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Mus musculus (house mouse)
Mus musculus
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Matches:
Conservative:
Mismatches:
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23.34
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AJ012160.1 GI:3805948
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Best Local Similarity:
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Q9P038 Q9Y4T7"
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LAVLPAGAPARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPP
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SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
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LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                    regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="trophoblast glycoprotein"
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AL544610 AA17072 AW662538 BE260089 BF306457 BF306926
BF314984 BI196133 BI562387 BM069633 BM670613
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                   Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
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complement(10004. .10982
                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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clone_lib="RPCI-3"
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                                                                                                                                                                                                                                                                                                                                                               map="q13-15"
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Center code: SC
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polyA\_site

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ROD 21-JUN-2005
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
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Submitted (13-UTM-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On May 4, 2005 this sequence version replaced gi:61656412.
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Center: Washington University Genome Sequencing Center
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Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
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                                                          /note="Clone_right_end: RP3-492P14"
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Matches:
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Mismatches:
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Contact: submissions@watson.wustl.edu
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121909
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Drafting center: WIBR
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                                                                                                                                                                                                                                                                                                          Indels:
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Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
Wilson, R. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 167046)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValLeuTyrLeuAsnArgLysGlylle 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-MAR-2005)
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Wilson, R.K.
Direct Submission
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This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
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If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous no comments or tags. If the criteria are I bases, then the region is duly annotated.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

## SOURCE INFORMATION:

The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/63 mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

This sequence is the entire insert of the clone. Location/Qualifiers

. .167046 source PEATURES

'organism="Mus musculus" /mol\_type="genomic DNA" /db\_xref="taxon:10090" /chromosome="9" clone="RP24-511A23"

note="Sequence derived from PCR product of genomic DNA" 31565. .31779
/note="Unresolved simple sequence repeat." clone\_lib="RPCI-24" .16712 misc\_feature ungure

46721. .46808 /note="Unresolved simple sequence repeat." .142347 142336. unsure ungure

'note="Sequence derived from one plasmid subclone."

ORIGIN

Conservative: Mismatches: Indels: Length: Matches: Gaps: 45.00 100.0% 100.0% 1.2e+03 Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: Pred. No.:

US-10-774-176-14 (1-9) x AC158516 (1-167046)

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AC128294/c RESULT 39

KEYWORDS LOCUS

DEFINITION ACCESSION VERSION ORGANISM REFERENCE AUTHORS

Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE.
AC128294
AC128294.3 GI:25083347
HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.
Rattus norvegicus (Norway rat)

Rattus norvegicus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroldea, Muridae, Murinae, Rattus.

1 (bases 1 to 210237)
Muzny, D.Marie., Metaker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyadi, A., Aydeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B., Carter, K., Carter, A., Chavez, D., Chang, C., Chan, Y., Chan, Y., Changas, V., Chavez, D., Chang, C., Chan, Y., Chan, Y., Chavez, D., Chang, C., Chang, C., Chan, Y., Chan, Y., Chavez, D., Chang, C., Chang, C., Chan, Y., Chan, Y., Chang, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Dalland, M., Darlan, R., Dangan, R., Garter, M., Ganta, R., Garter, R., Garter, R., Garter, R., Gabrer, R., Gabrer, R., Garter, R., Garter, R., Gabrer, R., Harandar, R., Handan, R., Handlin, C., Hamilton, C., Hamilton, C., Hamilton, R., Harandar, R., Handan, R., Mangan, R., Mangan,

(bases 1 to 210237) Worley, K.C. Direct Submission TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 210237)
Rat Genome Sequencing Consortium.
Direct Submission TITLE JOURNAL REFERENCE AUTHORS

COMMENT

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Nov 19. 2002 this sequence verseion replaced gi:2356504.

On Nov 19. 2002 this sequence verseion replaced gi:2356504.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgs.c.bcm.tmc.edu/projects/raf/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.

Center: Baylor College of Medicine

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On Nov 20, 2002 this sequence version replaced gi:22857070.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
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Rat Genome Sequencing Consortium.
Direct Submission
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2 (bases 1 to 239076)
Worley, K.C.
Direct Submission
ORGANISM
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AUTHORS
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TITLE
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**NOTE: This is a "working draft" sequence. It currently

**Consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 210237: contig of 210237 bp in length.
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Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
unordered pieces.
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AC106962.5 GI:25139469
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                           Web site: http://www.hgsc.bcm.tmc.edu/
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Conservative:
Mismatches:
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/note="clone_boundary
clone_end:Sp6
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/note="wgg end_extension
clone_end:T7"
2177. .144799
/note="clone_boundary
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208907. .210237
/note="wgs_end_extension
clone_end:Sp6"
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/db_xref="taxon:10116"
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Best Local Similarity:
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Sequencing of Mus musculus
Unpublished (2001)
3 (Dases I to 163959)
3 (Dases I to 163959)
Direct Submission
Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis MO 63108, USA
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-FBB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 163959)
McPherson,J.D., and Waterston,R.H.
                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
                                                                                                                                                   Sciurognathi, Muroidea; Muridea, Murinae; Mus.
1 (bases 1 to 163959)
Shah,N., Kozlowicz,A. and Meyer,R.
The sequence of Mus musculus BAC clone RP24-149D9
Unpublished (2001)
2 (bases 1 to 163959)
                                                                         Mus musculus (house mouse)
                                    AC131704.3 GI:30141995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 234710: contig of 234710 bp in length
71 224810: gap of unknown length
811 235924: contig of 1114 bp in length
925 236024: gap of unknown length
925 237314: contig of 1290 bp in length
9315 237414: gap of unknown length
9315 2397414: gap of unknown length
9315 2397414: gap of unknown length
9316 239076: contig of 1662 bp in length.
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Matches:
Conservative:
Mismatches:
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Center code: BCM
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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237315. .237414
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Direct Submission
Submitted (27-NOV-2003) Department of Genetics, Washington
Submitted (27-NOV-2003) Department of Genetics, Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
Submitted (26-APR-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 163959)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemister double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                     University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Apr 26, 2003 this sequence version replaced gi:28302028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: M_BB0149D09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                             ---- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
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NEIGHBORING SEQUENCE INFORMATION:

ROD 27-NOV-2003

AC131704 163959 bp DNA linear ROD 27-NOV-Mus musculus BAC clone RP24-149D9 from chromosome 12, complete

AC131704/c LOCUS DEFINITION

RESULT 41

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ValLeuTyrLeuAsnArgLysGlyIle 9

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US-10-774-176-14 (1-9) x AC106962 (1-239076)

Indels:

Best Local Similarity: Query Match:

Gaps:

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PAT 03-FEB-2004
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Matches:
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CQ736619
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This sequence is the entire insert of the clone. This clone is overlapped by AC122337.

Location/Qualifiers
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us-10-774-176-14.p2n.rge

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ACULW122 10066 bp DNA linear HTG 09-DEC-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
AC018122
                            PAT 10-OCT-2001
                                                                                                                                                                                                                  Isolated g-protein coupled receptors, nucleic acid molecules encoding gpcr proteins, and uses thereof as insecticidal targets patent: WO 0170980-A 64 27-SEP-2001; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10213448 by the submitter. This sequence mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases I to 10066)

Adams, M. and Venter, J. C.
Direct Submission
                                                                                                                        Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Mismatches:
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Drosophila melanogaster
                       4289 bp
Sequence 64 from Patent WO0170980.
AX254497.1 GI:16074220
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HTG; HTGS_PHASE2.
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Drosophila sp.
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RESULT 44
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ACCESSION
KEYWORDS
SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 02-FEB-2004
                                                                                                             Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                  Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 15076 27-SEP-2001;
PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila sp.

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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PB Corporation (NY) (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 4 clone RP11-124C9 map 4, LOW-PASS SEQUENCE SAMPLING.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 64168)

Birren, B., Linton, L., Nusbaum, C. and Lander, B.

Homo sapiens chromosome 4, clone RP11-124C9
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Web site: http://www-seq.wi.mit.edu
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Center clone name: 124_C_9
                                                                                                                          US-10-774-176-14 (1-9) x AC018122 (1-10066)
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2 (bases 1 to 64168)
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Homo sapiens (human)
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AC079003/c
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bp in length

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... or 100 bp in length se; contig of 695 bp in length se; gap of 100 bp se; contig of 706 bp in segue.
                                                                                                                                                                                                                                                                                                                               contig of 669 bp in length
gap of 100 bp
contig of 683 bp in length
contig of 680 bp in length
contig of 680 bp in length
gap of 100 bp
contig of 694 bp in length
gap of 100 bp
00 bp
f 704 bp in length
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g of 677 bp in length

f 100 bp in length

g of 652 bp in length

g of 697 bp in length

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g of 684 bp in length

f 100 bp

g of 686 bp in length

g of 686 bp in length

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1 of 701 bp in length
2 100 bp
3 of 667 bp in length
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gap of 100 bp
contig of 682 bp in length
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AF138924 111108 bp DNA linear PRI 02-OCT-2002
Homo sapiens chromosome 12 clone CTC-790L10 map 12p11.2, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 111108)
Taudien, S., Wen, G., Schilhabel, M., Menzel, U., Jahn, N., Baumgart, C. Dette, M. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-SRP-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 1 (bases 1 to 111108)
Lagemann, D. and Platzer, M.
Direct Submission
Submitted (02-OCT-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Oct 2, 2002 this sequence version replaced gi:14327767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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Sequencing vector: pUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 110433 bases at least Q40
Consensus quality: 110887 bases at least Q30
Consensus quality: 111058 bases at least Q30
Quality coverage: 9.56x.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 111108)
Taudien, S., Wen, G.P., Schilhabel, M., Menzel, U., Jahn, N.
Baungart, C., Dette, M. and Rosenthal, A.
Direct Submission
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Contact: gscj-submit@genome.imb-jena.de
------ Project Information
Center project name: H269
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Location/Qualifiers

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Length: Matches: Conservative: Mismatches: Indels:

2.07e+03 42.00 100.0% 88.9% 93.3%

> Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

Pred. No.:

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misc_feature	55034550457000 conserved.	ACCESSION AC022363	24 G1:11067115	
misc_feature	7.0000 prings cross age 5214 . 55401	S		
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Homon, J., Bandan, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Borde, S., Brieder, Brown, E., Brown, M., Brant, N.P.,

Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Burkett, C., Burrell, K.L., Byrd, N.C., Cleveland, C.D.,

Carter, M. Cavacos, S.R., Chacko, J., Chave, D., Chen, G., Chen, R.,

Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D.,

Cox, C., Coyle, M.D., Dathorne, S.R., David, N.R., Delgado, O.,

Denn, A.L., Ding, Y., Durbin, K.J., Earnhart, C., Edgar, D., Eddards, C.C.,

Elbaj, C., Emerling, S., Durbin, K.J., Earler, T. Ferraguto, D.,

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Jacobson, B., Martinez, E., Marche, S., Joudsh, S., Jouche, J., Lowis, C.,

Karlsoon, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Kracovic, J., Kursen, A., Ludier, S., Joudsh, S., Martinez, E., Martinez, M., 
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Submitted (02-FBB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Submitted (01-NOV-2000) Human Genome Sequencing Center, Departmen
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4 (bases 1 to 114933)
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AUTHORS
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                                                                                                                                  REFERENCE
                                                                                                                                                                     AUTHORS
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REFERENCE

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity (expect < 1e-34) to the BST and cDNA sequences Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
Worley, K.C.
Direct Submitssion
Submitted (21-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON NOV 1, 2000 this sequence version replaced gi:10645203.
GINFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggagtggtg (t) gtttgtagtc
atatacttag (a) catataaacg
aacagtttt (t) tgtggtgtt
caataattt (c) tattttaagt
aataatctta (a) ccacaaagat
gaggctgtgg (t) gaattaaata
gtcagtgtt (t) gcatttaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality fo a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cttagagtgg (t) gggataaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Distribution of Quality < 40
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aggagtggte (n) gtttgtagtc
atatacateag (n) catataaaca
aacagtttt (n) tgtggtgttc
caataaattt (n) tattttaagt
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gaggctgtgg (n) gaattaaata
gtcagtgtgt (n) gcatgttgac
aataatcaac (n) cactttaaaa
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450
400
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57888
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                       COMMENT
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Submitted (31-JUL-2004) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
On Jul 31, 2004 this sequence version replaced gi:13324738.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This sequence aubmission incorporates changes made during reevaluation of the assembly or fingerprint verification of the close. For further information about this sequence, including its close. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.org.
                                                                                                                                                                                                                            Direct Submission
Submitted (21-0CT-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
Classes 1 to 169385)
Celniker, S., Carlson, J., Wan, K., Pfeiffer, B., Frise, E., George, R., Hoskins, R., Stapleton, M., Pacleb, J., Park, S., Svirskas, R.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO22045 175837 bp DNA linear HTG 30-MAR-2000
Homo sapiens clone RP11-11G5, WORKING DRAFT SEQUENCE, 6 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 169385)

(calniker, S.B., Agbayani, A., Arcaina, T.T., Baxter, B., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Parfan, D.B., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, B., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, B., Shirk, R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BAC clone BACR14D22 (D1120)"
/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial BCORI in
DBACG3.6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
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Mismatches:
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Matches:
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AC022045.2 GI:7341884
HTG; HTGS PHASB1; HTGS_DRAFT.
HOWO SADIENS (human)
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42.00
100.0%
77.8%
93.3%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                 Rubin, G.M.
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SOURCE
ORGANISM
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                         REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .205
/note="Overlaps bases 73353. .73557 of clone AC022364"
/function="Overlaps with adjacent clone AC022364"
complement(2174. .3412)
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC012164 169385 bp DNA linear INV 31-
Drosophila melanogaster clone BACR14D22, complete sequence.
AC012164
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Phrap Value Range
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Mismatches:
Indels:
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Matches:
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7016...7067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AT_rich"
4696. .4718
/rpt_family="AT_rich"
5165. .5349
                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="RP11-1151B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="L1PA16"
566. .3605
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Location/Qualifiers
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'rpt_family="MIR"
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42.00
100.0%
88.9%
93.3%
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bases
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DB:
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ACCESSION
VERSION
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-JAN-2000) Whitehead Institute/MIT Center for Genome Submitted (25-JAN-2000) Whitehead Institute/MIT Center for Genome Steearch, 320 Charles Street, Cambridge, MA 02141, USA ON MAX 30, 2000 this sequence version replaced gi:6751775.
All repeats were identified using RepeatMasker:
All repeats were identified using RepeatMasker:
Streen, P. (1996-1997)
Arty://ftp.genome.washington.edu/RW/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Clohe name: 11 G.5
Sequencing vector: M113 M77815, 100% of reads
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 17439 bases at least Q40
Consensus quality: 17428 bases at least Q20
Consensus quality: 174815 bases at least Q20
Insert size: 175337; aum-of-contigs
Quality coverage: 5.9 in Q20 bases; sum-of-contigs
Quality coverage: 5.8 in Q20 bases; sum-of-contigs
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6025: gap of 100 bp

21447: contig of 15422 bp in length

21547; gap of 100 bp

50643: contig of 29096 bp in length

50743: gap of 100 bp

81519: contig of 30776 bp in length

81619: gap of 100 bp

127107: contig of 45488 bp in length

127207: gap of 100 bp

175837: contig of 48630 bp in length
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L3163
                     1 (bases 1 to 175837)
Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens, clone RP11-11G5
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1. .175837
             Hominidae; Homo.
                                                                                                            Inpublished
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organism="Homo sapiens" /mol\_type="genomic DNA

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nucleic search, using frame plus p2n model

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April 25, 2006, 10:26:14

US-10-774-176-13

Perfect score:

Sequence:

FLYLPRDVL 9

**BLOSUM62** 

Scoring table:

of hits satisfying chosen parameters: 4996997 segs, 3332346308 residues

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Total number

0.5

Xgapext Ygapext Fgapext Delext

Xgapop 10.0 , X Ygapop 10.0 , Y Pgapop 6.0 , F Delop 6.0 , D

summaries

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1000

Command line parameters:

ABX76333 AD880503 AD880503

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744 744 744

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Length

Query Match

Score

Result No.

genesequ20008:\* genesequ2001b8:\* genesequ2001b8:\* genesequ20028:\* genesequ2003a8:\* genesequ2003a8:\*

Geneseq 21:\* geneseqn1980s:\* geneseqn1990s:\*

Jatabase

geneseqn2003cs:

geneseqn2003ds: geneseqn2004as: geneseqn2004bs: geneseqn2005s:\*

Pred. No. is the number of res score greater than or equal to and is derived by analysis of

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Abv99349 Human Nov
Aaa27058 Human ST4
Aar89736 Nucleotid
Abr87174 cDNA enco
Ad56199 Human LRR
Ad56199 Human LRR
Ad56199 Human LRR
Ad56219 Human LRR
Ad56219 Human LRR
Ad13619 Human LRR
Ad036197 Human LRR
Ad03619 Human LRR
Ad03619 Human CDN
Ad16473 Human Full
Ad13631 Feline ST
Ad13631 Human Full
Ad126162 Human CDN
Ad27632 Human CDN
Ad2763 Mouse ST4
Ad126162 Human CDN
Ad41562 Plant cDN
Ad2763 Mouse ST4
Ad126169 Human CDN
Ad41562 Plant CDN
Ad41563 Human Nov
Ad41563 Human Nov
Ad469731 DNA enco
Ad6630 Human Dro
Adx06031 Cyclin-de
Adx06031 Cyclin-de
Adx06031 Cyclin-de
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Adx06031 Human Dro
Adx06031 Cyclin-de
Adx06031 Human Dro
Adx06031 Human CDN
Adx153063 Human CDN
Adx15313 DNA encod
Adx06031 Human CDN
Adx130527 Full leng
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-Q=/abss/ABSSWEB spool/US10774176/runat_24042006_165112_19185/app_query.fasta_1
-DB-N Geneseq -QFWT=fastap -SUFFX=p2n.rng -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -TRANS=human40.cdi -LIST=100
-UNTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USR=uS10774176 @CGN 1 1 3463 @runat_24042006_165112_19185 -VCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                              Search time 295.3 Seconds (without alignments) 203.123 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
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      ADX52485
ADX54092
ADX38778
ADX51945
ARA55815
AAF7320
AAF33388
                                                                          AAK78603
AAK78604
AAK78602
AAC77903
ABL06261
ADS6465
ADS6465
ADZ5461
                                                                                                               AAS26542
ABX73883
AAQ11412
ABS57556
ADX38776
                                 ADR85532
ABQ90320
                                               ADS03519
ABK52047
                                                     ADX27832
AAS26121
ABX73462
ADT44085
ADR84945
ADX29192
                                                                                                         ADQ86040
ADQ87091
                                                                                                                                    ACL67294
ABL19455
                                                                                                                                                     ADX38774
                                        ADR62836
                                                                                                                                 ADK16278
                                                                                                                                                         ADR62837
                                                                                                                                                  AAK90479
                                                                                                                                                            AAA37023
                                                                                                                                                                                    ABT07721 standard; DNA; 927 BP
                                                                                                                                                                                                                                              24-JAN-2002; 2002WO-US002242
                                                                                                                                                                                                                                                     24-JAN-2001; 2001US-0263965P
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1005
1014
1017
1020
1031
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1129
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1137
1140
WO200259377-A2.
                                                                                                                                                                                                                         Unidentified
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oldsymbol{n}
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9994
9995
9998
1009
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for descriping that are up or down-regulated in breast cancer calls. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07633 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

927

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

5.36 47.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

Ac167294 M. xanthu Ab119455 Drosophil Adc92799 E. faeciu Aba07320 Human pan

Adx38774 Human can Adr62837 Cotton cD Aaa37023 Human PRO Aak90479 Human

Query Match: DB:

Alignment Scores:

.. 8

Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast

(EOSB-) EOS BIOTECHNOLOGY INC

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Gish KC, Afar

Mack DH,

WPI; 2002-583738/62. N-PSDB; ABJ05564.

09-APR-2001; 2001US-00829472. 09-APR-2001; 2001US-0282698P. 04-MAY-2001; 2001US-0288590P. 29-MAY-2001; 2001US-0294443P.

2001US-0265928P

Claim 9; Page 372; 414pp; English

Adk45509 Streptoco Adx52485 Plant ful Adx52485 Plant ful Adx538778 Human can Adx138778 Human can Adx63120 Human can Adx63120 Human can Adx63120 Human can Adx62312 Plant ful Adx62316 Cotton cD Adx93519 Staphyloc Adx623047 cond acpeul Adx623047 cond acpeul Adx27462 Human nov Adx27462 Human can Adx78604 Human imm Adx661 cDNA enco Adx38010 Human tum Adx661 cDNA enco Adx601401 Bacterial Adx6161 CDNA enco Adx601401 Bacterial Adx73831 Human nov Adx1181 Rat cilia Adx38776 Human can Adx661 Human can Adx38776 Human can Adx38776 Human can Adx616278 Nanosrcha

cancer nucleic acids.

Lung cancer-associated polynucleotide, gene; ds; cytostatic; emphysema; antinfiammatory; antiasthmatic; non-small cell lung cancer; atelectasis; amall cell lung cancer; benign lession; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis. cancer-associated polynucleotide #197. PheLeuTyrLeuProArgAspValLeu 9 US-10-774-176-13 (1-9) x ABT07721 (1-927) ABX76333 standard; DNA; 927 BP 02-APR-2003 (first entry) 322 ABX76333; Lung RESULT 2 ABX76333 DX PX SX W W W W X BX PX X X X Y U Š

WO200286443-A2

31-OCT-2002

Unidentified

cocation/Qualifiers

Homo sapiens.

Key

1. .927 /\*tag=

WO2002102235-A2

27-DBC-2002

(EOSB-) BOS BIOTECHNOLOGY INC

Gish KC;

Mack DH,

WPI; 2003-167431/16.

P-PSDB; ADB80504.

12-APR-2002; 2002US-0372246P.

18-JUN-2001; 2001US-0299234P. 27-AUG-2001; 2001US-0315287P. 05-SEP-2001; 2001US-0317544P. 13-NOV-2001; 2001US-0350666P.

18-JUN-2002; 2002WO-US019297

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEXSEXEX
                                                                                                                                                                                                                                                                                                    transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a memmal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell ung cancer or other benign or precancerous leations, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, intersitial pulmonary disease, fibrosis, bronchiectasis. The genes, polymucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                  Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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                                                                                                                                                                                                                                                                                  Claim 22; Page 336; 453pp; English.
                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC
                                               10-MAY-2001; 2001US-0290492P.
109-NOV-2001; 2001US-0339245P.
113-NOV-2001; 2001US-033666F9.
29-NOV-2001; 2001US-034370P.
12-APR-2002; 2002US-0372246P.
             18-APR-2002; 2002WO-US012476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB80503 standard; DNA; 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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47.00
100.0%
100.0%
                                                                                                                                                                             WPI; 2003-093161/08.
P-PSDB; ABU56604.
                                                                                                                                                     Aziz N, Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB80503;
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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                          selectively
                                                                                                                                                                                     The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymucleotide that selectivel hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for the detection method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 TTCCTTTACCTGCCGCGGATGTGCTG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PheLeuTyrLeuProArgAspValLeu
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                                                                                                                                Claim 10; Page 297; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN38723 standard; cDNA; 927 BP
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47.00
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Best Local Similarity
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Local Similarity:

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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind and methods of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and nucleic acids. The nucleic acids, polypeptides and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune disease, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
inflammatory disease, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
                                                       retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 41; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ginsburg WM,
8, Watson SR,
                                                                                                                                                                                                                                                                                                              13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DRC-2001; 2001US-0335394P.
14-DRC-2001; 2001US-0343394P.
10-JAN-2002; 2002US-0347349P.
08-FRB-2002; 2002US-0355250P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-036809P.
04-APR-2002; 2002US-0370110P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2002; 2002US-0386614P.
                                                                                                                                                                                                                                                                             13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2002; 2002US-0372246P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-0397775P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2002; 2002US-0409450P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Afar D, Aziz N, Gir
Mack DH, Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-468649/44.
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                                                                                                                                                                                                  WO2003042661-A2.
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-2002;
                                                                                                                                                                                                                                      22-MAY-2003
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BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

Sequence 927

927

Length: Matches: Conservative:

5.36 47.00 100.0%

Percent Similarity:

Alignment Scores: Pred. No.:

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nuclead acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                            Human; p53 pathway; Leucine rich repeat capricious related protein; LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Mismatches:
Indels:
Gaps:
                                                                                                                  322 TICCITIACCIGCCGCGGAIGIGCTG 348
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                                                                                            1 PheLeuTyrLeuProArgAspValleu 9
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                                                             x ADN38723 (1-927)
                                                                                                                                                                                        AADS6198 standard; DNA; 973 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                  Human LRRCAPS related DNA #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belvin M, Schleithoff L, P.
Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.67
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Query Match:
                                                               US-10-774-176-13 (1-9)
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                                                                                                                                                                                                                      AAD56198;
                   Query Match:
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Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS;
                                                                                                                                                                    antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; notropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
337 TICCITIACCIGCCGCGGGAIGIGCIG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001; 2001US-0278999P.
27-MAR-2001; 2001US-0279036P.
28-MAR-2001; 2001US-0279344P.
30-MAR-2001; 2001US-0279995P.
02-APR-2001; 2001US-028023P.
02-APR-2001; 2001US-0280802P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0274849P.
2001US-0275235P.
2001US-0275578P.
2001US-0275579P.
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02-MAY-2001; 2001US-0288066P.
03-WAY-2001; 2001US-0288342P.
03-WAY-2001; 2001US-0288342P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0275601P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-0277791P.
22-MAR-2001; 2001US-0277833P.
23-MAR-2001; 2001US-0278152P.
26-MAR-2001; 2001US-0278894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-2001; 2001US-0280900P.
04-APR-2001; 2001US-0281194P.
13-APR-2001; 2001US-0283675P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0283675P.
2001US-0287424P.
                                                   ABV99349 standard; DNA; 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0277338P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0299303P
                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2002; 2002WO-US007288
                                                                                                                                Human NOV8a coding sequence
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                 WO200272771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-2001; 2
12-MAR-2001; 2
13-MAR-2001; 2
13-MAR-2001; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001; 2
14-MAR-2001; 2
16-MAR-2001; 2
19-MAR-2001; 2
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20-MAR-2001;
20-MAR-2001;
20-MAR-2001;
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18-JUN-2001;
19-JUN-2001;
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16-MAY-2001;
                                                                                                      27-JAN-2003
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          19-SEP-2002
                                                                              ABV99349;
                                        ABV99349
                          RESULT
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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli RA, Vernet CAM; Pena CRA, Burgess CB, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CB; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PP;
                     2001US - 0312903P.
2001US - 0318462P.
2001US - 0318470P.
2001US - 0325681P.
2001US - 033580P.
2001US - 0335301P.
2001US - 03323172P.
                                                                                             2001US-0332272P.
2001US-0333184P.
2001US-0333272P.
2001US-0332094P.
                                                                                                                            2001US-0337426P.
2001US-0338092P.
                                                                                                                                            2001US-0337185P
2002US-0345705P
                                                                                                                                                             2002US-00093463
                                                                                                                                                                             (CURA-) CURAGEN CORP.
             16-AUG-2001;
10-SBP-2001;
12-SBP-2001;
27-SBP-2001;
27-SBP-2001;
18-OCT-2001;
31-OCT-2001;
                                                                                             14-NOV-2001;
14-NOV-2001;
                                                                                                             14-NOV-2001;
21-NOV-2001;
                                                                                                                                                             08-MAR-2002;
                                                                              14-NOV-2001;
                                                                                      14-NOV-2001;
                                                                                                                              03-DEC-2001;
                                                                                                                                             04-DEC-2001;
                                                                                                                                                                                                                                     Zhong M;
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New NOVX polypeptides and polymucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.

WPI; 2002-732824/79.

P-PSDB; ABP70071.

Claim 16; Page 114-115; 619pp; English.

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of andicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disquences and proteins are useful for treating, concert, infectious diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases ancerial associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, parkinson's disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with obesity, metabolic syndrome X or wasting disorders associated with obesity, metabolic syndrome X or wasting disorders associated with obesity, metabolic syndrome X or wasting cidentification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, call proliferation, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods

Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

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     Length:
Matches:
Conservative:
Mismatches:
                                            Gaps:
     6.93
47.00
100.0%
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                           Best Local Similarity:
Query Match:
                     Percent Similarity:
Alignment Scores:
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x ABV99349 (1-1156) US-10-774-176-13 (1-9) (first entry)

Location/Qualifiers 1. 1263 /\*tag= a

/product= "5T4"

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Single chain antibody, ScFv; inflammatory disease, arthritis, cancer; hypersensitivity, autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiovalmonary disease; cardiovascular disease; gastrointeetinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                       Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
                                                  Nucleotide sequence of canine 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                              18-NOV-1999; 99WO-GB003859.
15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                                                                                                                                                                                                                                       13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-343805/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB83839.
                                                                                                                                                                                                                                        WO200136486-A2
                         23-JUL-2001
                                                                                                                                                                                                                                                                25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Myers KA;
AAF89736;
                                                                                                                                                Canis sp
                                                                                                                                                                          Key
 The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were incoulated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                         Human, TAA; tumour-associated antigen; anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
            Human 5T4 tumour-associated antigen gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PheleuTyrLeuProArgAspValleu 9
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 PheLeuTyrLeuProArgAspValLeu
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                                                                          照.
                                                                                                                                                                                                                                                                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                       99GB-00001739.
                                                                                                                                                                                                                                                                                                                           98GB-00025303.
                                                                         AAA27058 standard, DNA; 1263
                                                                                                                                                                                                                                                                                                    99WO-GB003859
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100.0%
100.0%
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Carroll MW, Myers KA;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-387735/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
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Best Local Similarity
Query Match:
DB:
                                                                                                                                                                                                                                                  WO200029428-A2
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                       27-JAN-1999;
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                                                                                                                                                                                                                                                                                                                           18-NOV-1998;
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Pred. No.:
                                                                                                                         22-AUG-2000
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                        553
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                                                                                                 AAA27058;
                                                              AAA27058
                                                  RESULT
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The specification describes the use of a single chain antibody (SCFV), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The SCFV antibody is useful in the manufacture of a disease medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The SCFV antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune disease, cancers, central nervous system disorders including Parkinson's disease, gastrointestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce SCFV of the invention
Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PheLeuTyrLeuProArgAspValLeu
                                                                                                                   Disclosure; Fig 26; 118pp; English.
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AAF89736 standard; DNA; 1263 BP

RESULT 8
AAF89736
ID AAF8

1 PheLeuTyrLeuProArgAspValLeu 9

Bb

AAD56199 standard; DNA; 1331

RESULT 10

AAD56199

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call prollferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                       encoding canine oncofoetal leucine-rich glycoprotein, 5T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product= "5T4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                             ABK87174 standard; cDNA; 1263 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 67; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                                                 (first entry)
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P-PSDB; AAU98693.
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                                                                                                                                                                                                                                                     07-0CT-2002
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                                                                                                                                                                   ABK87174;
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RESULT 9
                                  ABK8717
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Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.

Disclosure; Page 75-76; 99pp; English.

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Funke RP, Lioubin MN,

Plowman GD,

Belvin M, Schleithoff L, Pi Prancis-Lang H, Friedman L;

WPI; 2003-421410/39

(EXEL-) EXELIXIS INC.

22-OCT-2001; 2001US-0338733P. 15-PEB-2002; 2002US-0357600P. 01-MAR-2002; 2002US-0361196P.

21-OCT-2002; 2002WO-US033540

WO2003035831-A2

01-MAY-2003.

Homo sapiens.

p53 pathway; Leucine rich repeat capricious related protein;

LRRCAPS; cancer; gene therapy; ds.

Human;

Human LRRCAPS related DNA #6

(first entry)

07-AUG-2003

AAD56199;

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ56299 standard; cDNA; 2020 BP
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ID ADJ5
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Length: Matches: Conservative: Mismatches: Indels:

7.67 47.00 100.0% 100.0%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

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x ABK87174 (1-1263)

US-10-774-176-13 (1-9)

88

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Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
                                                                                              Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                   Human bladder cancer associated cDNA sequence SEQ ID NO:192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 296; 307pp; English
                                                                                                                                                                                                                                                                                                                         (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                   03-AUG-2001; 2001US-0310099P.
                                                                                                                                                                                                                                                                               13-NOV-2001; 2001US-0350666P.
                                                                                                                                                                                                            03-JUL-2002; 2002WO-US021338
                                        12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABR48236
                                                                                                                                                    WO2003003906-A2
                                                                                                                                                                                                                                       03-JUL-2001;
                                                                                                                          Homo sapiens
                                                                                                                                                                                16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                      Mack DH,
This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a proton oncogene that is amplified in neuroblastoms cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids for complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                        New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                       Human cDNA differentially expressed in MYCN activated cells SeqID 105
                                                                                human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; 88; MYCN activated cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.
                                                                                                                                                                                                                                                                                                                                                      Shohet JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 105; 27pp; English
                                                                                                                                                                                                                                                                                                                                                     Plon SE,
                                                                                                                                                                                                                          25-FBB-2002; 2002US-00084817
                                                                                                                                                                                                                                                      23-PEB-2001; 2001US-0270784P
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                      Stuart SG, Nuchtern JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US Patent Office at
                                                                                                                                                                                                                                                                               STUART S G.
NUCHTERN J G.
PLON S E.
SHOHET J M.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-635698/60
                                                                                                                                                                   US2003119009-A1
                                                                                                                                          Homo sapiens.
                           06-MAY-2004
                                                                                                                                                                                               26-JUN-2003.
ADJ56299;
                                                                                                                                                                                                                                                                                             (NUCH/)
(PLON/)
(SHOH/)
                                                                                                                                                                                                                                                                                  STUA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer.
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2003-201532/19.

Aziz N;

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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polymuclecide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC5095). ACC50951 to ACC51059 concode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated proteins given in haraquist cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic matchods, and for gene therapy, vaccine and/or antisense/inhibition applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Length: Matches: Conservative: Mismatches: Indels: Gaps:

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Percent Similarity: Best Local Similarity:

Best Local S Query Match:

Alignment Scores:

1 PheLeuTyrLeuProArgAspValLeu 9

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RESULT 12 ACC51052 ID ACC5

ACC51052 standard; cDNA; 2053 BP

JS-10-774-176-13 (1-9) x ADJ56299 (1-2020)

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Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lession; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                         Lung cancer-associated polynucleotide #196.
                                                                                                                                                                    2001US-0290492P.
2001US-0339245P.
2001US-0350666P.
2001US-0334370P.
                                                                                                                                                                                                                       (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                            18-APR-2002; 2002WO-US012476
                                                                                                                                                                                                      2002US-0372246P
        (first entry)
                                                                                                                                                                                                                                                       WPI; 2003-093161/08.
P-PSDB; ABU56603.
                                                                                                                                                                                                                                        Murray R;
                                                                                                           WO200286443-A2.
                                                                                                                                                                    10-MAY-2001;
09-NOV-2001;
13-NOV-2001;
29-NOV-2001;
                                                                                                                                                                                                       12-APR-2002;
                                                                                                                                                             18-APR-2001;
                                                                                         Inidentified
        02-APR-2003
                                                                                                                            31-OCT-2002
                                                                                                                                                                                                                                       Aziz N,
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Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polymucleotide that exhibits increased or decreased expression in lung cancer.

Claim 22; Page 335; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a blological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits con a sequence that is at least 80 % identical to a gene that exhibits compound that modulates a lung cancer associated for identifying a compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell ung cancer or other benign or precancerous lesions, e.g. atleetessis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, complyaema, bronchitis, intersitial pulmonary disease, fibrosis, bronchiectasis The genes, polymucleotides and polypeptides are useful confounds that modulate lung cancer, such as antibodies. Sequences invention

Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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                             Similarity:
                    Percent Similarity:
Alignment Scores:
                                    Query Match:
DB:
                             Best Local
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US-10-774-176-13 (1-9) x ABX76332 (1-2053)

PheLeuTyrLeuProArgAspValLeu 9

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comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                             Human; p53 pathway; Leucine rich repeat capricious related protein; LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                     Ξ
                                                                                                                                                                                                                                                                                                                                                   Identifying a candidate p53 pathway-modulating agent for treating
                                                                                                                                                                                                                                                                                                    Plowman GD, Funke RP, Lioubin MN,
           774
748 TICCTTTACCTGCCGCGGGATGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Page 73-74; 99pp; English.
                                                                                                                                                                                                                                         22-OCT-2001; 2001US-0338733P.
15-PRB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                  AAD56197 standard; DNA; 2053
                                                                                                                                                                                                                       21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                    Belvin M, Schleithoff L, P)
Francis-Lang H, Friedman L;
                                                                                         (first entry)
                                                                                                           Human LRRCAPS DNA #11
                                                                                                                                                                                                                                                                                 (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                 WPI; 2003-421410/39.
                                                                                                                                                                               WO2003035831-A2.
                                                                                       07-AUG-2003
                                                                                                                                                            Homo sapiens
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                                                                     AAD56197;
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucileacid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA

Seguence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

Alignment Scores:

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Length:
Matches:
Conservative:
Mismatches:
                                             Indels:
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                                                        Gaps:
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                                                                              US-10-774-176-13 (1-9) x AADS6197 (1-2053)
                                                                                                                                                                   AAD56200 standard; DNA; 2053 BP
13.5
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                      Percent Similarity:
Best Local Similarity:
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AAD56200

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, differential expression, cancer, angiogenic disorder;
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis;
inflammatory disease, autoimmune disease;
                                                                                                                                                                                                                                                                                                                                              ä
                                                                           pathway; Leucine rich repeat capricious related protein;
                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a candidate p53 pathway-modulating agent for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                              Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 76-77; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-774-176-13 (1-9) x AAD56200 (1-2053)
                                                                                           LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN38721 standard; cDNA; 2053 BP
                                                                                                                                                                                                                    21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                 22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                              Belvin M, Schleithoff L, P. Francis-Lang H, Priedman L;
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47.00
100.0$
100.0$
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                07-AUG-2003 (first entry)
                                             Human LRRCAPS DNA #12.
                                                                                                                                                                                                                                                                                                               (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-421410/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                        WO2003035831-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053
                                                                                                                          Homo sapiens
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                                                                                                                                                                                     01-MAY-2003
                                                                             Human; p53
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological call in a
conference of a pathological call in a
conference or absence of a pathological call in a
conference or absence of a pathological call in a
conference or by detecting a nocleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
conclet acid of the invention; antibodies which specifically bind a
conclet acid of the invention; use of such antibodies for drug targeting;
conclet and methods are useful for disgnosing, prognosing and treating
concer and other conditions such as psoriasis, ischaemia, heart disease,
concer and other conditions such as psoriasis, ischaemia, heart disease,
concer and other conditions such as psoriasis, ischaemia, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
concer sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; dewond healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gish KC, Glynne R, Hevezi PA;
Wilson KB, Zlotník A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aziz N, Ginsburg WM,
Murray R, Watson SR,
                                                                                                                                                                                                              2001US-0350666P.
2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
2002US-034771P.
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2002US-0355250P.
2002US-0356714P.
2002US-0359077P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-0397775P.
                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-0372246P.
2002US-0386614P.
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P-PSDB; ADN38722.
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Query Match:
DB:
                                                                                                                   WO2003042661-A2
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                                                                                                                                                                                                                                                                 03-DEC-2001;
                                                                                    Homo sapiens
                                                                                                                                                                                                                  13-NOV-2001;
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RESULT 1 ADL06473

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ADL06473;

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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating peoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S, Clark H, Jackman J, Schoenfeld J, Williams PM,
                                                                                                                                                                                                                   ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
TICCTITACCIGCGGGGAIGIGCIG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rrccrrraccrecececedargrere 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 355; 3069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer prognosis marker #1305.
                                                                        86
                                                                                                                                                                                   Antipsoriatic cDNA sequence #180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                        ADN03961 standard; cDNA; 2053
                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2003; 2003WO-US030907.
                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2002; 2002US-0414006P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR25444 standard; DNA; 2053
                                                                                                                                              01-JUL-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-305105/28.
P-PSDB; ADN03962.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                            WO2004028479-A2
                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                 08-APR-2004.
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748
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                                                                                                            ADN03961;
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                                                        ADN0396:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for represents or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillan KJ, Polakis P, Polson A, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                              Human; tumour-associated antigenic target; TAT; cell death; tumour;
                                                                                                                                                                                                                                                                           Human tumour-associated antigenic target (TAT) cDNA sequence #53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
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Gaps:
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                    US-10-774-176-13 (1-9) x ADN38721 (1-2053)
                                                        PheleuTyrLeuProArgAspValLeu
                                                                                                                                                                  ADL06473 standard; cDNA; 2053 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-2002; 2002US-0405645P.
23-SEP-2002; 2002US-0413192P.
15-OCT-2002; 2002US-0419008P.
15-NOV-2002; 2002US-0426847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-2002; 2002US-0404809P
                                                                                                                                                                                                                                                                                                                                     cancer; cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-2003; 2003WO-US025892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2003; 2003US-0484959P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desauvage FJ, Frantz G,
Spencer SD, Wu TD, Zhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-257144/24.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                        WO2004016225-A2
                                                                                                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Pred. No.:
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26-FEB-2004.

ds; breast cancer; prognosis; gene expression; diagnosis.

Ношо варіепв

PheLeuTyrLeuProArgAspValLeu

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Query Match: DB:

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Length:
Matches:
Conservative:
Mismatches:
Indels:

**Gaps**:

Wood WI;

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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the disgnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1305; 226pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   marker used in the method of the invention
                                                                                                                                                                                    (ROSE-) ROSETTA INPHARMATICS LLC.
                                                                                                                                                                                                       (NECA-) NETHERLANDS CANCER INST
                                                                                                                                             15-JAN-2003; 2003US-00342887.
                                                                                                     LS-JAN-2004; 2004WO-US001100.
                                                                                                                                                                                                                                                Van't Veer LJ, He Y;
                                                                                                                                                                                                                                                                                         WPI; 2004-593473/57.
                     WO2004065545-A2
                                                            05-AUG-2004.
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2053 9 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 13.5 47.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Score:

US-10-774-176-13 (1-9) x ADR25444 (1-2053)

Gaps:

Trectitacetecececedates σ PheLeuTyrLeuProArgAspValLeu 748 셤 ò

ACN38510 standard; cDNA; 2053 BP ACN38510;

RESULT 20

(first entry) 18-NOV-2004

Fumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.

Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukeemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss. 

Homo sapiens

WO2004030615-A2

15-APR-2004.

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nucleic acids,
                                                                                                                                                                                                                                                                                                                                                         New tumor-associated antigenic target polypeptides and nucleic aci
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2070; 7273pp; English.
29-SEP-2003; 2003WO-US028547.
                                                                   02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                             Wu TD, Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate cancer or tumor.
                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                 WPI; 2004-347921/32.
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide and capture and both relations and methods and compositions are norganic coid; an autibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; the treatment or TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT appression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, ovarian and selves and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acids may further be represents and penter invention 

Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

Alignment Scores:

2053 9 9 0 0 0 0 0 Matches: Conservative: Mismatches: Indels: Length: Gaps: 1 PheleuTyrLeuProArgAspValLeu 9 US-10-774-176-13 (1-9) x ACN38510 (1-2053) 13.5 47.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: 8

748 riccirraccióccococaroroció 774

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ADV35098 standard; cDNA; 2053 BP. RESULT 21 ADV35098

10-FEB-2005 (first entry)

ADV35098;

Human cDNA of an exemplary efficacy gene for BAD SeqID174.

human; 88; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant. 2XXX2XXXXXXXXXXXXXXXXXXXX

Homo sapiens.

US2003096264-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals convention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as well as Parkinson's and Alzheimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, notropic, antimanic and autidepressant. Furthermore, the screening etchod used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is different and every and second of the presence of a therapeutic compound and second of the compound and second of the compound and second of the compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell
                                                                                                                                                                                                                                                                                    Laeng P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    Hook D, Klimczak LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; SEQ ID NO 174; 39pp; English
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                                                                                                                                                                                                                                                                                    Evans D,
                                                                                                                                                                                                                                                                                                                                                                                                                                               contacted with the test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS87175 standard; cDNA; 2338 BP.
                                                                                                                                                                                                                                            (PSYC-) PSYCHIATRIC GENOMICS INC
                                                                                                                    07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-0325150P.
14-NOV-2001; 2001US-033347P.
18-JAN-2002; 2002US-034936P.
04-MAR-2002; 2002US-0361834P.
                                                                                                   2001US-0299151P
                                                            18-JUN-2002; 2002US-00175523
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                                                                                                                                                                                                                                                                                 Altar CA, Brockman JA,
Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                            WPI; 2004-118903/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity
                                                                                                 18-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                    22-MAY-2003
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Human; chromosome mapping; gene mapping; gene therapy; forensic;

DNA encoding novel human diagnostic protein #22979.

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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal genes. (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging olypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197.AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 22979; 103pp; English.
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                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                            31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                          Tang YT;
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                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73
                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABG22988
                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity.
                                         Homo sapiens.
                                                                                                                   11-0CT-2001.
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DB:
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The invention relates to primers for synthesising full length cDNA clones 30 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3' ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                           830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                  Ξ
                                                                                                                                                                                                                                                                                                                              Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English
                                   Human; full length cDNA; cDNA synthesis; oligo-capping; ss
Human full-length cDNA, SEQ ID NO: 2864.
                                                                                                                                                                                                                                     11-JAN-2000; 2000JP-00118774.
                                                                                                                                                                                                                     99JP-00194486.
                                                                                                                                                                                 07-JUL-2000; 2000EP-00114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic manipulation.
                                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB, AAM93333
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                                                                                                          BP1130094-A2
                                                                         Homo sapiens
                                                                                                                                              05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from BPO
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Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other; Alignment Scores:

Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;

2359 0 0 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

15.8 47.00 100.0% 100.0%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores:

Gaps:

1113

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AAK94254 standard; cDNA; 2361

PheLeuTyrLeuProArgAspValLeu 9

TTCCTTTACCTGCCGCGGATGTGCTG

1087

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RESULT 25 AAK94254

US-10-774-176-13 (1-9) x ADL30831 (1-2359)

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human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
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Length:
Matches:
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Mismatches:
Indels:
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                                                                                                                                                                                                   Full length human cDNA clone SeqID 2864.
                                                                                     PheLeuTyrLeuProArgAspValLeu 9
                                                                  US-10-774-176-13 (1-9) x AAK94253 (1-2359)
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15.8
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                  Percent Similarity:
Best Local Similarity:
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                                                                                                      1087
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                                                                                                                                                                ADL30831;
                                       Query Match
DB:
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Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

Homo sapiens EP1130094-A2

08-JUL-1999; 99JP-00194486. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765.

Homo sapiens

07-JUL-2000; 2000EP-00114089

05-SEP-2001

Human full-length cDNA, SEQ ID NO: 2866.

06-NOV-2001 (first entry)

AAK94254;

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA from both the 5' and 3' entl length human cDNA from both the 5' and 3' full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                             oligonucleotide primers (830 cDNAs) useful for synthesizing full
                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                     Kawai Y;
T, Koga I
                                                                                                                                                                                                                       Hayashi K, Ishii S,
K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 2864; 1340pp; English.
                                                                                                                                                                                                                                         Nagai
                                                                                                                                                                                                                       Isogai T,
                                                                                                                                                                                       (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                07-JUL-2000; 2003EP-00025638
                                                                                                   99JP-00194486
                                                                                                                                                                                                                                       Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                         Nishikawa T,
                                                                                                                                                                                                                                                                           WPI; 2004-204755/20.
                                                                                                                                                                                                                                                                                                                                             length human cDNAs
                                                                                                                                                                                                                                                                                             P-PSDB; ADL30832
EP1396543-A2
                                                                                                   08-JUL-1999;
                                 10-MAR-2004.
                                                                                                                                                                                                                         Ota I,
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New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. diabetes and cancer.

Claim 4; SEQ ID NO 127; 1368pp; English.

Muramatsu S, Ishizawa K;

Honda G,

Sugahara T, Matsuda A, (ASAH ) ASAHI KASEI KK

WPI; 2004-122214/12. P-PSDB; ADI26163.

16-MAY-2003; 2003US-0470836P.

```
The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA male useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length CDNA asily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                             830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE; immunogen; STATE activation; allergy; inflammation; state; immunogen; STATE activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                             Kawai Y;
T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding protein that promotes STAT6 activation #64.
                                                                                                                                                                                             Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                                             Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S,
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki
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                                                                                                                                                                in genetic manipulation.
               (HELI-) HELIX RES INST
                                                                                              WPI; 2001-524255/58.
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                                                                                                               P-PSDB; AAM93334
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Pred. No.:
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or carefully to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant or promote STAT6 activation. A transformant composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, chyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of the hyperactive diseases. Compositions are also useful in rheumatoid attricts, systemic lupus erythematosus, sepsis asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive detired to or inhibition of STAT6. The present sequence represents a processive details and preventing descention of stative definition of stative details and details when the present sequence or details and details when the details and details details descenting details and details details details details details details details 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Full length human cDNA clone SeqID 2866.
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #X#X#X#X#######X#X#X######
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2002US-0385912P. 2002UP-00377326. 2002US-0436467P. 2003JP-00137505

06-JUN-2002; 26-DEC-2002; 27-DEC-2002; 15-MAY-2003;

2002JP-00164257

05-JUN-2002;

05-JUN-2003; 2003WO-JP007123

WO2003104277-A2

18-DEC-2003

Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.

Claim 4; Page 68; 68pp; English.

(OXFO-) OXFORD BIOMEDICA UK LTD.

13-NOV-2000; 2000WO-GB004317.

13-NOV-2001; 2001WO-GB005004.

Carroll M;

WPI; 2002-557449/59. Myers K, Drury N,

P-PSDB; AAU98694

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cells.

Cr proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in disquestic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, this use useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The colls may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).

The present sequence encodes feline 574 protein
This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide primers (830 cDNAs) useful for synthesizing full
                                                                                                                                                                                                                                                                                                         Ë
                                                                                                                                                                                                                                                                            Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feline, cat, oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                        (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                     11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000BP-00114089.
                            07-JUL-2000; 2003EP-00025638
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47.00
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                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-204755/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length human cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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Pred. No.:
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DB:
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Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Feline 5T4 antigen protein"
                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                  Indels:
                                                                                                                                                                 661 riccrcrrcrisccrcssacaracis 687
                                                                                             Gaps:
                                                                                                                                           1 PheLeuTyrLeuProArgAspValLeu 9
                                                                                                                    US-10-774-176-13 (1-9) x ABK87175 (1-1260)
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1. .1260
/*tag= a
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                                  52.6
43.00
100.0%
88.9%
91.5%
                                                                                                                                                                                                                                                                                    Feline 5T4 antigen DNA.
                                                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                       ADB97513;
                                                                               Query Match:
DB:
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/product= "5T4 protein"

WO200238612-A2

16-MAY-2002

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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope of the 5T4 antigen. The invention further browning the statement of the 5T4 epitope; a uncleic acid sequence encoding the 5T4 epitope or a polyepitope string of the 5T4 epitope or a caid to a cell; a cell pulsed with the 5T4 epitope, a polyepitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid, a method comprising detecting the presence of the 5T4 epitope or its encoding nucleic acid in a subject, and a T cell line or clone capable of mucleic acid in a subject, and a T cell line or clone capable of specifically recognising the 5T4 epitope has cytostatic activity. The vaccine comprising the 5T4 epitope has cytostatic activity. The vaccine comprising the 5T4 epitope or its encoding nucleic acid and the vector system or cell is useful in the prevention and/or treament of a disease, partenent of a lagrace coff the 5T4 epitope or its nucleic acid and the vector system or cell is useful for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or preventing a disease. This polynucleotide sequence represents the feline or clone of the factor of a medicament for treating and/or preventing a disease. This polynucleotide sequence represents the feline or state of the invention.
                                                                                                                                                                                                                                                                                                                                                                   major histocompatibility complex class I peptide epitopes from human tumor-associated antigen, useful for preventing and/or treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                         Redchenko I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 67; 73pp; English.
                                                                                                                                                                                   OXFORD BIOMEDICA UK LTD
                                                                                                                               13-FEB-2002; 2002GB-00003419.
                                                                           13-FEB-2003; 2003WO-GB000670.
                                                                                                                                                                                                                                                                                                                                                                                                                            disease, particularly cancer.
                                                                                                                                                                                                                                      Carroll M, Kingsman S,
                                                                                                                                                                                                                                                                                       WPI; 2003-637141/60.
                                                                                                                                                                                                                                                                                                                  P-PSDB; ADB97520
                             21-AUG-2003.
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84000 Length: Matches: Conservative: Mismatches: Indels: TTCCTCTTCTTGCCTCGGGACGTACTG 687 PheleuTyrLeuProArgAspValLeu 9 US-10-774-176-13 (1-9) x ADB97513 (1-1260) 52.6 43.00 100.0% 88.9% 91.5% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 661 Query Match DB:

84000

Conservative: Mismatches: Indels:

52.6 43.00 100.0% 88.9% 91.5%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Gaps:

Matches: Length:

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Enterohaemorragic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 132.
                                                                                                                                                                                                                                  ds; gene; enterohaemorragic; anti-bacterial
                                           1 PheLeuTyrLeuProArgAspValLeu 9
US-10-774-176-13 (1-9) x ADB97452 (1-1260)
                                                                                                               ADC00087 standard; DNA; 86248 BP
                                                                                                                                                                          04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                Escherichia coli; 0157:H7
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ID ADC0
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                                                                                                                                gene; ds; feline; Major Histocompatibility Complex class II; MHC;
epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                               DNA encoding feline 5T4 protein.
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04-DEC-2003

ADB97452;

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Unidentified

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II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosling or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polymucleotide sequence represents the DNA
                                                                                                                                                                                                                                                                                                                                                                         New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a Major Histocompatibility Complex (MHC) class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                 /*tag= a
/product= "Feline 5T4 antigen protein"
          Location/Qualifiers
1. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 49; 63pp; English.
                                                                                                                                                                                                                                                                                    Kingsman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding for the feline 5T4 protein.
                                                                                                                                                                                                                                                 (OXFO-) OXFORD BIOMEDICA UK LID.
                                                                                                                                                                            13-FEB-2003; 2003WO-GB000618
                                                                                                                                                                                                               13-FEB-2002; 2002GB-00003420.
                                                                                                                                                                                                                                                                                    Harrop R,
                                                                                                                                                                                                                                                                                                                     WPI; 2003-663795/62.
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Percent Similarity:
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detecting which can b
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                                                                                                           The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific nucleic acid of the
                                                                   Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                                                                                                 Sequence 86248 BP; 22338 A; 20003 C; 21303 G; 22604 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA sequences from Escherichia coli strain O157:H7, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                     ds; acute haemorrhagic colitis; haemolytic uraemic syndrome;
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                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                     B. coli 0157 unique DNA sequence OZID_57.
                                                                                           Claim 2; SEQ ID NO 132; 2067pp; Japanese.
                                                                                                                                                                                                                                                      Gaps:
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                                                                                                                                                                                                                                                                                                                                         ACD19044 standard; DNA; 87563 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli; strain 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-2002; 2002US-00114170.
24-JAN-2002; 2002JP-00015959.
                 24-JAN-2001; 2001JP-00112010.
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PERNA N T.
PLUNKETT G.
                                 (UYTS-) UNIV ISUKUBA
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                                                   WPI; 2003-451640/43
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                             food poisoning.
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03-DEC-1999;
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21-AUG-2003
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                                                                                                                                                                  invention
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The invention relates to an isolated DNA molecule comprising an B. coll strain 0157:H7 sequence selected from a clostridial cytotoxin-like gene, a urease gene cluster. a RYX toxin-like gene cluster. a locus of a urease gene cluster. a RYX toxin-like gene cluster. a locus of antercoyte effacement and 2 genes from its associated lymphocytic phage cantercoyte effacement and 2 genes from its associated lymphocytic phage 10157:H7 can cause food polsoning, specifically acute hemomorphagic collitis (which can develop into haemolytic uraemic syndrome). Also included are an isolated DNA molecule comprising a nucleotide sequence identical to at least 25 contiguous nucleotides contained in DNA sequences selected from ACD18988ACD19242 (being 255 E.coli 0157 DNA sequences which are not count in B.coli K12), a recombinant DNA construction comprising the DNA above and a method for detecting E. coli 0157:H7 (ATCC 43895) in a sample of the 125 sequences. The DNA sequences are useful in detecting E. coli of the 255 sequences. The DNA sequences are useful in detecting E. coli infected with O157:H7, and in designing diagnostic probes which can be used to distinguish strain O157:H7 from strain K12 using molecular techniques. The present sequence is one of the 255 E. coli 0157:H7 DNA sequence (termed OZID_1-OZID255). Note: The sequence data for this patent clain form pat of form pat of form pat of form pat of fer printed specification, but was obtained in electronic format directly from the USPTO at USPTO at sequence OS field)
B. coli 0157:H7 in a sample, or in designing diagnostic probes
be used to distinguish strain 0157:H7 from strain K12 using
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immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer;
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                                                                                                                                                                                                                                                       Claim 16; SEQ ID NO 57; 33pp; English
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99GB-00001739.
99GB-00017995.
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response useful in vaccinating against and in treating tumors

Disclosure; Page 78-79; 79pp; English.

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tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were incculated with a virus expression vector containing the human or murine 574 gene sequence. The 574 antigen was shown to be teffective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant, 88; gene; transgenic, cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield;
carcinomas but has a highly restricted expression pattern in normal adult
                                                                                                                                                                                          U; 112 Other;
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Mismatches:
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                                                                                                                                                                                        Sequence 901 BP; 178 A; 246 C; 212 G; 153 T; 0
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Matches:
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28-APR-2003; 2003US-00425115
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producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region to plant with a recombinant DNA construct comprising a promoter region of the functional in a plant cell operably joined to a polymorelecide encoding a polypeptide associated with the property and growing the transformed collater. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant theoremse, for galactomannan production, for production of plant growth regulators, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions for improvement by collegate of carbohydrate, introgen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polymucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and carbohydrate, in particular for production, the present invention are useful in the field of biochemistry and flow, increasing plant tolerance to cold or heat, improving plant tolerance to plant pests or producing transgenic plants with improving plant folerance to plant pests or pathogens. They can also be used in physical carrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence data for this patent did controled forms part of the present sequence is one fet be sequenced analysis of the invention. Note: The sequence data for this patent did note the lettonic formst directly, from used in particular in the sequence data for this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 electronic format directly from USPTO at
segdata.uspto.gov/sequence.html?DocID=20040216190.
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Sequence 1268 BP; 438 A; 223 C; 245 G; 362 T; 0 U; 0 Other; m 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 225 40.00 100.0% 66.7% 85.1% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-774-176-13 (1-9) x ADT16562 (1-1268)

셤 8

AAA27059 standard; DNA; 1281 BP. AAA27059;

**AAA**27059 RESULT

(first entry) 22-AUG-2000

Mouse 5T4 tumour-associated antigen gene.

systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

Mouse, TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;

Mus musculus

WO200029428-A2

25-MAY-2000

99WO-GB003859 18-NOV-1999;

2002JP-00377326 2003JP-00137505 2003JS-0470836P

06-JUN-2002) 26-DEC-2002) 27-DEC-2002) 15-MAY-2003)

2002JP-00164257 2002US-0385912P

05-JUN-2002;

05-JUN-2003; 2003WO-JP007123

WO2003104277-A2.

18-DEC-2003.

Homo sapiens.

98GB-00025303. 99GB-00001739. 99GB-00017995. 18-NOV-1998; 27-JAN-1999; 30-JUL-1999; 

(TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160 Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors. The present sequence encodes the mouse 5T4 tumour-associated antigen Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other; Example 2; Page 78; 79pp; English. (OXFO-) OXFORD BIOMEDICA UK LTD. Carroll MW, Myers KA; WPI; 2000-387735/33. 

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ss; gene; human; signal transducer and activator of transcription STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                     Human cDNA encoding protein that promotes STAT6 activation #63.
       1281
7
2
0
0
      Length:
Matches:
Conservative:
Mismatches:
                                            Indels:
Gaps:
                                                                                        US-10-774-176-13 (1-9) x AAA27059 (1-1281)
                                                                                                                                                ADI26160 standard; cDNA; 2557 BP.
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        228
40.00
100.0%
77.8%
85.1%
                                   Best Local Similarity:
                          Percent Similarity:
Alignment Scores:
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                                             Query Match:
DB:
          Pred. No.:
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06-JUN-2002; 2002US-0385912P. 26-DEC-2002; 2002JP-00377326. 27-DEC-2002; 2002US-043647P. 15-MAY-2003; 2003JP-00137505. 16-MAY-2003; 2003US-0470836P.

05-JUN-2003; 2003WO-JP007123 05-JUN-2002; 2002JP-00164257

18-DEC-2003.

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for screening
                                                                                                                                                                                                                                                                                   The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergic diseases, inflammation, autoimmune diseases, diabetes, the preparation of the propertions disease and cancers. Compositions are useful for treating disease associated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATE compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a human cDNA encoding a protein which promotes STATE activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmuno disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                          signal transducer and activator of transcription 6 activation noting purified protein, for diagnosing and treating disease ciated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding protein that promotes STAT6 activation #62.
                                            Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2557 BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                            Muramatsu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
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                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 125; 1368pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-774-176-13 (1-9) x ADI26160 (1-2557)
                                            Honda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI26158 standard; cDNA; 2557 BP
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                                        Matsuda A,
(ASAH ) ASAHI KASEI KK
                                                                                 2004-122214/12.
                                                                                                                                                                                                             diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                        P-PSDB; ADI26161
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                                        Sugahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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No.
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STATE). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosling a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATE activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATG activity. The protein or nucleic acid is effectively useful for screenin compounds for treating and preventing disease associated with excessive activation or inhibition of STATG. The present sequence represents a human cDNA encoding a protein which promotes STATG activation.
                                                                                                                                                                                                                                                                                                                                                                                          promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 123; 1368pp; English.
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                                                                                                                                                                                                                                                                         Sugahara T, Matsuda A,
                                                                                                                                                                                                                                   (ASAH ) ASAHI KASEI KK
                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes and cancer.
                                                                                                                                                                                                                                                                                                               WPI; 2004-122214/12
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Best Local Similarity:
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cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss. Recombinant DNA construct; transformed plant; improved plant property, Bacterial polynucleotide #20330. 20-FEB-2003; 2003US-00369493 21-PEB-2002; 2002US-0360039P HINKLE G J. SLATER S C. GOLDMAN B S. US2003233675-A1 CHEN X CAO Y 18-DEC-2003. Bacteria. (HINK/) (SLAT/) (CHEN/) (COLD/) (CNOY/) 

Chen X, Goldman BS; Cao Y, Hinkle GJ, Slater SC,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 44017; 122pp; English

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the colymnation DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant with the improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not be proved the property that the property that the plant property the plant property that the plant property the plant property the plant property the plant property the plant plant property the plant p format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 2568 BP; 774 A; 484 C; 620 G; 690 T; 0 U; 0 Other;

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4000
                Matches:
Conservative:
Mismatches:
Indels:
         Length:
                40.00
100.0%
87.5%
85.1%
                        Percent Similarity:
Best Local Similarity:
gnment Scores:
                                        Query Match:
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US-10-774-176-13 (1-9) x ADT45579 (1-2568)

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ommosis;
                                                                                                                          carbohydrate;
                                                                                              Recombinant DNA construct; transformed plant; improved plant p
cold tolerance; heat tolerance; drought tolerance; herbicide;
pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbo
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polymucleotide; gene; ss.
BP
                                                                                 Bacterial polynucleotide #1264.
                                  ADS46521/c
ID ADS46521 standard; cDNA; 2571
                                                                                                                                                                                               20-FEB-2003; 2003US-00369493.
                                                                    02-DEC-2004 (first entry)
                                                                                                                                                                    US2003233675-A1.
                                                                                                                                                                                  18-DEC-2003
                                                       ADS46521;
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Chen X, Goldman BS; Hinkle GJ, Slater SC, Cao Y,

21-FEB-2002; 2002US-0360039P.

CAO Y. HINKLE G J. SLATER S C. CHEN X.

(CAOY/) (SLAT/) (CHEN/) (HINK/)

GOLDMAN B S.

(GOLD/)

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 24951; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant cauch as maize or soybean. The method of producing a transformed plant to such as maize or soybean. The method of producing a transformed plant to such as maize or soybean. The method of producing a plant with the carecombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the polynucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or a drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or peats, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved light, production or improved galactomannan condition, improved light, production or improved galactomannan production, this sequence represents a bacterial polynucleotide used in the scope of the invention. When sequence data for this patent did cont form part of the printed specification but was obtained in electronic format from USPTO at sequence.

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AAC66548;
Query Match:
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                                                                                                                          AAC66548
                                                                                                            RESULT
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                                                                                                                                              represent sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                              Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma call lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes, base sequence data of which are applicable as tumour markers and reagents in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF97787 to AAF97829 represent PCR primers used in the exemplification of the present invention, and AAF97891 to AAF97829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs.
                                                                                                                                                                                                                                                                                                                  Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer; tumour suppressor; human 1p36 homozygosity deletion domain; tumour; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a homozygosity deletion domain co-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34488 BP; 9654 A; 6717 C; 6926 G; 11191 T; 0 U; 0 Other;
 T; 0 U; 0 Other;
                                  Length:
Matches:
Conservative:
Mismatches:
775 A; 484 C; 621 G; 691
                                                                                   Indels:
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                                                                                                                                                            TCCTTTATCTTCCTAAAGATGTT 196
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                                                                                                                                              1 PheLeuTyrLeuProArgAspVal 8
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                                                                                                                                                                                                                     AAF97854 standard, DNA, 34488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-00245962
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Seguence 2571 BP;
                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Pred. No.:
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                       Alignment Scores:
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                                                                       Best Local
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34488

Length:

Matches: Conservative: Mismatches:

1.03e+04 40.00 100.0% 66.7%

Percent Similarity: Best Local Similarity:

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The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromsome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIRIA and KIRIB proteins. The sequences disclosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in disease disgnosis and population studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12 nucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, kinesin-like protein, HKLP, KIF1, cell division, cancer,
intracellular transport, neurological disorder, infertility,
biallelic marker, spontaneous abortion, neonatal chromosome disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.
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                                                                                  US-10-774-176-13 (1-9) x AAF97854 (1-34488)
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                                                                                                                                   1 PheleuTyrLeuProArgAspValLeu
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Best Local Similarity:
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canine microarray; drug screening; toxicity assay; environmental pollutant; cellular response; gene expression profile; toxic response; liver necrosis; fatty liver disease; protein adduct formation; hepatitis; dog; ds.

Canis familiaris. WO2004063324-A2

29-JUL-2004

Novel canine microarray-related DNA sequence SeqID587

(first entry)

21-OCT-2004

```
The sequence is upstream of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 olds overlected brobe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites on the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for gpecification and indexed herein (see below). The sequences upstream and compatream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The consistent of in vitro amplification of the corresp.

The sequence of clentify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used in genetic identification, gene
                                                                                                                                                                            PCR; selection; primers, OPTIPRIM; breeding; cattle, parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                            Sequence upstream from a microsatellite from clone TGLA423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108 BP; 37 A; 13 C; 18 G; 40 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Table 7; Page 339; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - mapping, and selective breeding.
                  AAQ34023 standard; DNA; 108 BP.
                                                                                                                                                                                                                                                                                                                                             92WO-US000340,
                                                                                                                                                                                                                                                                                                                                                                                91US-00642342
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
                                                                                                                                                                                                                                                                       WO9213102-A1
                                                                                                                                                                                                                                                                                                                                             LS-JAN-1992;
                                                                                       25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                          06-AUG-1992.
                                                                                                                                                                                                                                     Bos taurus.
                                                     AAQ34023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        field.)
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New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell living organism.

Wei T;

Porter M,

Diggans JC,

WPI; 2004-561890/54.

03-MAY-2002; 2002US-0377240P. 05-MAY-2003; 2003WO-US013853

(GENE-) GENE LOGIC INC. (PFIZ ) PFIZER PROD INC

Claim 1; SEQ ID NO 587; 41pp; English

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This invention is related to a novel isolated canine nucleic acid
sequences and the construction of canine microarrays containing a
significant portion of the canine genome. The isolated canine nucleic
acid sequences of the invention may be useful for drug screening and
coxicity assays. The invention is therefore useful for assessing the
impact, including toxicity, of a compound, pharmaceutical agent or
environmental pollutant on a cell or living organism. The methods are
useful for detecting genes that are up- or down-regulated in canines in
disease state. The sequences are useful as diagnostic agents or markers
to detect a cellular response in a sample individually or as part of
a conducting electronic Northerns that allow the user to determine that
modulate gene expression or activity. The database is useful for
producing electronic Northerns that allow the user to determine the cell
type or tissue in which a given gene is expressed and to allow
controllar tissue or cell. The methods are useful for determining the
particular tissue or cell. The methods are useful for determining the
similarity of a toxic response to one or more individual compounds. The
methods are useful for predicting at least one toxic response or the
similarity of a toxic response to one or more individual compounds. The
methods are useful for predicting at least one toxic response or the
similarity be toxing themethods are also useful for predicting or elucidating
the toxins. The methods are also useful for predicting or elucidating
the potential cellular pathways influenced, induced or modulated by the
compound or test agent due to the similarity of the expression profile
compound or test agent due to the similarity of the expression profile
compound or test agent the toxin which was known toxin. The present sequence
compound or test agent the toxin as a profile induced by a known toxin. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 584 BP; 149 A; 107 C; 127 G; 167 T; 0 U; 34 Other;
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8
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Conservative:
Mismatches:
Indels:
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100.0$
75.0$
83.0$
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Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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Length: Matches: Conservative: Mismatches: Indels:

100.0% 75.0% 83.0% 21 39.00

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

BP.

ADQ49285 standard; DNA; 584

RESULT 43 ADQ49285/ ADQ49285,

PheLeuTyrLeuProArgAspVal 8

Н 80

8

US-10-774-176-13 (1-9) x AAQ34023 (1-108)

US-10-774-176-13 (1-9) x ADQ49285 (1-584)

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Gaps:

83.0\$

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Human NOV4b encoding cDNA SEQ ID NO:47.
                                             US-10-774-176-13 (1-9) x AEB53920 (1-753)
                                                                                                       159 Trrcreraccrrecedadr 179
                                                                                                                                                                   ACC62259 standard; cDNA; 937 BP.
                                                                           1 PheLeuTyrLeuProArgAsp
                                                                                                                                                                                                                               23-JUN-2003 (first entry)
                                                                                                                                                                                                   ACC62259;
Query Match:
                                                                           ઠે
                                                                                                       셤
                                                                                                                                                                     The present invention relates to methods of screening cancer-linked genes and expression products for cancer diagnosis, and for screening potential anti-cancer agents. Specifically claimed is a method of identifying (M1) an agent that modulates activity of cancer-related genes, by contacting a compound with a cell expression and detecting difference in expression relative to when the compound is not present. Also claimed are methods of identifying (M2) an anti-neoplastic agent, by contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene activity with a compound first identified as a cancer related gene activity with a compound first identified as a cancer related gene activity with a compound first identified as a cancer related gene condition and detecting a decrease in the neoplastic, or administering agent identified by (M1) to an animal exhibiting a cancer condition and detecting a decrease in the cancerous condition. Also given the protein (I), which has at least one immunogenic fragment; an antibody that reacts with a protein; an immunoconjugate comprising the antibody and a cytocoxic agent. The agent is useful for treating cancer, by contacting a cancerous cell in vivo with an agent having activity by eliciting the production of cytotoxic I lymphocytes specific for the specification. The agent is also useful for treating cancer in an animal by eliciting the production of cytotoxic I lymphocytes specific for the proteins are anion transport proteins specific for prostate cancer. The protein sequence is cDNA encoding a prostate cancer. The protein CGI-96, unigene cluster Hs.360940.
                                                                                                                                                                                                                             screening; diagnosis; cancer; prostate tumor; cytostatic; drug screening;
antibody therapy; immunoconjugate; immuno-diagnosis; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying agent that modulates activity of cancer-related gene, by contacting compound with cell, to promote expression of gene, and detecting difference in expression of gene relative to when compound is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 753 BP; 184 A; 194 C; 205 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                   cDNA encoding prostate cancer-specific protein, seqid 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 67; 131pp; English.
                                  540 TATTTGTATTTACCCAGGGACATT 517
               1 PheLeuTyrLeuProArgAspVal 8
                                                                                                                                                                                                                                                                anion transport protein; gene; ss
                                                                                                         AEB53920 standard; cDNA; 753 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not present, to identify agent.
                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-2005; 2005WO-US000040
                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2004; 2004US-0534419P
                                                                                                                                                                   06-OCT-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weigle B, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-563837/57
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                                                                                                                                       AEB53920;
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anorectic; immunosuppressive; cytostatic; antidiabetic; antinfertility; haemostatic; antinfertility; haemostatic; antinfertility; haemostatic; antinfertility; haemostatic; antinfertility; haemostatic; antinfertility; gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderms; congenital heart defect; aortic stenosis; valve disease; transplantation; tuberous sclerosis; obesity; congenital adrenal hyperplasis; diabetes; prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer; fertility; haemophilia; hypercoagulation; graft versus host disease; didopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia; crohn's disease; multiple sclerosis; infectious disease; cancer; cancer; madelessis; infectious disease; cancer; cancer; disease; immune disorder; haematopoietic disorder; dyslipidaemia;
Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
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E, Chant JS, Chaudhuri A;
R, Bisen AJ, Bllerman K;
Gorman L, Guo X, Gusev VY,
Lepley DM, Li L, Liu X;
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Catterton B,
Edinger SR,
Giot L, Gor
Leach MD, Le
                                                                                                                                                                                                                                                                                                                                                  metabolic syndrome X; gene; ss
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2001US-0323519P
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Burgess CB, Casman SJ, Ca
Crabtree J, Dipippo VA, E
Gangolli EA, Gerlach VL, U
Kekuda R, Khramtsov NV, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-03
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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14-DEC-2001;
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17-MAY-2002;
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Length: Matches: Conservative: Mismatches:

199 39.00 100.0%

Percent Similarity: Best Local Similarity:

Pred. No.:

sapiens.

Homo

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JM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M; Rieger DK, Rothenberg ME, Shenoy SG, Shinkets RA; C, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ; J, Zhong M;
                                                     Spaderna SK,
                                                                                    Zerhusen BD,
     Malyankar UM,
                               Pena CEA,
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WPI; 2003-313241/30.

P-PSDB; ABR54190

Novel human proteins and nucleic acid encoding the proteins, useful for diagnosis, treatment and prevention of disorders involving the human protein or nucleic acid e.g. cardiac and neurological disorders.

Claim 20; Page 118-119; 460pp; English.

The present invention describes isolated human NOVX proteins, where X is

1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in

ABR542167 to ABR54226. NOVX sequences have antiatheroscolerotic, cardiant,

phypotensive, dermatological, anorectic, immunosuppressive, cytostatic,

antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,

antidatic, metabolic, immunomodulator, neuroprotective, nootropic,

antiparkinsonian and antilipaemic activities, and can be used in gene

therapy. NOVX proteins are useful for treating or preventing a pathology

associated with the human disease. NOVX nucleic acids, proteins and

associated with the human disease. NOVX nucleic acids, proteins and

antibodies can be used in the treatment and diagnosis of cardiomyopathy,

attherosclarosis, hypertension, congenital heart defects, acrtic stenosis,

valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,

congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic

disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,

hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host

disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,

infectious disease, parkinson's disease, immune disorders,

haematopolete, disorders, danceranders, dand metabolic syndrome x.

Alzheimer's disease, Parkinson's disease, immune disorders,

congenitation, diopathic thrombogypepenic purpura, graft versus host

disease, AIDS bronchala, cancer, fertility, haemophilia,

hypercosquibation, ridiopathic strombogypepenic purpura, graft versus host

alzheimer's disease, parkinson's disease, immune disorders,

Alzheimer's disease, anoresent graft propes for human NOVX

sequences, which are used in examples from the present invention.

Abs. human hyperplasente a human trypsinogen protein given in comparison with the human NOV35b protein in the exemplification of the present invention

Seguence 937 BP; 217 A; 257 C; 258 G; 205 T; 0 U; 0 Other;

937 0 0 0 Matches: Conservative: Mismatches: Indels: Gaps: Length: 39.00 100.08 100.08 83.08 Percent Similarity: Best Local Similarity: Alignment Scores: Best Local S Query Match: 

US-10-774-176-13 (1-9) x ACC62259 (1-937)

g 8

RESULT 46 AAL57532 

AAL57532 standard; cDNA; 945 BP

AAL57532;

(first entry) 06-NOV-2003 cDNA encoding human homologue of fruit fly kraken.

Anorectic, antinflammatory; cardiant; hypotensive; antidiabetic; neuroprotective; pharmaceutical composition; body-weight regulation; thermogenesis; metabolic; obesity; Syndrome X; insulin-resistance; eating disorder; cachexia; diabetes mellitus; hypertension; gallstone; pancreatic dysfunction; arteriosclerosis; coronary heart disease; gene; hypercholesterolaemia; dyslipidaemia; osteoarthritis; ROS defence; ss; reactive oxygen species; neurodegenerative; mitochondrial; gene therapy; human; kraken.

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The invention relates to a novel pharmaceutical composition comprising a nucleic acid molecule or polypeptide which is a human homologue of a Drosophila melanogaster polypeptide or polynucleotide. The composition of the invention may be utilised during the diagnosis, study, prevention and treatment of diseases related to body-weight regulation and thermogenesis including metabolic disorders such as obesity, Syndrome X and insuling cresistance syndrome and eating disorders e.g. cachexis, diabetes mellitus, hypertension, pancreatic dysfunctions, arteriosolerosis, coronary heart disease, hypercholesterolaemia, dyslipidaemia, coronary heart disease, hypercholesterolaemia, disorders related to reactive osteoarthritis and gallstones. Furthermore, disorders related to reactive neurodegenerative disorders or mitochondrial disorders. Flanally, the composition of the invention may be useful in gene therapy. The current sequence is that of the cDNA encoding the human homologue of fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pharmaceutical composition, useful for the manufacture of an agent for diagnosing, treating or preventing disorders related to body-weight regulation and thermogenesis, e.g., metabolic diseases such as obesity.
                                                                                          /*tag= a
/product= "Human homologue of fruit fly kraken protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Broenner G;
                                                                                                                                                                                                                                                                                                                                                                                                  (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Steuernagel A, Molitor A, Eulenberg K,
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 17B; 144pp; English.
                                                                                                                                                                                                                                                                                                  28 FEB-2002; 2002EP-00004687.
25-APR-2002; 2002EP-00009475.
18-JUN-2002; 2002EP-00013329.
30-DEC-2002; 2002EP-00029081.
                                                                                                                                                                                                                           24-JAN-2003; 2003WO-EP000738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-627418/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AA023978.
                                                                                                                                                   WO2003061681-A2
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                                                                                                                                                                                        31-JUL-2003
                                                      Key
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Sequence 945 BP; 217 A; 261 C; 254 G; 213 T; 0 U; 0 Other;

Matches: Conservative: Mismatches: Indels: Length: 100.0% 100.0% 83.0% 39.00 Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Score:

24 0 0 0 0

US-10-774-176-13 (1-9) x AAL57532 (1-945)

371 TTTCTGTACCTTCCCCGAGAT 1 PheLeuTyrLeuProArgAsp

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ADQ87521 standard; cDNA; 945 RESULT 47

BP.

07-OCT-2004 (first entry)

ADQ87521;

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human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
    Human tumour-associated antigenic target (TAT) cDNA sequence #4399.
                                                                                                                                 Claim 1; SEQ ID NO 4399; 5504pp; English.
                                                                  18-OCT-2002; 2002US-0418988P.
                                                         LS-OCT-2003; 2003WO-US029126
                                                                           (GETH ) GENENTECH INC.
(WUTD/) WU T D.
(ZHOU/) ZHOU Y.
                                      WO2004060270-A2.
                                                                                               Zhou Y;
                             Homo sapiens.
                                               22-JUL-2004.
                                                                                               tu TD,
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New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer WPI; 2004-534300/51.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SRQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above comprising the above expression vector; (a) a process for producing a polypeptide; (4) an isolated polypeptide comprising (a) an amino acid sequence encoded by the full-notetide sequences; (b) an amino acid sequence encoded by the full-notetide sequences; (b) an amino acid sequence encoded by the full-notetide sequences; (b) an amino acid sequence encoded by the full-notetide sequences; (b) an amino acid sequence encoded by the full-comprising the above polypeptide fueed to a heterologous polypeptide comprising the above polypeptide fueed to a heterologous polypeptide; (c) an isolated antibody that binds to the above polypeptide; (f) a process comprising the antibody; (8) an isolated oligopeptide; (7) a process composition of matter comprising to the above polypeptide; (f) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above polypeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the container; (12) method of the growth of the cell is at least in part dependent upon a growth the protein of persented above protein; (14) a method of containing the protein ammanal; (15) a method of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing or cell promise of the above contained with increased expression or activity of the above protein; and (17) a method of hinding an antibody, oligoprotein; and (17) a method of hinding an antibod of hinding an antibod of hinding an antibod of hinding an antibod of preventing or treating cancer. The composition is also used for preparing medicament for the therapeutic treatment or diagnostic detection of a sill proliferative disorder or cancer. The present sequence represents a protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, human TAT cDNA sequence from the present invention.

Sequence 945 BP; 217 A; 261 C; 254 G; 213 T; 0 U; 0 Other;

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Length:
Matches:
Alignment Scores:
Pred. No.:
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gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma; congenital heart defect; acrtic stenosis; valve disease; transplantation; tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes; prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer; fertility; haemophilia; hypercoagulation; graft versus host disease; idiopathic thrombocycopenic purpura; AIDS; bronchial asthma; anorexia; Crohn's disease; cancer;
                                                                                                                                                                                                                                                                                      anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility; haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                     cancer-associated cachexia; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia;
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Chaudhuri A;
Ellerman K;
                                                                                                                                                                                                                                                                             Human; NOVX; antiatherosclerotic; hypotensive; cardiant;
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Chant JS,
Eisen AJ,
  Conservative:
              Mismatches:
Indels:
                                        Gaps:
                                                                                                                                                                                                                                                  Human NOV4c encoding cDNA SEQ ID NO:49.
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Catterton E,
Edinger SR,
                                                                  US-10-774-176-13 (1-9) x ADQ87521 (1-945)
                                                                                                                   351 TTTCTGTACCTTCCCCGAGAT 371
                                                                                                                                                                       ACC62260 standard; cDNA; 1058 BP
                                                                                            PheLeuTyrLeuProArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolic syndrome X; gene; ss.
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2001US-0341144P.
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06-SBP-2002; 2002US-00236417
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E, Casman SJ, C
J, Dipippo VA,
100.0%
100.0%
83.0%
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 Percent Similarity:
Best Local Similarity:
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05-MAR-2002;
03-MAY-2002;
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Burgess CE,
Crabtree J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2001;
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                              Query Match:
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                                                                           Patturajan M;
Gusev VY,
Gangolli RA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X; Malyankar UM, Miller CE, Ort T, Padigaru M, Pattura Pena CEA, Riger DK, Rothenberg ME, Shenoy SG, Shimkets RA; Spaderna SK, Spytek KA, Taupler RJ, Twomlow N, Vernet CAM, Zerhusen BD, Zhong M;
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WPI; 2003-313241/30. P-PSDB; ABR54191.

Novel human proteins and nucleic acid encoding the proteins, useful diagnosis, treatment and prevention of disorders involving the human protein or nucleic acid e.g. cardiac and neurological disorders.

Claim 20; Page 119; 460pp; English.

hypotensive, dermatological, anotectic, imminosuppressive, cytostatic, antidabetic, antidetility, haemostatic, antidabetic, antidetility, haemostatic, antidabetic, antidabetic, antidabetic, metabolic, immunomodulator, neuroprotective, noctropic, antidatabetic, metabolic, immunomodulator, neuroprotective, noctropic, antidatabetic, metabolic, immunomodulator, neuroprotective, noctropic, associated with a NoVX protein in humans and for treating a syndrome associated with a NoVX protein in humans and for treating a syndrome associated with the human disease. NoVX nucleic acids, proteins and antibodies can be used in the treatment and diagnosis of cardiomyopathy, alversosilenosis, proteins and antibodies can be used in the treatment and diagnosis of cardiomyopathy, alverdise can be used in the treatment and diagnosis of cardiomyopathy, valve disease, tuberous sclerosis, scleroderma, obesity, transplantation, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disease, anorexia, cancer. sesociated caches, metabolic disease, anorexia, cancer-associated cachesia, cancer, hemanopoietic disorders, anorexia, cancer-associated cachesia, cancer, Alzheimer's disease, anorexia, cancer-associated cachesia, cancer, Alzheimer's disease, Parkinson's disease, immune disorders, heman NOVX sequences, which are used in examples from the present invention.

ARS4277 represents a human trypabinogen protein given in comparison with the human NOV35b protein in the exemplification of the present invention The present invention describes isolated human NOVX proteins, where X is 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,

Sequence 1058 BP; 243 A; 295 C; 284 G; 236 T; 0 U; 0 Other;

1058 7 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 296 39.00 100.0% 100.0% 83.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: ₽ 9

US-10-774-176-13 (1-9) x ACC62260 (1-1058)

364 TTTCTGTACCTTCCCCGAGAT 384 PheLeuTyrLeuProArgAsp

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AEB53915 standard; DNA; 1165 BP. **A**BB5391

RESULT 49

AEB53915;

(first entry) 06-OCT-2005 DNA encoding prostate cancer-specific protein, seqid 62.

screening; diagnosis; cancer; prostate tumor; cytostatic; drug screening; antibody therapy; immunoconjugate; immuno-diagnosis; immunotherapy; anion transport protein; ds; gene; splice variant.

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The present invention relates to methods of screening cancer-linked genes and expression products for cancer diagnosis, and for screening potential anti-cancer agents. Specifically claimed is a method of identifying (Mt) an activate modulates activity of cancer-related genes, by contacting a compound with a cell expressing a gene under conditions promoting the expression of gene, and detecting difference in expression relative to when the compound is not present. Also claimed are methods of identifying (M2) an anti-neoplastic agent, by contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator by (M1), and detecting a decrease in the neoplastic, or administering agent identified by (M1) to an animal exhibiting a cancer condition and detecting a decrease in the cancerous condition. Also given a tip a protein (I), which has at least one immunogenic fragment; an antibody that reacts with a protein; an immunoconjugate comprising the protein the agent is useful for treating cancer, or antibody and a cytotoxic agent. The agent is useful for treating cancer, and animal and activity against an expression produced encoded by a gene sequence given in the specification. The agent is also useful for treating cancer in an animal, and an expression produced encoded by a gene sequence given in the proteins are anion transport proteins appealing prostate cancer. The protein and sequence is variant 4 DNA encoding a prostate cancer. The present and anion transport proteins appear protein appears and a protein and anion transport proteins appears to prostate cancer. The protein and anion transport proteins appears to prostate cancer. The appear are anion transport proteins appears to prostate cancer. The appear are anion transport proteins appears to protein a protein and anion transport proteins are cancer. The appears are anion transported to a protein appears and a protein appears and a protein and anion transport and anion transported and a protein appears appears and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contacting compound with cell, to promote expression of gene, and detecting difference in expression of gene relative to when compound is
                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying agent that modulates activity of cancer-related gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1165 BP; 273 A; 319 C; 325 G; 248 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 62; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, unigene cluster Hs.360940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not present, to identify agent.
                                                                                                                 04-JAN-2005; 2005WO-US000040.
                                                                                                                                                                                06-JAN-2004; 2004US-0534419P
                                                                                                                                                                                                                                            (AVAL-) AVALON PHARM
                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-563837/57.
                                                                                                                                                                                                                                                                                                        Weigle B, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AEB53916
WO2005067629-A2.
                                                           28-JUL-2005
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Matches: Conservative: Mismatches: Indels: Length: 331 39.00 100.0% 100.0% 83.0% Similarity: Percent Similarity: Best Local Similari Alignment Scores: Query Match: DB:

1165 7 0 0 0

US-10-774-176-13 (1-9) x AEB53915 (1-1165)

439 419 rrrcreracerrecedadar 1 PheLeuTyrLeuProArgAsp

ADI40459;

ADI40459 standard; DNA; 1241 BP

RESULT 50 AD140459

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22-APR-2004 (first entry)

Human purified secretory polynucleotide (sptm), seq id 152 

Antiarteriosclerotic; antipsoriatic; cytostatic; secretory molecule;

Homo sapiens

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The invention relates to isolated purified secreted polynucleotides (sptm) (1), and the polypeptides (SPTM) encoded by sptm. A polypeptide encoded by (1) is used to identify a compound which binds to it. A microarray comprising (1) is used to generate a transcript. (1) is used to screen a compound for effectiveness in altering expression of (1). Is used to assess toxicity of a test compound. An agonist or antagonist identified by a new method is used in a pharmaceutical composition. The secretory molecules are used to diagnose or treat conditions, diseases or disorders associated with cell signaling e.g. arteriosclerosis, psoriasis, and cancer. Sequences given in ADI40308-ADI40468 represent human purified secretory polynucleotides of the invention, and those given in ADI40369-ADI40631 represent the polypeptides they encode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GB, Jackson JL; Yu JY, Tuason O, Yap PB, Amshey SR, Dam TC, Liu TF, Gerstin EH; Peralta CH, Lewis SA, Chen AJ, Marwaha R, Lan RY, Urashka MB; Kristnam SR, Kolluru V, Panesar IS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated secreted polynucleotide for diagnosing or treating conditions, diseases or disorders associated with cell signaling e.g. arteriosclerosis, psoriasis, and cancer.
agonist; antagonist; gene therapy; antisense; human; secretory; purified secretory polynucleotide; sptm; toxicity; arteriosclerosis; psoriasis; cancer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim la; SEQ ID NO 152; 486pp; English
                                                                                                                                       15-JAN-2003; 2003WO-US001605.
                                                                                                                                                                  17-JAN-2002; 2002US-0349413P.
                                                                                                                                                                                                           INCYTE GENOMICS INC.
                                                                                                                                                                                                                      JONES A L.
DAHL C R.
GIETZEN D.
CHINN J.
DUFOUR G E.
YU J Y.
TUASON O.
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KRISTNAM S R.
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P-PSDB; ADI40622.
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AMSHEY S R.
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PERALTA C H.
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LIU T F.
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHEN A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAN R Y.
                                                                                   WO2003062385-A2.
                                                         Homo sapiens
                                                                                                            31-JUL-2003.
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(LEWI/)
(CHEN/)
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Sequence 1241 BP; 321 A; 291 C; 281 G; 348 T; 0 U; 0 Other;

1241 7 0 0

Matches: Conservative: Mismatches: Length:

39.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

Alignment Scores: Pred. No.:

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Indels:
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                              US-10-774-176-13 (1-9) x ADI40459 (1-1241)
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                                                   1 PheLeuTyrLeuProArgAsp
83.0%
10
Query Match:
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Search completed: April 25, 2006, 12:32:33 Job time : 341.3 secs

AX316086 Sequence
AX467371 Sequence
CQ711678 Sequence
CQ7837282 Primer fo
CQ782724 Sequence
AX074786 Homo sapis
BD127283 Primer fo
CQ782726 Sequence
AX961916 Sequence
AX074790 Homo sapi

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AB168308 AL012159 AL121977 AF527803 AC000048 AL449423 AC040173 AC040173 AC05231 AF063339 BC087011

Perfect score: Sequence: Scoring table:

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ACO02318 Homo sapi AC166847 Bos tauru Continuation (112 Continuation (113 AL161650 Human DNA AC145796 Xenopus t AC006063 Homo sapi

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Score

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us-10-774-176-13.p2n.rge

	AC1091 AC1156: AC1126 AC1126 AC1136 AC1136 AC1045 AC167 AC167 AC667 AC667 AC667 AC6666 AC6666	BV2342 BV2342 BC093899 AL590111 BV48651 BV5649 BV5704 AX27438 AX27438 AX27438 AX27438 AX36551.	CQ491185 Sequence CQ497050 Sequence AX829180 Sequence AX833269 Sequence AX833269 Sequence AX833269 Sequence AX0782420 Sequence AX074492 Homo sapi AX508662 Sequence AX074492 Homo sapi AX508610 Homo sapi AX508601 Homo sapi AX5080853 Sequence CQ491584 Sequence CQ491584 Sequence CQ580853 Sequence CQ580853 Sequence AX63757 Pan trogl AC09444 Rattus no AC084621 Caenorhab BX294390 Homo sapi AR659650 Sequence AC087213 Rattus no
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37 78.7 159914 9 37 78.7 160193 14 37 78.7 160376 4	C 957 37 78.7 160775 9 AC125158 C 958 37 78.7 160845 2 AC079606 C 959 37 78.7 160979 14 AC055679	37 78.7 161001 8 37 78.7 161012 14 37 78.7 161143 8	37 78.7 161250 37 78.7 161280 37 78.7 161407	37 78.7 161482 14 37 78.7 161523 8	968 37 78.7 161547 8 969 37 78.7 161613 14 970 37 78.7 161672 14	37 78.7 161692 14 37 78.7 161955 8	973 37 78.7 161970 14 974 37 78.7 162149 14	37 78.7 162215	37 78.7 162918 8 37 78.7 162975 2	979 37 76.7 163036 0 980 37 78.7 163371 15 981 77 78 7 163377 16	37 78.7 163404 14 37 78.7 163788 5	984 37 78.7 163900 9	985 37 78.7 164075 14 986 37 78.7 164096 14 987 37 38.7 164170 14	37 78.7 164404 4 37 78.7 164404 4	37 78.7 164783 9 8 37 78.7 164823 14	992 37 78.7 165510 14	7 78.7 166125 14 7 78.7 166297 14	37 78.7 166594 9 37 78.7 166689 14	37 78.7 167288 14 37 78.7 167531 5 37 78.7 167548 8	TIE	AX829164	DEFINITION Sequence 57 IFOM FACENC WOU ACCESION AX829164 GI:39838931	S Homo sapiens (	zoa; ria;	REFERENCE 1 DITTERED TO THE THE TAIL OF AND THE THEORY AND THE THEORY WAS TO THE THEORY OF AND THE THEORY OF THE THE THEORY OF THE THE THEORY OF THE THE THEORY OF THE	TITLE Methods of diagnosis of breast cancer, comportant patent: WO 02059317A, 57 01.AUG-2002;	EUS BIOLECINOLOGY, INC. (US EATURES LOcation/Qualifier source 1927 / Organism="Homo sa	,

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Mamalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Bllard, P.M. and Myers, K.A.
                                                                                                                                    Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
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Location/Qualifiers

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Sequence 1 from Patent WO0029428.
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 1 05-DEC-2001;
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Location/Qualifiers
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Hominidae; Homo.
1 (Dases 1 to 2359)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
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                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
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Myers, K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.
and Stern, P.L.
Isolation of a cDNA encoding 5T4 oncofetal trophoblast
glycoprotein. An antigen associated with metastasis contains
leucine-rich repeats
J. Biol. Chem. 269 (12), 9319-9324 (1994)
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Sequence 17612 from Patent WO02068579.
CQ731678
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                          664 TICCICIACIIGCCICGCACGICCIG 690
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5T4 gene; 5T4 oncofoetal antigen.
Homo sapiens (human)
    1 PheLeuTyrLeuProArgAspValLeu 9
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Location/Qualifiers
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Direct Submission
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18 2 (Dases 1 to 2359)
18 1 sogal, T. and Otsuki, T.

Direct Submission

Submitted (125-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(Email:genomics@hri.co.jp, Tel:81-438-52-3997, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA hibrary construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; CDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                               AK074786 2159 bp mRNA linear PRI 03-SEP-2002 Homo sapiens CDNA FLJ90305 fis, clone NT2RP2000694, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Salto, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojiuma, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Nimoniya, K.

NEDO human cDNA sequencing project
Unpublished
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Mismatches:
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STHPLYLPROVLAQLPBLIADLSNBSLYSLIYVSRWLTHESELHESDNALKYLHNG
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                                  22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                               C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualiflers
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Mammalía, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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PI YURI KAWAL,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
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Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Sequence 2864 from Patent BP1396543.
CQ782724 GI:45502667
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Location/Qualifiers
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RESULT 12

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REFERENCE AUTHORS JOURNAL

COMMENT

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SNHELYZLPEDVLAQLPSLIRHIDLSNNSLVSLTYVSFRNLTHLESILHLEDNALKYLHNG
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LAVLPAGAPARRPPLABLAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPP
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                      Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Staté activation gene
Patent: WO 03104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                                                               Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2866 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Matches:
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Mismatches:
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/mol Exref="taxon:9606"
426. 1688
/note="unnamed protein product"
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1. 2361
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426. 1688
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Hominidae; Homo.
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                                                                                                  TITLE
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                     REFERENCE
                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (Dases 1 to 2161)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
                                                                                                                                                              BD127283 2161 bp DNA linear PAT I
Primer for synthesizing full-length CDNA and use thereof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2714 22-JAN-2002; HELIX RESEARCH INSTITUTE
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Sequence 2866 from Patent EP1396543.
CQ782726
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Location/Qualifiers
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                                                                1087 TTCCTTTACCTGCCGCGGATGTGCTG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .2361
/organism="Homo saplens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                          PheLeuTyrLeuProArgAspValleu 9
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U8-10-774-176-13 (1-9) x AK074786 (1-2359)
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JP 2002017375-A/2714
22-JAN-2002
                                                                                                                                                                                                                             BD127283.1 GI:2322228
JP 2002017375-A/2714.
Homo sapiens (human)
Homo sapiens
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FEATURES

RESULT 13 CQ782726 LOCUS

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PAT 14-JAN-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba, 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Sconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA full insert construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
TLAELGGEHFRYPLDNHPWYCDCHMADMYTMLKETBYVQGKORLTCAYPEKMRNYL
LELNSADLDCDPILPSPSLQTSYYFLGIVLALIGAIFLLUVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK074790 2361 bp mRNA linear PRI 09-UUL-2005 Homo sapiens cDNA FLJ90309 fis, clone NT2RP2000903, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Yamamoto,J., Wakamatsu,A., Kimura,K., Sakamoto,K., Hatano,N.,
Kawai,Y., Ishil,S., Saito,K., Kojima,S., Sugiyama,T., Ono,T.,
Okano,K., Yoshikawa,Y., Aotsuk,K., Sasaki,N., Hattori,A.,
Okumura,K., Nagai,K., Sugano,S. and Isogai,T.
Signal Sequence and Keyword Trap in silico for Selection of
Full-Length Human cDNAs Encoding Secretion or Membrane Proteins
from Oligo-Capped CDNA Libraries
DNA Res. 12, 117-126 (2005)
                                                                                                                                                          2361
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Conservative:
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/db_xref="taxon.9606"
/clone="NT2RP2000903"
/cell_line="NT2"
/cell_type="texatocarcinoma"
                                                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                  PheLeuTyrLeuProArgAspValLeu 9
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3 (bases 1 to 2361)
1sogai,T. and Otsuki,T.
Direct Submission
                                                                                                                                                        2.99
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Best Local Similarity:
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AK074790
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AUTHORS
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JOURNAL
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Hominidae; Homo.

Is (bases 1 to 2379)

Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haiseh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Bromstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X. (Gibbs, R.A.,
Bantear, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchen, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerchield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerztion and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

AL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC037161 29-JUN-2004
Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317
IMAGE:4138906), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Submitted (03-5872-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
/clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3
/note="cloning vector: pCoursor cells after 2-weeks
retinoic acid (RA) induction"
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Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help desk
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Matches:
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Indels:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lab host:
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AUTHORS
TITLE
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                   Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskelllo,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov Series: IRAL Plate: 26 Row: m Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.

Location/Qualifiers
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TLABLQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKARNYL
LELNSADLDCDPILPPSLQTSYVPLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MpGGCSRGPAAGDGRLRLARLALVILGWVSSSSPTSSASSFSSS
APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lavlppagafarrpplaelaalinlsgsrldevragafehlpslrqldshnpladlspf
Afsgsnasvsapsplvelilinhivppederqnrsfegmvvaallagralggerrlela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Muscle, rhabdomyosarcoma"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
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|db_xref="GeneID:7162"
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/mol_txref="texxon:9606"
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AB168308.1 G1:67967899
oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
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site: http://www.nisc.nih.gov/
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/db_xref="MIM:190920"
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Nemaryce, Nemearacy, Condete, Ceremiter, Vertebrets, Buteleoscomi, Cercoptifical Butheria; Butchcidae, Cercoptificalizes, Macaca.

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LAVLPAGAFARRPPLAELAALNI.SGSRLDEVRGGAFEHLPSIRQLDI.SHNPLAYI.SPP
RSGSSNAS, ISAPSPLVAELILMHIVPPDDKRQMSR BEGAVAALVAGKALQGI.HILELA
SNHFLYI.PRDVLAQLPSLRYLDLSNNS.LVSPSTRYLTHLESI.HILEDNALKYLHNG
TLAELQGLPHVRVFLDNNPWVCDCHMADMYTWLKQTGVVQGKORLTCAPPEKARNRVL
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                                                                  LBINSADLDCDPILPPSLQTSYVFLGIVLALIGAĪPLIVLYLNRKGIKKMHNIRDAC
RDHMEGYHYRYBINADPRLTNLSSNSDV*
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Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   King, K.W., Sheppard, P.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="5T4" oncofetal trophoblast glycoprotein"
/protein_id="CAA09930.1"
/db_xref="GI:3805947"
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
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Homo sapiens (human)
Homo sapiens
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Biochim. Biophys. Acta 1445 (3), 257-270 (1999)
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Matches:
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2698. .2703
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2704. .2709
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3431. .4693
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1. .5551
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/gene="5T4"
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Myers, K.A.
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Libert Submitted (13-MXY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Chone requests: clonerequest@sanger.ac.uk Cn Dec 15, 2000 this sequence version replaced gi:11558491.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: KBMB, Sw., SWISSPROT, Tr., TREMBL, Wp., WORNERP, Information on the WORNERP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6

RP3-492Pl4 is from the library RPCI-3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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/ db_xref="InterPro: IPR001611"
/ db_xref="InterPro: IPR003591"
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Human DNA sequence from clone RP3-492P14 on chromosome 6q13-15

Gontains a single stranded DNA binding protein pseudogene, the TPBG

gene for trophoblast glycoprotein (5T4-AG) and a CpG island,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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HTG; CpG island; TPBG.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 121909)
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3517. .4690
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF527803 28-770 bp DNA linear PRI 23-OCT-2003 Homo sapiens cyclin-dependent kinase inhibitor 2A (CDKN2A) gene, complete cds, alternatively spliced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (08-JUL-2002) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
170 cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: http://egp.gs.washington.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 28770)

Rieder, M.J., Livingston, R.J., Daniels, M.R., Montoya, M.A.,

Rieder, M.J., Livingston, R.S., Nguyen, C.P., Nguyen, D.A., Poel, C.L.,

Chung, M.-W., Miyamoto, K.B., Nguyen, C.P., Nguyen, D.A., Poel, C.L.,

Robertson, P.D., Schackwitz, W.S., Sherwood, J.K., Witrak, L.A. and
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                                                                                                                                                                                                                                                                                                                    Indels:
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100.0%
100.0%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                        US-10-774-176-13 (1-9)
                                                                                                         misc_feature
                                                                                                                                                                                                   Alignment Scores:
                                  polyA_site
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AF527803
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFSGSNASVSAPSPLVELILMHIVPPEDERQMRSFEGMVVAALLAGRALQGIERLELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRALTHLESLHLBDNALKVLHNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="trophoblast glycoprotein"
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Center: Wellcome Trust Sanger Institute
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                                                                                                      Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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            VECTOR: pCYPAC2
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Lacture (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Canbridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk clone requeste: clonerequest@sanger.ac.uk cn Nov 15, 2001 this sequence version replaced gi:15795445.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Swi, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-14912 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. Por further details see
                                                                                                                                                                                                                                                                                                                                                                                                            AL449423

Human DNA sequence from clone RF11-14912 on chromosome 9 Contains the CDENZA gene for cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4), the gene for susceptibility protein NSG-x methylthioadenosine phosphorylase (MSAP), the 3' end of a variant of the MTAP gene for methylthioadenosine phosphorylase (MSAP), the 3' end of the CDKN2B gene for cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL449423.14 GI:16944057
HTG; CDK4; CDKNZA; CDKNZB; CpG island; LOC51198; MSAP; MTAP; NSG-x.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 300); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                               Matches:
Conservative:
Mismatches:
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Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and 4 CpG islands, complete sequence.
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                                                                                                                                                          Indels:
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1 (bases 1 to 101155)
                                                                                    46.00
100.0%
88.9%
97.9%
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                                                                                                                                Best Local Similarity:
Query Match:
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                                                                                                          Percent Similarity:
                                           Alignment Scores:
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VERSION
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                                                                 Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACO00048 34669 bp DNA linear PRI 09-APR-2003
Homo saplens Chromosome 9p21 Cosmid Clone c66, complete sequence.
AC000048
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Joons="666"
/note="Left Neighbor sequenced in this center: 34a5. Right
Neighbor sequenced in this center: c86."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (30-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (Dasea 1 to 34669)

Burlan, D.M., Mitchell, N. and Roe, B.A.

Homo saplem: Cosmid Clone c66 encoding the p16/CDK-INK4 gene Unpublished
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On Sep 15, 1999 this sequence version replaced gi:5801678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Department of Chemistry And Biochemistry
The University of Oklahoma
Center code:UOKNOR
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                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sveen, L., Olopade, F.I. and Rowley, J.D.
Unpublished
3 (bases 1 to 34669)
                                                                                                                                                                                                                                                                                                                                                                                                  14453 TTCCTGTATCTCCCCAGAGATATTCTA 14479
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                                                                                                                                                                                                                                                                                                                            US-10-774-176-13 (1-9) x AF527803 (1-28770)
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88.9%
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Best Local Similarity:
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                                                                                                                                         Alignment Scores:
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                                             variation
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AC000048/c
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pi6, inhibits CDK4)"

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197753 TTCCTGTATCTCCCCAGAGATATTCTA 197727
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grrpiqvmmgsarvaellilhgaepncadpatltrpvhdaaregfildtivvilhraga
rldvrdamgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdipd"
                                                                                                                                                                                                                                                                PRI 26-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 250000)
Yokota,J., Kohno,T., Inoue,K. and Kitagawa,Y.
Yokota,J., Kohno,T., Inoue,K. and Kitagawa,Y.
Submitted (25-APR-2001) Takashi Kohno, National Cancer Center Research Institute, Biology Division; 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan (B-mail:tkohno@gan2.res.ncc.go.jp, Tel:81-3-3542-2511(ex.4652), Pax:81-3-3542-0807)
                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kohno,T., Inoue,K., Kitagawa,Y., Hayashi,Y., Matsuo,Y.,
Mizoguchi,H. and Yokota,J.
Prevalent Involvement of Illegitimate V(D)J Recombination in
Chromosome 9p21 Deletions in Lymphoid Leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join(185617. .185630,188290. .188596, 192072. .192221)

//gene="plac/CDKNZA"

complement (join(185617. .185630,188290. .188596, 192072. .192221))
                                                                                                                                                                                                                                                    ABUGUBUB 250000 bp DNA linear Homo sapiens gene for p16/CDKN2A, complete cds. AB060808
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/chromosome="9"
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PheLeuTyrLeuProArgAspValLeu 9

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AL Unpublished

State Submission

Library Submission

AL Unpublished

State State State

AL Submitted (11-APR-2000) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 192971)

Alamos National Laboratory.

Alamos National Laboratory.

By Cabmitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

4 (bases 1 to 192971)

By Cabmission

AL Submission

Drive, Walnut Creek, CA 94598, USA

Alamos National Laboratory.

By Cabmission

AL Submission

AL Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

Alamos National Laboratory.

Drivet Submission

AL Submission

AL Submitted (07-APR-2003) DOE Joint Genome Institute

WWW-jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los Alamos

National Laboratory

WWW-shgc. stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Restimated Total Number of Errors is 0.1.

NOTE: Unsure number of dinucleotide repeat copies 72468-73310. The

number of missing bases by PCR is 500.
ACC40173 192971 bp DNA linear PRI 07-APR-2003
Homo sapiens chromosome 16 clone RP11-65J21, complete sequence.
ACC40173
                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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72468. .73310
/note="NOTE: Unsure number of dinucleotide repeat copies
72468-73310. The number of missing bases by PCR is 500."
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1 (Dasse 1 to 192971)

DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_tref="taxon:9606"
/chromosome="16"
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Homo sapiens chromosome 16 clone CTD-2502C11, complete sequence. AC092291.3 GI:29124062
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                                                                                                                                                                                                                                             DOB Joint Genome Institute.

DOB Joint Genome Institute.

Direct Submission

Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-SEP-2001) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 194551)

DOB Joint Genome Institute, Stanford Human Genome Center and Los
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Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
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                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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(Lobasea 1 to 194551)

10 John Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
Location/Qualifiers
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Rattus norvegicus
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/clone="CTD-2502C11"
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Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Muridae; Murinae; Rattus.

1 (bases 1 to 2333)

1 (bases 1 to 2333)

2 (bases 1 to 2333)

3 Euchan, V.L.

Buchman, V.L.

Direct Submission

L. School of Biomedical Sciences, University of St. Andrews, Bute Medical Buildings, St. Andrews, Pife KY16 9TS, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAAFLASGSAQPPPAERCPAACECSEAARTVKCVNRNILEVPADLPPYVRNLFITGNQ
MTVLPAGAFRQPPLADLAVLNLSGNHLKEVGAGAFEHLPGIRRLDLSHNPLTNLSAF
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HHLELASNNFOTLPROLLDQLPSLKFLDLARNSLVSLTYASFRNITHLESLHLESLALBGL
KVLHNSTLARNGGLARVLLDQLPSLKFLDLRNSLVSLTYASFRNITHLESLHLESNAL
KVLHNSTLARNGGLARVRVFLDNNPWVCDCYNADMYSWLKETRVYPDKARLTCARPER
MRNRGLLDLTSSDLDCDATLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
1 (bases 1 to 2361)
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                               l. .2333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="5T4"
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/gene="5T4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Meb site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPGAGSRQPSAGDGRLRLARLALVLLGWVSASAPSSSLPSSTS
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TFAGSNVSVSTPSPLLELILLMHTVPPEDQRQNGSFEGWVAFRGWVAAALRSGLALRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-shgc.stanford.edu
Contect: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-DEC-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GeneID:83684"
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Director MGC Project.
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AUTHORS
TITLE
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COMMENT
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HHLELASNHFLYLPRDILDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
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Lobases 1 to 210337)

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

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Anyalebechl, V., Aoyagla., Andodej, M., Baca, B., Baden, H.,

Baldwin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, P.,

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Cardenas, V., Carter, C., Davy, Carroll, L., De Anda, C., Dederich, D.,

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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eagen, C., Evang, C.A., Falls, T., Fan, G.,

Fernandez, S., Filley, M., Flaggy, N., Forbes, L., Ponter, M., Gebregeorgis, S., Geer, K., Gill, R., Grady, M., Guevara, M.,

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Itu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

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Shetty, J., Shettspey, A., Soott, G., Shatsans, S., Shen, H.,

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Shetty, J., Shettspey, Sheety, S., Soott, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACI28294 210237 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE.
ACI28294
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC128294.3 GI:25083347
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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44.00
100.0%
88.9%
93.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 28
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23265004.

The sequence in this sequence version replaced gi:23265004.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (19-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 210237)
Rat Genome Sequencing Consortium.
Direct Submission
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valase, R., Vora, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warng, G., Wang, S., Warren, R., Weoden, H., Worley, F., Williams, G., Willaon, R., Wieczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederchausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the finished sequence as soon as it is available and the accession number will be preserved.

1 210237; contig of 210237 bp in length.
Location/Qualifiers
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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clone_end:T7"
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                                                                                                                                                                                                                                                                                                        (bases 1 to 210237)
                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
                                                                                                                                                                                                                                                                               Unpublished
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Rature norvegicus

Rature norvegicus

Rature norvegicus

Rature norvegicus

Rature norvegicus

Rature norvegicus

Sciurognathi; Muroides; Murinae; Rattus

1 (bases 1 to 239076)

Ruzny, D.Marie.

Rature norvegicus

Rature n
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HTG; HTGS PHASB1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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/note="clone_boundary
clone_end:Sp6
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                                                                                                                                                                                                                                                                                        end_sequence:BH360465"
208907. .210237
/note="wgs_end_extension
clone_end:Sp6"
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                                                                                                                                  end_sequence:BH360464"
                              /note="clone_boundary
clone_end:T7
2177. .144799
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AX467373.1 GI:21900603
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Worley, K.C.

Worley, K.C.

Worley, K.C.

Bujor Submission

Direct Submission

Baylor Plaza, Houston, TX 77030, USA

Direct Submission

Bylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:22857070.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/txt/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the eatimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence eads. Both end sequences and whole genome shotgun sequence cases. Both end sequence sequence reads. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome shotgun sequence cases.
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Parul,H., Perez,A., Perez,L., Ferantkoch,C.,
Plopper,F., Poindexter,A., Pepovic,D., Primus,B., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,B., Reeves,K., Regier,M.A., Raigh,R.,
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Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiss,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
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Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villssans,D., Waldron,L., Walker,B., Wang,J.,
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Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Proceedings of the state o
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NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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COMMENT

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 16-JUL-2002
4711 234810: gap of unknown length
4811 235924: contig of 1114 bp in length
5225 236024: gap of unknown length
6025 237314: contig of 11290 bp in length
7315 237414: gap of unknown length
7315 239076: contig of 1662 bp in length
7415 239076: contig of 1662 bp in length
7415 239076: contig of 1662 bp in length
7415 239076: contig of 1662 bp in length
7401 £1988 Rattus norvegicus"
7402 XIVE = "Cascon: 10116"
7616 April = "Cascon: 10116"
7617 11. 234810
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Matches:
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Mismatches:
Indels:
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Polypeptide
Patent: WO 0238612-A 3 16-MAY-2002;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers

    1260
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                                                                                                                                                                                                                                                                                                                                                /estimated_length=unknown
237315. .237414
/estimated_length=unknown
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/estimated_leng
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INV 21-SEP-2004

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AX821533

REFERENCE AUTHORS

TITLE

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PEATURES

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Direct Submission
Submitted (05-AR-2004) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
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Submitted (28-JUN-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
5 (bases 1 to 26599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-APR-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
6 (bases I to 26599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-UUL-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (21-SEP-2004) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
On Apr 5, 2004 this sequence version replaced gi:20198805.
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-NOV-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                 WormBase Consortium
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
                                                                                            U40187 linear INV
Caenorhabditis elegans cosmid F11H8, complete sequence.
                                                                                                                                                                                          Caenorhabditis elegans
Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
1 (bases 1 to 26599)
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Department of Genetics, Washington University
St. Icuis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-NOV-1995) Robert Waterston
4 (bases 1 to 26599)
                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 26599)
Menezes, S. and Menezer, S.
The sequence of C. elegans cosmid F11H8
Unpublished (2001)
661 TTCCTCTTCTTGCCTCGGGACGTACTG 687
                                                                                                                                                                                  Caenorhabditis elegans
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8 (bases 1 to 26599)
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                     PAT 10-DEC-2003
                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Pissipedia, Pelidae,
Pelinae, Pelis.
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Pelis.
                                                                                                                                                                                                                      Carroll, M.M., Kingsman, S.M. and Redchenko, I.M. MHC class I peptide epitopes from the human 5t4 tumor-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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Matches:
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                       DNA
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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AX821533
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Sequence 1 from Patent W003068815.
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Felis catus
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Best Local Similarity:
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Best Local Similarity:
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                                                 ACCESSION
VERSION
KEYWORDS
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ORGANISM
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Pred. No.:

ORIGIN

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source

FEATURES

REFERENCE AUTHORS TITLE

JOURNAL

Pred. No.:

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ORIGIN

SOURCE

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 32

셤 8

AX821548

St.

email: submissions@watson.wustl.edu and jes@sanger.ac.uk

IICE: This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections ce, or longer because we provide a small overlap between neighboring submissions

gene

8

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one ml3 subclone.

http://www.wormbase.org/db/seq/sequence?name=F11H8;class=Sequence For a graphical representation of this clone sequence and its

## NEIGHBORING CLONE INFORMATION

The 5' clone is C06E8, 2400 bp overlap; the 3' clone is R01H2, 200 bp overlap. Actual start of this clone is at base position 2397 of F11H8; actual end is at 11501 of R01H2.

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (Pr Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (communication), the (http://www.ddbj.nig.oc.jp/c-elegans/html/CE INDEX.html) and The C. elegans ORPeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proceins from Blacks analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kant's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Location/Qualifiers Res., 25, 955-964).

gene

SCOS

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12674. .12675
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Conservative: Mismatches: Length: Matches: Indels: 43.00 100.0% 77.8% 91.5% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: Score:

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4156. 6006
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Yersinia pestis CO92 putative hemolysin activator protein
encoded by GenBank Accession Number CAC91296"
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Qdsfyinvswdalntaysehpewfsglusgden"
                                                                27297 bp DNA linear BCT 24-FEB-2004 coli strain CL3 serovar Oll3:H21 pathogenicity island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shen,S., Mascarenhas,M., Rahn,K., Kaper,J. and Karmali,M.A.
Direct Submission
Submitted (14-APR-2003) Laboratory for Poodborne Zoonoses, Health
Canada, 110 Stone Road West, Guelph, Ontario NIG 3W4, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Bacteria, Protecbacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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gene encoded by GenBank Accession Number AE005311"
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gene encoded by GenBank Accession Number AE005311"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen, S., Mascarenhas, M., Rahn, K., Kaper, J.B. and Karmal, M.A. Bvidence for a Hybrid Genomic Island in Verocytotoxin-Producing Bscherichia coli CL3 (Serotype 013:HZ1) Containing Segments of EDL933 (Serotype 0157:H7) O Islands 122 and 48 Infect. Immun. 72 (3), 1496-1503 (2004)
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PAT 17-JUN-2003

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Nucleic acid molecule and polypeptide specific to intestinal hemorrhagic hemorrhagic pathogenic Escherichia coli 0157:H7, and method of use thereof Key Location/Qualifiers source 1.86248 /organism='Escherichia coli 0157:H7'.
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HIDEO HAYASHI,HIDEO SHINAGAWA,KOZO MAKINO,TETSUYA HAYASHI,SHIN
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CI2N15/09,CI2N15/09,A61K31/7088,A61K39/00,A61K48/00,A61P31/04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C07K16/12, C12M1/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/
                 BD184766
Nucleic acid molecule and polypeptide specific to intestinal hemorrhagic pathogenic Escherichia coli 0157:H7, and method of use
                                                                                                                                                                                                                                                              Nucleic acid molecule and polypeptide specific to intestinal hemorrhagic pathogenic Escherichia coli 0157:H7, and method of use Patent: JP 2002355074-A 2 10-DEC-2002; PRESIDENT OF UNIVERSITY OF TSUKUBA
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                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
[ Lobase 1 to 86248]
Hayashi, H., Shinagawa, H., Makino, K., Hayashi, T., Onishi, S., Hattori, M. and Kurokawa, K.
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Bscherichia coli 0157:H7
Bscherichia coli 0157:H7
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gvlgsqaslqissgtlmnqkgalkagtdmlleggdvsnqrgtlaagrdlnahlnvlen
                                                                                                                         LENRNSGDRGGVISQEPMILNAGTLDSTAGVLLSGDALSLTAGVVNNTSGQVVANGLL
GWNSQALNNQSGLIQGRGISINTAGQTLDNRRGTLNSLQBLTVSTGAMDNRGGTVGAK
TTADLSTTSLDNREGGRLVSEGBLRLHTGGLQNSHGQIQSVGDMLLNSVRGVVDNVSG
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SVAGNFLGNMANNLLVGANHEGHADSTTQSAVSAGNITIRDTQSQKQDVADLKRDAAH
ANQTLSPIFDREKEQQRLQQAQLIGBIGNQVADIARTEGQIAGEKAKRDPAALNQARA
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GGAVPYLAELIKQTTPDGAGRVATHAVVNAALSLAQGKNALAGAAGAATGEVVGMLAT
OMYGKPVSELSETEKQTVSTLATVAAGLAGGLVGDSGASAVAGAGSGKTTVENNALSF
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MIAGAWYLGSAASAGKVLGGGLLGLAANSGYQIYDLNQPQNANKSWDYLGSATSFTTG
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/gene="S5"
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Query Match:
DB:
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PAT 20-JUN-2002

Unclassified. 1 (bases 1 to 87563) Blattner, P.R., Burland, V., Perna, N.T., Plunkett, G. and Welch, R.

Unknown

ORGANISM

Percent Similarity:

RESULT 35

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Alignment Scores:

gene

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Score:

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from base 1100001 (AE005174 Escherichia coli O157:H7
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AROUS174_03 300
AROUS174_04 400
AROUS174_05 500
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AB005174_43
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Pred. No.:
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Unclosed fied.
Unclassified.
1 (bases 1 to 87563)
1 batter 1 to 87563)
Sequences 0. E. Oli 0157.
Patent: US 6855814-6 57 15-PRB-2005;
Wisconsin Alumni Research Foundation; Madison, WI
Location/Qualifiers
1. 87563
/organism="unknown"
/mol_type="genomic DNA"
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Sequences of E. coli 0157
Patent: US 6365723-A 57 02-APR-2002;
Location/Qualifiers
1. .87563
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                            AR637510 87563 bp I Sequence 57 from patent US 6855814. AR637510 AR637510.1 GI:62771252
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AE005174 02
AE005174 03
AE005174 05
AE005174 05
AE005174 06
AE005174 07
AE005174 07
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Pred. No.:
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AE005174 11/C
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AUTHORS
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from base 1400001 (BA000007 Escherichia coli 0157:H7
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BA000007 44
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Pred. No.:
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BA000007_26
BA000007_27
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AC091229 04
WPCOMMENT
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Birren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Barten, B., Linton, L., Bucklagalter, B., Brown, A., Burket, G., Baddwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Castle, A., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Perreira, P., Fitzhugh, W., Gage, D., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Jones, C., Kann, L., Karatas, N., Klein, J., MacWan, P., McCark, M., McKernan, K., McPheeters, R., McCartby, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connell, P., Piani, C., Pollara, V., Raymond, C., Riley, R., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vonsiller, H., Viel, R., Vo, A., Wilson, B., Wu, X., Myman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Travers, M., Trigillio, J., Direct Submission
                                                                                                                                                                                     134580 bp DNA linear HTG 27-APR-200 MA Spansone 13 Clone RPI1-354D13 map 13, WORKING DRAFT SEQUENCE, 22 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:7342149. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L7802
Center clone name: 354 D 13
Center clone name: Statistics
Sequencing vector: M13; M77815; 100% of reads
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Homo sapiens chromosome 13, clone RP11-354D13
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 Mismatches:
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AC025359.3 GI:7656790
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
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of AC091229 from base 400001 (AC091229 Rattus norvegicus clone CH
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Continuation (5 of 6
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Continuation {5 of 7
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AC091242_0
                AC091229_01
AC091229_02
AC091229_03
AC091229_05
AC091229_06
AC091229_07
AC091229_07
AC091229_08
AC091229_09
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                                            NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Quality coverage: 3.4 in Q20 bases; agarose-fp Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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contig of 1183 bp in length
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL BEFERENCE TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

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DEFINITION ACCESSION

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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                         SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or barin genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                              NEICHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
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Submitted (08-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 16, 2002 this sequence version replaced gi:22830488.
                                                                                                                                                                                                                                                        ROD 08-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (10ases 1 to 157393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 157393) McPherston, T.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-SEP-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Guarchontoglires; Glires; Rodentia; Guarchontoglires; Musinae; Mus. 1 (bases 1 to 15739)

Cordes, M., Haglund, K., Spalding, L., Schatzkamer, K. and
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                                                                                                                                                                                                                                   AC124199 157393 bp DNA linear ROD 08-N
Mus musculus BAC clone RP23-312B17 from 8, complete sequence
AC124199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mangiapanello, L.
The sequence of Mus musculus BAC clone RP23-312B17
Unpublished (2001)
2 (bases 1 to 157393)
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Summary Statistics
Center project name: M_BA0312B17
                                                                                                                                    120120 TTCCTCTACCTACCCAGAGATGTC 120097
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McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of Mus musculus
Unpublished (2001)
3 (bases 1 to 15793)
McPherson, J.D. and Waterston, R.H.
                                                      US-10-774-176-13 (1-9) x AC025359 (1-134580)
                                                                                                          œ
                                                                                                       1 PheLeuTyrLeuProArgAspVal
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                 AC124199.3 GI:25046693
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/note="Likely pseudogene (HMM Sc=33.19 / Sec struct Sc=-10.52)"

product="tRNA-Ser"

24108. .24261

repeat\_region

MAPPING INFORMATION: restriction digest

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HTG 19-JUN-2002
                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Gliree, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 184940)
                                                                                                                                                                                                                                                                                                                                                         AL672264 184940 bp DNA linear HTG 19-JUN-20
Mus musculus chromosome 16 clone RP23-407N15, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 18377 bases at least Q30
Consensus quality: 18492 bases at least Q30
Consensus quality: 184092 bases at least Q20
Insert size: 184440; sum-of-contigs
Insert size: 175303; 5.1% error; agarose-fp
Quality coverage: 17.17x in Q20 bases; sum-of-contigs Quality
coverage: 18.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41746: contig of 41746 bp in length 41846: gap of 100 bp 111308: contig of 6946 bp in length 111408: gap of 100 bp 114732: contig of 3224 bp in length 114732: gap of 100 bp 171805: gap of 100 bp 171805: gap of 100 bp 175266: contig of 3361 bp in length 175366: gap of 100 bp 184940: contig of 9574 bp in length 184940: contig of 9574 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://mrcseq.har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                  AL67266.2 GI:19309835
HTG; HTGS PHASE1; HTGS CANCELLED
Mus musculus (house mouse)
                                                      91227 TTTCTGTACCTGCCTAGAGATGTG 91250
US-10-774-176-13 (1-9) x AC124199 (1-157393)
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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AUTHORS
TITLE
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Matches:
Conservative:
Mismatches:
Indels:
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7.ppt family="Alu"
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43.00
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SOURCE
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lacture (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: vega@sanger.ac.uk Clone requeste: olone-request@sanger.ac.uk on May 20, 2001 this sequence version replaced gi:13356481.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 http://www.sanger.ac.uk/HGP/Christ RPI-11.2 constructed by the group of Pleter de Jong. Purther details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL354821 200087 bp DNA linear PRI 18-MAY-2005
Human DNA sequence from clone RPI1-538N17 on chromosome 13,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mismatches:
Indels:
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clone_end:T7
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Matches:
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Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Сарв:
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ragment chain:1"
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AL354821.21 GI:14160928
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1 (bases 1 to 200087)
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TITLE
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KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (Dases 1 to 20180)
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Admas, C., Alder, J., Angulano, D., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anglebechi, V., Aoyagi, A., Ayodeji, M., Barastead, M., Benammed, F., Balden, D., Bandaranaike, D., Barber, M., Barastead, M., Benammed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Brager, C., Bagan, A., Escetto, M., Eugene, C., Evans, C.A., Falle, T., Fernandez, S., Finley, M., Ganta, R., Garcia, A., Garrer, M., Guevara, W., Gunaranez, B., Haaland, W., Hawlak, P., Hawlers, R., Hanilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, S., Hladun, S.L., Hodgson, A., Hogues, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Sequence confirmed by AC025359. Sequenced by WIBR." 87417. .87635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACI10466 210180 bp DNA linear HTG 11-OCT-2002
Rattus norvegicus clone CH230-248B3, WORKING DRAFT SEQUENCE.
AC110466
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 300); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8209. .8302 _ _ _ MDES. Sequenced by WIBR." | 7/note="Sequence from AC025359. Sequenced by WIBR." | 7/190. .87416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Sequence from AC025359. Sequenced by WIBR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Clone_right_end: RP11-538N17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Clone_left_end: RP11-538N17"
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-774-176-13 (1-9) x AL354821 (1-200087)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-538N17"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.98e+03
43.00
100.0%
100.0%
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AL672244/c
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Submitted (13-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 210180)

33 At Genome Sequencing Consortium.

Direct Submission

34 Genemalited (11-0CT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 9, 2002 this sequence version replaced gi:21741386.

The sequence in this sesembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Mithin each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-seaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
             Holling, B., Howells, S., Hulyk, S., Hume, J., Idleblid, J., Jackbon, L., Jackbon, L., Jackbon, L., Jackbon, L., Jackbon, L., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Kelly, S., Kelly, L., Lebow, H., Levan, J., Levis, L., Liu, T., Liu, M., Liu, Y., Loulseged, H., Levan, J., Levis, L., Liu, S., Liu, J., Liu, M., Liu, M., Malloger, S., Longacre, S., Lopez, J., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Manjun, A., Mahneshwari, M., Mallodarine, M., Malloy, K., Martine, R., Mangum, B., Mangum, B., Mapua, P., Morris, C., Minja, R., Montemayor, J., Moore, S., Morris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, J., Peraz, L., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Pasternak, S., Radhlin, R., Reeves, K., Regier, M., Riggs, F., Railly, M., Ren, Y., Reuter, M., Richards, S., Shan, H., Shetter, W., Savery, G., Scherer, S., Scotle, R., Shateman, S., Shen, H., Shetty, J., Sodergren, E., Song, K.-Z., Sorelle, R., Sosa, J., Shateman, S., Shen, H., Shetty, J., Shvattebey, A., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Vals, R., Vals, R., Vals, R., Warsen, V., Walse, R., Warsen, J., Warren, R., Walser, R., Warsen, V., Walse, R., Walser, R., 
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 196785 bases at least 040
Consensus quality: 198352 bases at least 020
Consensus quality: 198352 bases at least 020
Statisted insert size: 200019; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgs-help@bom.tmc.edu
Contact: hgr-help@bom.tmc.edu
Center project Information
Center project name: GRNK
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Center code: BCM
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Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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COMMENT

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Direct Submission
Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2003 this sequence version replaced gi:24527417.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL672244 243114 bp DNA linear ROD 04-FEB-2003
Mouse DNA sequence from clone RP23-4318 on chromosome 16, complete
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html

* NOTE: This is a "working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 210180: contig of 210180 by in length.
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8
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Matches:
Conservative:
Mismatches:
Indels:
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| Organism="Rattus norvegicus"
|mol_type="genomic DNA"
| db xref="taxon:10116"
| clone="CH230-24883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1230
/note="wgs_end_extension
clone_end:Sp6"
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/note="clone boundary
clone_end:Sp6
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/note="clone_boundary
clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL672244.15 GI:28193396
HTG.
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100.0%
91.5%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                         During sequence assembly date is compared into overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSRORT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP HEALD or the RECIL-23 Mouse BAC Library and the RECIL-23 Mouse BAC Library and the RECIL-23 Mouse BAC Library and the sequence of the WORMPEP database can be found at the RECIL-23 Mouse BAC Library and the sequence of the WORMPEP database can be found at the RECIL-23 Mouse BAC Library and the sequence of the WORMPEP database can be found at the RECIL-23 Mouse BAC Library and the second the worm of the
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Rattus norvegicus clone CH230-unknown, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 247964)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,
                                                                                                                                                        During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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HTG; HTGS_PHASE1; HTGS_DRAPT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Matches:
Conservative:
Mismatches:
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                                         Web site: http://mrcseq.har.mrc.ac.uk
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                                                                              Contact: mouseg@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="RPCI-23"
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Center code: UK-MRC
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ORIGIN

FEATURES

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, M.L., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delagado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Daper, H., Degan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Beans, C., Farnandez, S., Finley, M., Flaggi, N., Porbes, L., Foster, M., Foster, P., France, C., S., Garner, T., Garza, M., Gebregocrgis, B., Geer, K., Gill, R., Grady, M., Guevra, M., Gebregocrgis, B., Geer, K., Gill, R., Grady, M., Hamilton, C., Hamilton, K., Harnandez, R., Hines, S., Hladu, S.L., Haddun, S.L., Hodgson, A., Hoguse, M., Hollins, B., Howells, S., Hladu, S.L., Hodgson, A., Hoguse, M., Hollins, B., Howells, S., Hlaw, J., Cardy, M., Hernandez, R., Molly, S., Kelly, S., Kelly, S., Kally, S., Man, S., Mayor, M., Marnandez, R., Mayor, M., Marnandez, R., Mayor, M., Marnandez, S., Mayor, M., Marnandez, S., Mayor, S., Kally, S., Mayor, S., Marren, R., Well, K., Walle, R., Marren, R., Well, K., Walle, R., Marren, A., Walle, R., Marren, A., Walle, R., Marren, A., Walle Submitted (10-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequence and the feature Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Unpublished 2 (bases 1 to 247964) Rat Genome Sequencing Consortium. Center project name: KZSP Direct Submission

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 211194 bases at least Q20
Estimated insert size: 204976; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                            1 28079: contig of 28079 bp in length
18080 28179: gap of unknown length
18180 51936: contig of 23757 bp in length
1819 52096: gap of unknown length
1819 520902: contig of 177866 bp in length
1819 235002: gap of unknown length
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1819 235971: gap of unknown length
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1819 241096: contig of 1034 bp in length
1819 247964: contig of unknown length
1819 247964: contig of 1768 bp in length
1819 247964: contig of 7768 bp in length
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Db 212028 TTCCTGTATCTCCTAGGGATCTG 212005 Search completed: April 25, 2006, 20:27:22 Job time : 3131.7 Becs

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protein

Run on:

Sequence:

Title: Perfect

Total number

88

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Adn38721 Cancer/an Adn08721 Cancer/an Adn08721 Antipoori Adr2544 Breaat ca Adn38510 Tumour-as Adv35098 Human CDN Ad430833 Human Full leng Ad430833 Human Full leng Ad430833 Human CDN Ad13083 Full leng Ad43083 Full leng Ad43083 Full leng Ad43083 Full leng Ad43083 Human CDN Ad126160 Human CDN Ad126169 Human CDN Ad126169 Human CDN Ad25198 Human TNF Ad26529 Human TNF Ad26529 Human TNF Ad265207 Oligonucl Abd4266 Oligonucl Abd4266 Oligonucl Abd4269 Oligonucl Abd4269 Oligonucl Abd4269 Oligonucl Abd4269 Oligonucl Abd4269 Human hCG Ad464289 Oligonucl Abd4289 Oligonucl Abd4289 Oligonucl Abd4289 Human Can Ad37319 Human Dol Abx8396 Corn ear-Ad36519 Human SIR Ad817919 Human SIR Ad81796 Human SIR Ad813101 Prokaryot Ad862019 Bacterial Adx1189 Plant full Adx1149 Plant full Adx11499 Plan
                               Abv99349 Human NOV
Abk87175 CDNA enco
Adb97513 Feline 5T
Adb97452 DNA encod
Aaa27058 Human 5T4
Apk87174 CDNA enco
Aab87174 CDNA enco
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Adj5629 Human cDN
Acc51052 Human bla
Abx76332 Lung canc
Add56197 Human LRR
Add56200 Human LRR
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Adx14584 Plant ful
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Ac156146 Human col
Abt07721 Breast ca
Abx76333 Lung canc
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203.123 Million cell updates/sec
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                                                                                                                              2006, 10:26:14 ; Search time 295.3 Seconds
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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73.9 4842 12 73.9 4842 12	73.9 4842 12 73.9 4842 12 73.9 4842 12 73.9 5010 4 73.9 5015 2 73.9 5015 2 73.9 5015 6 73.9 5015 6	73.9 651.46 2 73.9 6703 2 73.9 7924 6 73.9 7924 6 73.9 7921 4 73.9 10351 4 73.9 12706 4 73.9 12706 4 73.9 12706 14 73.9 12091 14 73.9 16091 14 73.9 19026 10	73.9 27781 10 73.9 29220 4 73.9 29220 4 73.9 29220 10 73.9 39220 10 73.9 33352 10 73.9 33352 10 73.9 33352 10 73.9 33352 10 73.9 33352 10 73.9 3558 14 73.9 3660 10	4 73.9 52211 11 ACN44892 4 73.9 65854 4 AAK86282 4 73.9 76798 6 ABN97454 4 73.9 76798 14 ADN50502 4 73.9 81905 6 ABC65024 4 73.9 81905 6 ABC67198 4 73.9 110000 2 AAT42063 11 4 73.9 110000 2 AAT42063 11 4 73.9 110000 10 ACF65386 09 4 73.9 110000 10 ACF65386 09 4 73.9 110000 10 ACF65386 10 4 73.9 110000 11 ABD32566 02 4 73.9 110000 12 ABN20250 4 73.9 110010 13 ABD32566 02 4 73.9 110218 11 ACN44744 7 73.9 11389 12 ADJ19197 7 73.9 112637 6 ABN83124 7 73.9 172637 6 ABN83124	
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us-10-774-176-12.p2n.rng

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Aat42223 Human TAT
Aat79597 TATA-bind
Abz13389 Arabidops
Aat58563 DNA seque
Aax56852 A. thalia
Aah17937 Human CDN
Aad34303 Human CDN
Aad34303 Human DWI
Aad134309 Human CDN
Ad31354 Plant Ful
Ad163169 Human Ova
Aac49880 Arabidops
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Ac13153 Arabidops
Adx50311 Plant ful
Adx17512 Arabidops
Adx5031 Plant ful
Adx17512 Arabidops
Adx5031 Rice cDN
Adx16583 Human CDN
Adx50577 Plant ful
Adx1786 Rat gene
Adx5326 Nuclear ful
Adx37268 Nuclear fal
Ach97334 Klebsiell
Aca28118 Prokaryot
Aca2064 Prokaryot
Aff00794 Bacrerial
Abn68764 Streptoco
Aa878645 DNA encod
Ab111645 DNA encod
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Ab119703 Drosophil
Acq70737 TATA-bind
Ab119703 Drosophil
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AAD34303
AD116268
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AAC40588
ADO81502
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ACL36459
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ADZ62274
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AAH13852
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## ALIGNMENTS

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Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                Bovine BST associated with lactation/muscle/fat deposition #5770.
                   ABX40605 standard; cDNA; 343 BP
                                                           (first entry)
                                                           20-FEB-2003
                                        ABX40605;
RESULT 1
         ABX40605
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Bos Taurus

US2002137139-A1

26-SEP-2002

24-SEP-2001; 2001US-00960352.

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The invention relates to a purified nucleic acid molecule associated with catation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences.

(C) appearing as ARX34836-ARX48947, or complements of them. Also included are if under to a promoter and a 3' non-translated sequence that acid linked to a promoter and a 3' non-translated sequence that cfunctions in the call to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and cf polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and cc fissue comprising a level or pattern of a molecule in a bovine cell or tissue complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) complementary nucleic acid permits the detection of the molecule; and (b) ceterating the level or pattern of the complementary nucleic acid permits the detection of the molecule; and complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the sequence or pattern of the complementary nucleic acid sequence acid sequence tago nucleic acid sequence complementary nucleic acid sequence tago nucleic acid sequence complementary nucleic acid sequence tago nucleic acid sequence acid sequence acid sequence tago nucleic acid sequence complementary nucleic acid sequence complementary nucleic acid sequence acid sequence complementary nucleic acid sequence complementar
                                                                                                                                                                                                                                                                                                                          New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                             Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 5770; 245pp; English.
                                                                                                                                                                                                                             Tao N,
12-JAN-1999; 99US-0115707P.
                                                                                                                                                                                                                             Byatt JC, Mathialagan N,
                                                                              (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                 WPI; 2003-110599/10.
                                                                                                                                           TAO N.
WARREN W C.
                                                                                                                                           (TAON/)
(WARR/)
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Sequence 343 BP; 40 A; 146 C; 108 G; 49 T; 0 U; 0 Other;

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w w o o o o
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       Length:
Matches:
Conservative:
Mismatches:
Indels:
      1.34
46.00
100.0%
100.0%
                               Best Local Similarity:
                        Percent Similarity:
Alignment Scores:
Pred. No.:
                                     Query Match:
DB:
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US-10-774-176-12 (1-9) x ABX40605 (1-343)

173 AACCTCTTCCTCACGGCAACCAGCTG 199 σ 1 AsnLeuPheLeuThrGlyAsnGlnLeu 셤 ਨੇ

ACL56146 standard; cDNA; 505 ACL56146 23235335<u>8</u>

RESULT 2

ACL56146;

BP

(first entry) 24-MAR-2005

Human colon cancer differentially expressed polynucleotide, SEQ ID:2281.

Differential expression; diagnosis; therapy; drug screening; cancer; neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;

Gene, ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.

2001US-0263965P. 2001US-0265928P. 2001US-00829472. 2001US-0282698P. 2001US-0288590P.

24-JAN-2002; 2002WO-US002242

24-JAN-2001; 09-APR-2001;

02-FEB-2001;

WO200259377-A2

01-AUG-2002

Unidentified

(EOSB-) EOS BIOTECHNOLOGY INC

Gish KC, Afar D;

Mack DH,

2002-583738/62.

N-PSDB; ABJ05564.

29-MAY-2001; 2001US-0294443P

09-APR-2001;

Breast cancer-associated gene sequence 29

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The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which are differentially expressed in colon cancer cells. The invention also relates to vectors and host cells comprising a differentially expressed polynucleotide of the invention; a method for detecting a cancerous phydiaucleotide of the invention; a method for detecting a cancerous cell by detection of a gene product of the polynucleotides; a method for inhibiting a cancerous phenotype of a cell by inhibiting a gene product of the polynucleotides; a method of treating an individual with cancer by administration of a medulator of a gene product of the polynucleotides; and an isolated antibody that specifically binds to a polypeptide encoded by one of the 9672 polynucleotides. The polynucleotides, polypeptides, antibodies, and methods are useful for the detection of cancerous cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the diagnosis, prognosis and management of cancer; for the diagnosis, prognosis and management of cancer; for the diagnosis, prognosis and management of cancer; for the identification of therapeutic targets for cancer chemotherapy; and for the treatment of cancer, especially colon cancer and metastasized colon cancer, but also breast or pancreatic cancer. The polynucleotides are also useful as a source of probes or primers for use in diagnostic methods. The differentially expressed polynucleotides or their encoded proteins can additionally be used as vaccines to modulate primary immune responses for the prevention or treatment of cancer. The present sequence represents a specifically claimed polynucleotide which is differentially expressed in colon cancer. Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                   New isolated polynucleotides, which are differentially expressed in colon cancer cell, useful for treating cancer, e.g. colon cancer, breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 505 BP; 68 A; 202 C; 149 G; 85 T; 0 U; 1 Other;
                                                                                                                                                                                                                      Garcia PD;
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2281; 97pp; English.
                                                                                                                                                                                                                      Escobedo J,
                                                                                                                                                                                                                                                                                                                  cancer, or pancreatic cancer.
                                                                                                                         13-MAY-2004; 2004WO-US015421,
                                                                                                                                                      03-JUN-2003; 2003US-0475872P
                                                                                                                                                                                                                      Randazzo F, Moler E,
                                                                                                                                                                                       (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                    WPI; 2005-075421/08
                                                            WO2005000087-A2
                             Homo sapiens.
                                                                                           06-JAN-2005
 88.
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Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast

Claim 9; Page 372; 414pp; English.

cancer nucleic acids

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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or preast cancer cells. Gor detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development, DNA sequences ABT0763 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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DB:
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Length: Matches: Conservative: Mismatches:

2.1 46.00 100.0% 100.0%

Score: Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

Indels:

AACCICITICCTIACCGGCAACCAGCIG 200

174

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RESULT

ABT07721 standard; DNA; 927

(first entry)

14-NOV-2002

ABT07721;

ABT07721 ID ABT1 XX XX ABT0 XX ABT0

AsnLeuPheLeuThrGlyAsnGlnLeu

US-10-774-176-12 (1-9) x ACL56146 (1-505)

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283 AACCTCTTCCTTACCGGCAACCAGCTG 309

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in cased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal lawing lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating a modulatory compound identified are insequenced to other benign or precancerous leasions, e.g. atelectasis, emphysema, bronchtis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchactasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences compounds that modulate lung cancer, such as antibodies. Sequences
                                                                              Lung cancer-associated polynucleotide, gene, ds; cytostatic, emphysema, attinflammatory, antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                          Lung cancer-associated polynucleotide #197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 336; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2002; 2002US-0372246P
                                                                                                                                                                                                                                                                                                                                                    18-APR-2002, 2002WO-US012476
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093161/08.
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02-APR-2003
                                                                                                                                                                                                                                                                                                         31-OCT-2002
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other; invention

927 Conservative: Mismatches: Length: Matches: Indels: 4.26 46.00 100.0% 100.0% Percent Similarity: Best Local Similarity Alignment Scores: Pred. No.: Query Match: DB:

AsnLeuPheLeuThrGlyAsnGlnLeu

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US-10-774-176-12 (1-9) x ADB80503 (1-927)
Percent Similarity:
Best Local Similarity:
                                                        Query Match:
                                                          JS-10-774-176-12 (1-9) x ABX76333 (1-927)
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Matches: Conservative: Mismatches: Indels: Gaps:

4.26 46.00 100.0% 100.0%

Length:

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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
blological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
determining tumour prognosis, early detection of pre-cancerous lesions,
and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                             cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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                                                                                                                               Ovarian cancer-associated transcript #34.
                                                                                                                                                                                                                                                                  cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 297; 332pp; English.
                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-0317544P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-2001; 2001US-0299234P.
                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002; 2002WO-US019297
                             ADB80503 standard; DNA; 927
                                                                                              (first entry)
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P-PSDB; ADB80504.
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                                                              ADB80503;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as anglogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting;
                                                                                                                                                                                                                              Human; differential expression; cancer; angiogenic disorder; librotic disorder; psortlasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                           detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                  Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glynne R, Hevezi PA;
B, Zlotník A;
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Wilson KE,
                               AACCICTICCITACCGGCAACCAGCIG 309
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            1 AsnLeuPheleuThrGlyAsnGlnLeu
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R, Watson SR,
                                                                                                         B
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14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347311P.
10-JAN-2002; 2002US-0347349P.
08-PEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355714P.
20-PEB-2002; 2002US-0359077P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0350666P.
2001US-0332464P.
2001US-0334393P.
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04-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
                                                                                                       ADN38723 standard; cDNA; 927
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2002US-0397775P.
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                                                                                                                                                                  (first entry)
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P-PSDB; ADN38724.
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Mack DH,
                                            283
                                                                                                                                     ADN38723;
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Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                                                      treating
                         polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as pecriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal anevascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
methods of screening for modulators of activity or expression of the
                                                                                                                                                                                                                                                                             Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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2001US-0274194P.
2001US-0274322P.
2001US-0274322P.
2001US-027449P.
2001US-0275578P.
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2001US-0275579P.
2001US-0275579P.
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2001US-0276994P.
2001US-0277239P.
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2001US-0278152P
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Best Local Similarity:
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12-MAR-2001;
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22-MAR-2001;
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23-MAR-2001;

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26-MAR-2001; 2001US-0278894P.
27-MAR-2001; 2001US-0278999P.
28-MAR-2001; 2001US-0279036P.
28-MAR-2001; 2001US-0279036P.
30-MAR-2001; 2001US-0279344P.
02-APR-2001; 2001US-028082P.
02-APR-2001; 2001US-028090P.
04-APR-2001; 2001US-028090P.
04-APR-2001; 2001US-028090P.
04-APR-2001; 2001US-028090P.
03-MAY-2001; 2001US-0289367SP.
03-MAY-2001; 2001US-0289367P.
03-MAY-2001; 2001US-0289367P.
03-MAY-2001; 2001US-0289342P.
03-MAY-2001; 2001US-0289342P.
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2001US-0312903P.
2001US-0318462P.
2001US-0318770P.
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2001US-0291190P.
2001US-0291099P.
2001US-0291240P.
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2001US-0299303P.
2001US-0299310P.
2001US-0304354P.
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2001US-0330380P.
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14-NOV-2001; 2001US-0332272P.
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03-DEC-2001; 2001US-0337426P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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18-JUN-2001)
19-JUN-2001)
19-JUN-2001)
10-JUL-2001)
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10-SEP-2001;
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16-MAY-2001;
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31-OCT-2001;
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Š Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ;
Boldog FL, Li L, Zerhueen BD, Tchernev VT, Gangolli EA, Vernet CAM,
Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK;
Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE,
Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.

Claim 16, Page 114-115; 619pp; English.

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABB70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disquosing diseases such as metabolic disorders, diabetes, obsesity, infectious diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 5T4, and the polynucleotide sequences encoding them. The 5T4 proteins are expressed in
disease, immune disorders, haematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunocherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                            Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                               therapeutic or diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK87175 standard; cDNA; 1260 BP
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                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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useful in a pharmaceutical commosition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammacory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus (es). The present sequence encodes feline 574 protein
significant proportion of tumours. The sequences of the invention are
888888888888888888888888
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                             Location/Qualifiers
1. .150
/+teg= a /product= "Peline 574 antigen protein"
       1260
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       Length:
Matches:
Conservative:
Mismatches:
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                                                               US-10-774-176-12 (1-9) x ABK87175 (1-1260)
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                                                                                                                               ADB97513 standard; DNA; 1260 BP
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      6.08
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                                                                                                                                                                               Peline 5T4 antigen DNA.
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P-PSDB; ADB97520.
                   Score:
Percent Similarity:
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Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                             Unidentified
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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further provides a polypeltope string comprising the 5T4 epitope; a mucleic acid sequence encoding the 5T4 epitope atring of the 5T4 epitope; a westor system capable of delivering the 5T4 epitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope, a polypeltope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 5T4 epitope in conjunction with an MHC class in molecule. The 5T4 epitope has cytostatic activity. The vaccine comprising the 5T4 epitope has cytostatic activity. The vaccine comprising the 5T4 epitope in its encoding nucleic acid and the vector system or call is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for diagnosing or presence of the 5T4 epitope or its mucleic acid. The T cell line or clone consense and for detecting the presence of the 5T4 epitope or its mucleic acid. The T cell line or clone consense.
                                                                                                                                                                                                                                                                                                                                                                               preventing a disease. This polynucleotide sequence represents the feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                    5T4 antigen coding DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 AACCTCTTCTCACCGGCAATCAGCTG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding feline 5T4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2003; 2003WO-GB000618
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46.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-663795/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
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Best Local Similarit
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90
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P-PSDB; ADB97455

major histocompatibility complex class I peptide epitopes from human tumor-associated antigen, useful for preventing and/or treating a

Disclosure, Page 67; 73pp; English

disease, particularly cancer.

Nev

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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 514 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for detecting the presence of a peptide or uncleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 574 protein.
           New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, TAA; tumour-associated antigen; anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                            Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 AACCICITCCICACCGGCAAICAGCIG 306
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                                                                  Disclosure; Page 49; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA27058 standard; DNA; 1263 BP
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99GB-00001739.
99GB-00017995.
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                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X444X8X000000000000X8
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Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.

(OXFO-) OXFORD BIOMEDICA UK LTD

Myers KA;

Carroll MW,

WPI; 2000-387735/33.

The present sequence encodes the human 5T4 tumour-associated antigen

Example 2, Page 78, 79pp, English.

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(TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metestasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen fueble can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bebbington CR, Carroll MW, Bllard FM;
                                                                                                                                                                             Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
                                                                                                                                                                                                                           1263
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                           AACCTCTTCCTTACCGGCAACCAGCTG 309
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                                                                                                                                                                                                                                                                                                                                         US-10-774-176-12 (1-9) x AAA27058 (1-1263)
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1. .1263
/*tag= a
/product= "5T4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bb
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02-MAR-2000; 2000GB-00005071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-343805/36.
P-PSDB; AAB83839.
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                                                                                                                                                                                                                                                          Percent Similarity:
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The specification describes the use of a single chain antibody (SCFV), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The SCFV and is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The SCFV antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system diseases including Parkinson's disease, periodontal diseases, cardiovascular
                                                                                                                                                     diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-related diseases, and other immune disorders. The present sequence encodes a 5T4 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                          Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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/product= "5T4 protein"
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Pred. No.:
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                                                                                                                                                                                                                                                                                                           Query Match:
DB:
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Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.

Claim 1; Page 67; 68pp; English.

(OXFO-) OXFORD BIOMEDICA UK LTD.

L3-NOV-2000; 2000WO-GB004317.

Myers K, Drury N, Carroll M;

WPI; 2002-557449/59. P-PSDB; AAU98693.

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concorderal leucine-rich glycoproteins known as 574, and the polymucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell compositions, in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(se). The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
               present invention relates to the isolation of canine and feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; p53 pathway; Leucine rich repeat capricious related protein;
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                                                                                                                                                                                                                                                                                                                                               Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 AACCTCTTCCTCACGGCAACCAGCTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 75-76; 99pp; English
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human LRRCAPS related DNA #6.
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Best Local Similarity:
Query Match:
DB:
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucilation is read of its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
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8888888888888888

Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                     AACCICITICCITIACCGGCAACCAGCIG 339
                                                                   Gaps:
                                                                                                              AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                                         UB-10-774-176-12 (1-9) x AAD56199 (1-1331)
         6.48
46.00
100.0%
100.0%
                                            Similarity:
                                 Percent Similarity:
Alignment Scores:
                                                                                                                                     313
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                                                        Query Match:
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No.:
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ADJ56299 standard; cDNA; 2020 BP

(first entry) 06-MAY-2004

ADJ56299;

Human cDNA differentially expressed in MYCN activated cells SeqID 105.

human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; 88; MYCN activated cell.

Homo sapiens.

JS2003119009-A1.

26-JUN-2003.

25-FEB-2002; 2002US-00084817

23-FEB-2001; 2001US-0270784P

STUART S G. NUCHTERN J G. PLON S E. SHOHET J M. (NUCH/) (PLON/) (SHOH/) STUA/)

Shohet JM; Plon SE, Stuart SG, Nuchtern JG,

WPI; 2003-635698/60

New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the

Claim 1; SEQ ID NO 105; 27pp; English

This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a proto-oncogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules RESULT 15
ADJ56299
ADJ56299
XX
ADJ56299
XX
ADJ56299
ADJ56

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as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the US Patent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to accept as 80 % identical to a table of sequences (see ACCS0951 to ACCS1059). ACCS0951 to ACCS1059 encode the human bladder cancer-associated proteins given in ABR48146 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bladder cancer associated cDNA sequence SEQ ID NO:192.
                                                                                                                                                                                                                      Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                    ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC51052 standard; cDNA; 2053
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-035066FP.
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ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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2053
9
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         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                            1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                          x ACC51052 (1-2053)
         10.7
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                           Percent Similarity:
Best Local Similarity:
                                                                          US-10-774-176-12 (1-9)
Alignment Scores:
Pred. No.:
                                             Query Match
DB:
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AACCICITCCITACCGGCAACCAGCTG 393 367

Bb. standard; DNA; 2053 RESULT 17 ABX76332 셤 

ABX76332; ABX76332

Lung cancer-associated polynucleotide #196.

(first entry)

02-APR-2003

Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

Unidentified

WO200286443-A2

31-0CT-2002

18-APR-2002; 2002WO-US012476

18-APR-2001; 2001US-0284770P. 10-MAY-2001; 2001US-0290492P. 09-NOV-2001; 2001US-0339245P. 13-NOV-2001; 2001US-0330666P. 29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P.

(ROSB-) EOS BIOTECHNOLOGY INC

Murray R; Aziz N, WPI; 2003-093161/08. P-PSDB; ABU56603. Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased cancer expression in lung

Claim 22; Page 335; 453pp; English

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological

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compound that patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancerassociated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous leadings, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of identifying a candidate p53 pathway
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Mismatches:
Indels:
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 2053
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Francis-Lang H, Friedman
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                                                                                                                                                                                                                                                                                 invention
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DB:
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other; gene therapy. The present sequence is human LRRCAPS DNA

2053 9 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

10.7 46.00 100.0% 100.0%

Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

Gaps:

US-10-774-176-12 (1-9) x AAD56200 (1-2053)

AACCTCTTCCTTACCGGCAACCAGCTG 393

367

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RESULT 20 ADN38721

ADN38721 standard; cDNA; 2053 BP

1 AsnLeuPheLeuThrGlyAsnGlnLeu

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modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
       888888888888888
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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Human; p53 pathway, Leucine rich repeat capricious related protein;
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Matches:
Conservative:
Mismatches:
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15-FBB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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                                                                                    Percent Similarity:
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Query Match:
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gnment Scores:
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110

AADS 6200

120

AADS 6200

120

AADS 6200

AADS 62
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39 Human; differential expression; cancer; angiogenic disorder;

17-JUN-2004 (first entry)

ADN38721;

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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gish KC, Glynne R,
Wilson KE, Zlotnik
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Murray R, Watson SR,
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2002US-0355250P.
2002US-0356714P.
2002US-0359077P.
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2001US-0335394P.
2001US-0340376P.
2002US-0347211P.
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2002US-0370110P.
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2002US-0397845P.
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20-FEB-2002;
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Mack DH,
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capticious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent—biased activity, where a citivity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in
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Plowman GD, Funke RP,

Belvin M, Schleithoff L, P Francis-Lang H, Priedman L;

WPI; 2003-421410/39.

EXEL-) EXELIXIS INC.

Disclosure, Page 76-77, 99pp; English.

Hevezi PA; A;

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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; antibodies which specifically bind a and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids is polypeptides, and methods are useful for diagnosing, prognosing and treating antibodies and other conditions such as psoriately, inschemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may
                                                              proteins (ADN38683-ADN40064)
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                                                                                                                                                                                                                                                                                                    also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                  Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                              invention relates to nucleic acids and
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Matches:
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                               Claim 8; SEQ ID NO 39; 1385pp; English
a nucleic acid in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-774-176-12 (1-9) x ADN38721 (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AsnLeuPheLeuThrGlyAsnGlnLeu
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2002US-0413192P.

2002US-0419008P.

2002US-0426847P.

2003US-0484959P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; cytostatic; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desauvage FJ, Frant
Spencer SD, Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-257144/24.
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Best Local Similarity:
Query Match:
DB:
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15-NOV-2002;
02-JUL-2003;
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23-SEP-2002;
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Pred. No.:
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P-PSDB; ADLO6552

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The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polymucleotide and polymeptide sequences. Also disclosed is an antibody that binds to a TAT polymptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for represents a human TAT CDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel polynuclectide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a
      New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                              Claim 1; SEQ ID NO 53; 319pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-774-176-12 (1-9) x ADL06473 (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AsnleuPheleuThrGlyAsnGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antipsoriatic cDNA sequence #180.
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                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                             Alignment Scores:
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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the disgnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
corresponds to one of the polynucleotides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; breast cancer; prognosis; gene expression; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 1305, 226pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                                                                                                                                                                                             367 AACCICTICCTIACCGGCAACCAGCIG 393
                                                                                                                                                                                                                        1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                                                                                                                                        US-10-774-176-12 (1-9) x ADN03961 (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                  Breast cancer prognosis marker #1305.
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                                                                                                                             Best Local Similarity:
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                                                                                              Score:
Percent Similarity:
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                                                              Alignment Scores:
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acids, an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide, and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
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                                                                    AACCTCTTCCTTACCGGCAACCAGCTG 393
                                           1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
US-10-774-176-12 (1-9) x ADR25444 (1-2053)
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                                                                                                                                                                           ACN38510 standard; cDNA; 2053
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                                                                                                                                                                                                                                                                  18-NOV-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer or tumor.
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Alignment Scores:

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Alignment Scores:

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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals caffected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as the treatment of neuropsychiatric and neurodegenerative disorders of this invention exhibit various activities including neuroleptic, continuals and autidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease signature, neuropsychlatric, neurodegenerative, schizophrenia,
bipolar affective disorder, BAD; autism, Parkinson's,
Alzheimer's disease, neuroleptic, nootropic, antimanic, antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schlzophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contexted with the test compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; 88; multi-parameter high throughput screening; MPHTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA of an exemplary efficacy gene for BAD SegID174.
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07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-0335150P.
14-NOV-2001; 2001US-033047P.
18-JAN-2002; 2002US-0349936P.
04-MAR-2002; 2002US-0361834P.
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Palfreyman M, Rajan P;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (I) is useful in gene therapy techniques to reserve normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cylypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in cepponsible for genetic disorders or other traits to assess biodiversity
differentially expressed in the presence of a therapeutic compound and represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                         Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                             2053
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                               AAS87175 standard; cDNA; 2338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631
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23-AUG-2000; 2000US-00649167.
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46.00
100.0%
100.0%
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P-PSDB; ABG22988.
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                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200175067-A2.
                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS87175;
                                                                                                                                 No.:
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Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the two-moton. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 Primers useful for synthesizing full length cDNA clones and their use
and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WTPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                             Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, full length cDNA; cDNA synthesis; oligo-capping; ss
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Matches:
Conservative:
Mismatches:
Indels:
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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P-PSDB; AAM93333.
                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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IID AAK6

AAK6
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonuclectide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
                                                                                                                                                                                                                                                                                                                                human, medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
           Length:
Matches:
Conservative:
Mismatches:
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                                                                   Indels:
                                                                                                                                                 106 AACCTCTTCCTTACCGGCAACCAGCTG 732
                                                                                                                                                                                                                                                                                                      Full length human cDNA clone SeqID 2864.
                                                                              Gaps:
                                                                                                           US-10-774-176-12 (1-9) x AAK94253 (1-2359)
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                                                                                                                                                                                                                    ADL30831 standard; cDNA; 2359
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-001183865.
07-JUL-2000; 2000RP-00114089.
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Best Local Similarity:
Query Match:
                                     Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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                                                                Query Match:
DB:
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            Pred. No.:
                                                                                                                                                                                           RESULT 28
                                                                                                                                                                                                          ADL30831
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ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

Human cDNA encoding protein that promotes STAT6 activation #64.

(first entry)

22-APR-2004

ADI26162;

ADI26162 standard; cDNA; 2361 BP.

ADI26162

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clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length CDNA easily without any special methods. The present sequence is a full length human cDNA of the three printed special close the sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T, Hayashi K, Ishii S, Kawai Y;
a T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                    Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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0
                                                                                     AACCTCTTCCTTACCGGCAACCAGCTG 732
                                                                                                                                                                                                                                                                   Human full-length cDNA, SEQ ID NO: 2866.
Gaps:
                                                                  1 AsnleuPheleuThrGlyAsnGlnLeu 9
                               US-10-774-176-12 (1-9) x ADL30831 (1-2359)
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The mucleic acid is useful for diagnosting a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening expressing the protein is useful for screening expressing the protein is useful for screening composition. A transformant compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation or inhibition of STAT6. The present sequence repressiblem of STAT6 activation.
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promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. signal transducer and activator of transcription 6 activation

Claim 4; SEQ ID NO 127; 1368pp; English.

diabetes and cancer.

Ishizawa K;

Muramatsu S,

Honda G,

Ř

(ASAH ) ASAHI KASEI

Sugahara T, Matsuda A,

WPI; 2004-122214/12 P-PSDB; ADI26163.

2002US-0385912P. 2002JP-00377326. 2002US-0436467P.

05-JUN-2003; 2003WO-JP007123

05-JUN-2002; 06-JUN-2002; 26-DEC-2002; 27-DEC-2002;

WO2003104277-A2 Homo sapiens

18-DEC-2003

15-MAY-2003; 2003JP-00137505. 16-MAY-2003; 2003US-0470836P.

Seguence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;

Alignment Scores:

708 AACCICITCCITACCGCCAACCAGCIG 734

AsnLeuPheLeuThrGlyAsnGlnLeu

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US-10-774-176-12 (1-9) x AAK94254 (1-2361)

2361 0 0 0 0

Length: Matches: Conservative: Mismatches:

12.6 46.00 100.0% 100.0%

Similarity:

Query Match:

Best Local

Percent Similarity:

Alignment Scores:

1 AsnLeuPheLeuThrGlyAsnGlnLeu 9

BP.

AAA27059 standard; DNA; 1281

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RESULT 32
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ID AAA2
                                                                                                                                                                                           %XCCCCCCCCCCXXX11X8X1X8X838X6X6X6X6X6XXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
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oligo-capping method; ss; gene.
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  Length:
Matches:
Conservative:
Mismatches:
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                                                                                               Indels:
                                                                                                                                                                                                                                       AACCTCTTCCTTACCGCAACCAGCTG 734
                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full length human cDNA clone SeqID 2866.
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-001183865.
07-JUL-2000; 2000BP-00114089.
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                                                Percent Similarity:
Best Local Similarity:
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                                                                                                 Query Match:
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ADLIA0833
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ADLIA0833
ADLIA0833
ADLIA083
ADLIA08
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Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.

(OXFO-) OXFORD BIOMEDICA UK LTD.

Carroll MW, Myers KA; WPI; 2000-387735/33.

99GB-00001739.

27-JAN-1999; 30-JUL-1999;

99WO-GB003859 98GB-00025303

18-NOV-1999; 18-NOV-1998;

25-MAY-2000.

WO200029428-A2 Mus musculus.

Mouse; TAA; tumour-associated antigen; anti-tumour; cytostatic; Immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;

Mouse 5T4 tumour-associated antigen gene

Mouse;

22-AUG-2000 (first entry)

AAA27059;

```
The present sequence encodes the mouse 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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Example 2; Page 78; 79pp; English.
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44.00
100.0$
88.9$
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ADI26160
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638 G; 533 T; 0 U; 0 Other;

Sequence 2361 BP; 506 A; 684 C;

2361 0 0 0 0

Conservative: Mismatches: Indels:

12.6 46.00 100.0% 100.0% 12

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores: Pred. No.:

Score:

US-10-774-176-12 (1-9) x ADL30833 (1-2361)

Length: Matches:

Mismatches:

Best Local Similarity:

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Bystemic lupus erythematosus; sepsis; asthma; allergic rhinitis;
ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS
                                                                             88; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; dlabetes; hyperlipidaemia; infection; cancer; Th1 hyperactive disease; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                         New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                           Human cDNA encoding protein that promotes STAT6 activation #63
                                                                                                                                                                                                                                                                                                                                        Ishizawa K;
                                                                                                                                                                                                                                                                                                                                        Muramateu S,
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ADI26160 standard; cDNA; 2557 BP
                                                                                                                                                                                                                                                    2002US-0385912P.
2002JP-00377326.
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15-MAY-2003; 2003JP-00137505.
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                                                                                                                                                                                                                     05-JUN-2003; 2003WO-JP007123
                                      (first entry)
                                                                                                                                                                                                                                                                                                                                        Sugahara T, Matsuda A,
                                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASBI KK.
                                                                                                                                                                                                                                                                                                                                                            2004-122214/12.
                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ADI26161
                                                                                                                                                                           NO2003104277-A2
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                              16-MAY-2003;
                                                                                                                                                                                                                                           35-JUN-2002;
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                                       22-APR-2004
                                                                                                                                                                                                18-DEC-2003
                  AD126160
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Claim 4; SEQ ID NO 125; 1368pp; English diabetes and cancer

The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression a activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases. Inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease. Compositions are also useful in rheumatoid arthritis, osteoarthitis, systemic lupus erythematosus, sepsis, asthma, allergic thinitis, ischaemic heart diseases, subarachnoid heemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive human chars and a protein and preventing disease associated with excessive human chars and a contrain and a protein has effectively useful for screening compounds for treating and preventing disease associated with excessive human chars and a contrain and a protein has effectively useful for screening compounds for treating and preventing disease associated with excessive human chars and a contrain a contrain a contrain a contrain a contrain and a contrain and a contrain a contrain and a contrain a contrain a contrain a contrain a contrain a human cDNA encoding a protein which promotes STAT6 activation

Sequence 2557 BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;

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2557
8
                          Conservative:
         Length:
Matches:
        37.1
44.00
100.0%
                          Percent Similarity:
Alignment Scores:
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useful for the producing an antibody, which involves administering the useful for the producing an antibody, which involves administering the useful for the producing an antibody, which involves administering the protein or is epitope-bearing fragments to a non-human animal as an antigen. The mucleic acid is useful for disgnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for grounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATE activation such as allergic diseases, inflammation, autoimmune diseases. Compositions are useful for treating disease associated with STATE activation and/or prevention for treating disease associated with STATE activation and/or prevention are treating disease. Compositions erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage,
                                                                                                                                                                                                                                                                                                                                                                   se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
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                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding protein that promotes STAT6 activation #62
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                 Indels:
                                                                                                                            838 AACCTTTCCTTACCGGCAACCAGATG 864
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                                    Gaps:
                                                                                                           AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                      US-10-774-176-12 (1-9) x ADI26160 (1-2557)
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                                                                                                                                                                                                                      BP.
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2002US-0436467P.
2003JP-00137505.
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88.9$
95.7$
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27-DEC-2002;
15-MAY-2003;
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                   Query Match:
DB:
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retrieved from the WIPO website.

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viral hepatitis and AIDS. The protein has efficient promoting STAT6 activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse; murine; cancer; psoriasis; ulcerative colitis; inflammation; ischaemic heart disease; thrombosis; immune disorder; bacterial disorder; viral disorder; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises 744 novel mouse DNA sequences (genes). The DNA sequences of the invention are useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischemic heart disease, thrombosis, immune disorders. bacterial disorders and viral disorders. The present nucleic acid represents a mouse DNA sequence of the invention. NOTE: The present DNA sequence is not shown in the specification, but has been
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heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mouse nucleic acid molecules and polypeptides, useful for cancer, psoriasis, ulcerative colitis, inflammation, ischemic disease or thrombosis.
                                                                                         512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;
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                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                        AACCTTTTCCTTACCGGCAACCAGATG 864
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                                                                                                                                                                                                                                                                        AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                                                                                                                                                                                           (1-2557)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FIVE-) FIVE PRIME THERAPEUTICS INC.
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05-DEC-2002; 2002US-0431145P.

05-DEC-2002; 2002US-0431605P.

09-UN-2003; 2003US-047662IP.

09-UN-2003; 2003US-047663IP.

08-UUL-2003; 2003US-04852IPP.

08-UUL-2003; 2003US-04852IPP.
                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel mouse gene sequence #612.
                                                                                                                                                                                                                                           US-10-774-176-12 (1-9) x ADI26158
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                                                                                                                                                                                                                                                                                                                                                               AD035939 standard; DNA; 2557
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44.00
100.0%
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                                                                                         Sequence 2557 BP;
                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 35218.
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Sequence 2557 BP; 610 A; 794 C; 688 G; 465 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                    AACCTTTTCCTTACCGCAACCAGATG 37
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                                                                                                                                                                                                                                                     ABL27915 standard; DNA; 2820
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11-JUL-2000; 2000US-00614150.
                                      37.1
44.00
100.0$
88.9$
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100.0$
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91.3$
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                              Alignment Scores:
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                                                                                                                                                                                                                                                                                 ABL27915;
                                                                                               Query Match:
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Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                   Human TNFSF11 carcinoma associated gene, SEQ ID NO:1316.
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ADA02798 standard; DNA; 52754 BP.
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                                                                                                 06-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                         WO2003057146-A2
                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morris DW;
                                                  ADA02798;
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 35215.
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Gaps:
                                                                                                                                 864 AATCTATTTCTCACTGGGAACCAA 887
                                            US-10-774-176-12 (1-9) x ABL27915 (1-2820)
                                                                                               1 AsnLeuPheLeuThrGlyAsnGln 8
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
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ABL:7914,
AC ABL:
AC ABB:
AC
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acid sequences from mouse and human (ADAD1482-ADAD3034), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, inpubora or leukaemia) or a propensity to carcinoma by determination of the sequence carcinoma carcinoma cardia, proteins and antibodies are also useful as therefore of the invention. Note: The complete sequence data for this sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52754 BP; 15093 A; 10533 C; 11422 G; 15706 T; 0 U; 0 Other;
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Length:
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Gaps:

42.00 100.0% 100.0% 91.3%

Best Local Similarity:

Percent Similarity:

Alignment Scores:

3355 AATCTATTTCTCACTGGGAACCAA 3332

RESULT 38 ADA02798

1 AsnLeuPheLeuThrGlyAsnGln 8

US-10-774-176-12 (1-9) x ABL27914 (1-5278)

RESULT 39

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(MORR/) MORRIS D W.
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                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid, useful for treating carcinomas, lymphomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 52754 BP; 15093 A; 10533 C; 11422 G; 15706 T; 0 U; 0 Other;
                                                                                                                                                                                    is, cytostatic; gene therapy; vaccine; carcinoma; lymphomas; neoplasm; adenocarcinoma; sarcoma; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2001; 2001US-000041113.
08-NOV-2001; 2001US-0052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-0034650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAGR-) SAGRES DISCOVERY
                         ADB72536 standard; DNA;
                                                                                                                                                                                      ds, cytostatic;
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                                                                                                                                              Human TNFSF11 gene
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                   Homo sapiens
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New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
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02-MAR-2001; 2001US-00798586.
02-DEC-2002; 2002WO-US038582.
                                                            30-NOV-2001; 2001US-00997722.
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                                                                                                                                                                              Engelhard EK;
                                                                                                                        (SAGR-) SAGRES DISCOVERY
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The invention relates to new recombinant nucleic acids. The invention also relates to a host cell comprising a recombinant nucleic acid or expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a method of screening for a bioactive agent capable of modulating the actroinmed actually of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of diagnosing carcinoma or propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a corporation or activation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprising the nucleotide sequence. A method of diagnosing carcinoma comprising the nucleotide sequence. A method of diagnosing carcinoma comprising the nucleotide sequence. A method of diagnosing carcinoma comprising the expression of method of diagnosing carcinoma comprising the expression of the gene from a second normal tissue type from the first individual and comparing the expression of the gene from the first individual has carcinoma. A method of inhibiting the carcinomas comprises administering to a patient an inhibitor of CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The protein encoded by the nucleic acid. The nucleic acid are useful for protein and promaring an agent for the capacitor of the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preparing a composition for diagnosing or treating carcinoma e.g., leukaemia or lymphoma. This sequence represents a human carcinoma associated (CA) nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was
                                                                                                                                                                          New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 64; 29pp; English.
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                                                        Worris DW, Engelhard EK;
(ENGE/) ENGELHARD B K.
                                                                                                                    WPI; 2004-328562/30.
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Sequence 52754 BP; 15093 A; 10533 C; 11422 G; 15706 T; 0 U; 0 Other;

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        Length:
Matches:
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                                 Mismatches:
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       5.49e+03
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Alignment Scores:
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US-10-774-176-12 (1-9) x ADM74393 (1-52754)
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16134 CACCTATTCTTAACAGGCAATCAGCTA 16160 1 AsnleuPheleuThrGlyAsnGlnLeu

ADZ12653 standard; DNA; 65274 BP ADZ12653; ADZ12653 2×2×2×2×2×2

(first entry) 16-JUN-2005

Human cancer-associated genomic DNA #14.

Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;

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the antigen or its antigen binding fragment, a composition comprising the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of thinbiting expression of a CA nucleic acids. The antibody is useful for detecting for detecting CA nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA crost from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the cancer cells in an individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer and for inhibiting expression of a CA gene in a cell. This sequence represents human cancer—associated genomic DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid array useful for detecting cancer associated nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid array for detecting a cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises two or more nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 173; 198pp; English.
                                                                                                                                                                                          23-SEP-2004; 2004WO-US031617.
                                                                                                                                                                                                                                        23-SEP-2003; 2003US-00669920
                                                                                                                                                                                                                                                                                                                                        Malandro MS;
cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-273395/28.
                                                                                          WO2005031001-A2
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                                               Homo sapiens.
                                                                                                                                          07-APR-2005
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Conservative: Mismatches: Indels: Length: Matches: US-10-774-176-12 (1-9) x ADZ12653 (1-65274) 7.03e+03 41.00 100.0\$ 88.9\$ 89.1\$ Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

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ABL14244 standard; cDNA; 37091 BP. ABL14244

RESULT 43

ABL14244;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 37214.

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us-10-774-176-12.p2n.rng

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide for detecting cytosine methylation SEQ ID NO 29197.
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                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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ADF77343_13
ADF77343_14
ADF77343_15
ADF77343_16
ADF77343_19
ADF77343_19
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                       Query Match:
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ABQ42606/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                            Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 37214; 21pp + Sequence Listing; English.
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Matches:
Conservative:
Mismatches:
Indels:
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11-JUL-2000; 2000US-00614150.
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87.0%
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P-PSDB; ABB70141.
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CONLINUATION

WP Sequence By
WP ADF7734

WP ADF7734
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particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the for determining the degree odisclosure of the invention 888888888888

Sequence 792 BP; 119 A; 94 C; 297 G; 282 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 39.00 88.9 88.9 84.8 Percent Similarity: Best Local Similarity: gnment Scores: Query Match: Alignment S Pred. No.:

x ABQ42606 (1-792) US-10-774-176-12 (1-9)

166 AACCICITICCITACCGACAACCAACTA 140 6 AsnLeuPheLeuThrGlyAsnGlnLeu

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ABQ42607 standard; DNA; 792 BP 셤

ABQ42607;

(first entry) 12-JUL-2002

Oligonucleotide for detecting cytosine methylation SEQ ID NO 29198

drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; Human; cytosine

Homo sapiens

WO200218632-A2

07-MAR-2002

01-SEP-2001; 2001WO-EP010074

01-SBP-2000; 2000DB-01043826. 05-SBP-2000; 2000DB-01044543.

(EPIG-) EPIGENOMICS AG.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA. WPI; 2002-371829/40.

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Guetig

Berlin K,

ပဲ

Piepenbrock

olek A,

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least noe member of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs 

nervous, cardiovascular, gastrointestinal and respiratory systems etc...particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABO13410-ABO44121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disorders of the central Sequence 792 BP; 282 A; 297 C; 94 G; 119 T; 0 U; 0 Other; 792 8 0 1 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: a wide range of diseases, e.g. cancer, disclosure of the invention 1112 39.00 88.9% 88.9% 84.8% Best Local Similarity: Percent Similarity: Alignment Scores: ij Query Match: 88666666666888

(1-792)US-10-774-176-12 (1-9) x ABQ42607

AACCTCTTCCTTACCGACAACCAACTA 653 σ 1 AsnLeuPheLeuThrGlyAsnGlnLeu

ABQ42584/c RESULT 47

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ABQ42584 standard; DNA; 795

BP

ABQ42584;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 29175.

Human, cytosine methylation, 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens

WO200218632-A2.

07-MAR-2002

01-SEP-2001; 2001WO-EP010074

01-SEP-2000; 2000DE-01043826. 05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG

ä Guetig Berlin K, Olek A, Piepenbrock C,

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons comprises losis and prognosis, com chemically treated DNA. diagnosis from chemi

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of

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oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (ii) for differentiation of cell or tissue types and for stratus of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                        Sequence 795 BP; 132 A; 94 C; 313 G; 256 T; 0 U; 0 Other;
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Best Local Similarity:
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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA. Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. Guetig D; Berlin K, 01-SEP-2001; 2001WO-EP010074. 01-SEP-2000; 2000DE-01043826 05-SEP-2000; 2000DE-01044543 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2002-371829/40 WO200218632-A2 Homo saptens 07-MAR-2002 

Claim 1; SEQ ID NO 26835; 122pp; English

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG<sup>21</sup>, present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

Claim 12; 56pp + Sequence Listing; 56pp; German.

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
degree of hybridisation to both classes is determined from the label on the analysicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
                                                              and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation abgains of many C residues to be determined simultaneously. AbQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; acoudit tolerance; heat tolerance; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polynucleotide; gene; ss.
                                                                                                                                                                                                                                     Sequence 795 BP; 256 A; 313 C; 94 G; 132 T; 0 U; 0 Other;
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39.00
88.9*
88.9*
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SLATER S C.
CHEN X.
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Best Local Similarity
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Oligonuclectide for detecting cytosine methylation SEQ ID NO 29176.

(first entry)

12-JUL-2002

ABQ42585;

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymuclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising an improved property. The plant is a crop plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maigned property comprises transforming a plant with the ecombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant with the polymucleotide or polypeptide is useful for producing plant properties. The recombinant DNA construct is useful for producing plant with the collected or polypeptide, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmocit conditions up pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or updake, by modification of protein yield and/or content, improved plant growth and development under at least one stress condition. This sequence represents a bacterial polymuclectide used in the scope of the invention. Note: The sequence data for this patent did formar from INPAD at sendata many proved plant growth was obtained in electronic formar from INPAD at sendata many proved plant many proved plant propertication between the plant propertication between the plant propertication between the plant propertication between the sequence represents a bacterial polymuclectide used in the formal propertication between the plant propertication between the plant propertication between the plant propertication between the plant propertication between the
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Conservative:
Mismatches:
Indels:
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24-FRB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-018930P.
17-MAR-2000; 2000US-0189374P.
17-MAR-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0205515P.
07-JUN-2000; 2000US-0205515P.
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Pred. No.:
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DB:
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2000US-0225757P.
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Barash SC, Ruben SM; Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 25737; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM9921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to

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supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the uncleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK8764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1000

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Database

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14 AC103202 AC103202 Rattus 14 AC056280 AC056280 Rattus 14 AC05805 AC05605 Rattus	14 AC1054159 AC054159 14 AC105600 14 AC105600 AC107404 14 AC105498 AC107404 14 AC105498 AC105498 14 AC10552 AC1420595 14 AC120595 AC120599 14 AC120509 AC1623509 14 AC162352 AC1623509	14 AC136646 14 AC097042 14 AC09142 14 AC116235 14 AC111885 14 AC111885 14 AC11685 14 AC16474 14 AC09445 14 AC09478		14 AC131350 14 AC091513 14 AC095513 14 AC10554 14 AC115513 14 AC115570 14 AC122969 14 AC02749 14 AC027165	ALIGNMENTS  graph DNA linear PAT 12-DEC-2003  Gr:39838931  (human)  hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	and Afar,D. s of breast cancer, compositions and ators of breast cancer -A 57 01-AUG-2002; Lalifiers "Homo sapiens"
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OS Homo sapiens (hunan)
PN JF 2002530060-A/1
PD 17-SFP-2002 1902 2000582415
PP 18-NOV-1999 GB 9901739.4 PR 18-NOV-1999 GB 9917995.4
PR 18-NOV-1999 GB 9917995.4
PP MILES WILLIAM CARROLL, KEVIN ALAN MYERS
PC C1ZN15/09, A61K39/00, A61K48/00, A61P35/00, C07K19/06, C07K19/00, PC C12N15/00
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OXFORD BIOMEDICA LTD
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  Carroll, M.W. and Myers, K.A.
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Mammalia, Butheria, Laurasiatheria, Carnivora, Pissipedia, Pelidae,
Pelinae, Pelis.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1263)
                                                                                                                                                                                                                                                                                                                                   linear
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Indels:
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. .1260
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Sequence 1 from Patent W003068815.

AX821548.1 GI:39724930
                                                                                                                                                                                                                                              280 AACCTCTCCTCACCGGCAATCAGCTG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AsnleuPheLeuThrGlyAsnGlnLeu 9
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Homo sapiens (human)
Homo sapiens
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Pelis catus
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Polypeptide.
BD249731
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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1263 9 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

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PAT 15-SEP-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                       Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
1. 1263
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Matches:
Conservative:
Mismatches:
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                                                                                  Sequence 1 from Patent WO0029428.
AX025011
AX025011.1 GI:10184932
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283 AACCTCTTACCGGCAACCAGCTG 309
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PAT 16-JUL-2002
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Canis sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Buthería, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 03-FEB-2004
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Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                             DNA
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                                                                                                                                                                                                                                                                                              Polypeptide
Patent: WO 0238612-A 116-MAY-2002;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 1 from Patent W00238612.
AX467371 GI:21900602
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             US-10-774-176-12 (1-9) x AX316086 (1-1263)
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CQ731678.1 GI:42308932
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Homo sapiens
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Best Local Similarity: 1
Query Match:
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CQ731678
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                              Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W.,
Ellard, F.M. and Myers, K.A.
Antibodies
                                                                                    linear
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Matches:
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Indels:
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/nole="5T4"
                                                                                    DNA
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PA
                                                                                                                                                      synthetic construct
synthetic construct
other sequences, artificial sequences.
                                                                                                                                                                                                                                                       Patent: WO 0136486-A 14 25-MAY-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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AX316086 1 from Patent RP1160323.
AX316086.1 GI:17899278
Gaps:
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Homo sapiens
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Pred. No.:
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AX149553
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AX316086
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BD127282 2359 bp DNA linear PAT 18-SBP-2002 Primer for synthesizing full-length cDNA and use thereof. BD127282
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JP 2002017375-A/2713
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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JP 2002017375-A/2713.
Homo sapiens (human)
Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
I (bases I to 2359)
Ota T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koga,H.
Trimer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Conservative:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
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Pred. No.:
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                                                          misc_RNA
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SHRTYLVBROVLAQLBELLHULGSNBSLVSLTYSPRULTHESELHLESBLHEDDNALKVTHNG
TLABLQGLBHIRVELDINNPWVCDCFBADMVTMLKETEVVQGKORLTCAYPERGRNRVL
LELNSADLDCDPILPPSLQTSYVPLGIVLALIGAIFLLVLYLNRGIKKWMHNIRDAC
                                                                                                                                                                                                                                                                                        PRI 18-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer
Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryogycan, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukamalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 2053)

Myers, K.A., Rahl-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.

1 solation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains J. Biol. Chem. 269 (12), 9319-9324 (1994)
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                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                             2053 bp RNA linear
Homo sapiens 5T4 gene for 5T4 oncofoetal antigen.
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373. .966
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Length:
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Conservative:
Mismatches:
Indels:
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5T4 gene; 5T4 oncofoetal antigen.
Homo sapiens (human)
Homo sapiens
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misc_RNA
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HS5T4OA
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BD127283 2361 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof.
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
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Homo sapiens (human)
Homo sapiens (human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 2361)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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HELIX RESEARCH INSTITUTE
OS Home sapiens (human)
PN JP 2002017375-A/2714
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
ALAVLPAGAFRRPPLARLAINLSGSRLDGVRAGPFEHLPSIAQLDLSRPPLADLSPP
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                                                                                                                                                      PAT 17-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS/
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LELNSADLDCDPILPPSLQTSYVPLGIVLALIGAIFLLVLYLYLNRKGIKK"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                   Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004; Research Association for Biotechnology (JP) Location/Qualifiers
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                      CQ782724 2864 from Patent EP1396543.
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                                                                706 AACCTCTTCCTTACCGGCAACCAGCTG 732
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              US-10-774-176-12 (1-9) x BD127282 (1-2359)
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US-10-774-176-12 (1-9) x AX961916 (1-2361)
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AK074790
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ALAVDAGARRRPPLALALINLSGSRLDBVRAADRAFREILPSLAQLDLSHPLADLSPF
AFGSSNASVSAPSPLYELI LAHT VPPEDERQORSFEGHVAALLAGRALGGLRSLELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /proteIn id="CAP85961.1"
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RDHMEGYHYRYEINADPRLTNLSSNSDV*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 17-MAR-2004
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C C12P21/02,C12Q1/68//C12P21/08,G06P17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers

T CDS
Location/Qualifiers
Location/Qualifiers
                                                                 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
   PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2866 10-MAR-2004; Research Association for Biotechnology (JP)
Location/Qualifiers
   YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
                                                                                                                                                                                                                                                                                                   2361
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Matches:
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426..1688
                                                                                                                                                                                  1. .2361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708 AACCTCTTCCTTACCGGCAACCAGCTG 734
PI YURI AAN......
SHINICHI KOJIMA,
PI TERSUJI OTSUKI,HISASHI KOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koga, H.
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Pred. No.:
Score:
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DB:
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                    FEATURES
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AFSGSNASYGAPSPLVELILMHIVPPEDERQNRSFEGMVVAALLAGRALQGERELELA
SNHFLYLPRDVLAQLPSLRHIDLSNNSLVSLTYVSFRNLTHLESLHHEDNALKVLHNG
TAZELGGEHRIRVELDNNPWCDCHMADMYTMLKETEVVQGKORLTCAYPEKMRNVL
LEINSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLGAIFLLYLYLNRKGIKKWMHNIRDAC
RDHMGGYHYRYEINADPRLTNLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLFBVPTDLPAYVRNLFLTGNQ
LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPF
                                                                                                                                                                                                                                                                                                           PAT 14-JAN-2004
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                              linear
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Indels:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualiffers
1. 2361
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Seguence 127 from Patent WO03104277.
AX961916
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                                                                                                                                                                                          708 AACCTCTTCCTTACCGGCAACCAGCTG 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708 AACCTCTTCCTTACCGGCAACCAGCTG 734
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KEYWORDS
SOURCE
ORGANISM
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Hominidae, Homo.

Straubsberg, E.L., Felngold, E.A., Grouse, L.H., Derge, J.G.,
Klausner R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavan, T.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mulahy, S.J., Bosak, S.A., McKenn, P.L.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Garcia, A.M., Madan, A., Kodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing waryland;

Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Shther,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karline,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-SBP-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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On Aug 19, 2003 this sequence version replaced gi:22713382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                           REFERENCE
AUTHORS
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TITLE
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3 (bases 1 to 2381)

5 sogai, T. and Otsuki, T.

6 lirect Submission

1 Submitted (15-MRA-2002) Takao Isogai, Helix Research Institute,

1 Submitted (15-MRA-2002) Takao Isogai, Helix Research Institute,

2 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba, 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

8 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Rey Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2379 bp mRNA linear PRI 29-JUN-2004 Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317 IMAGE:4138906), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                         Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawat-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Atsuka, S., Sagaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                     Oceuki, T., Ota, T., Nishikawa, T., Hayashi, K., Suzuki, Y., Yamamoto, J., Wakamateu, A., Kimura, K., Sakamoto, K., Hatano, N., Yawai, Y., Ishii, S., Saito, K., Kojima, S., Sugiyama, T., Ono, T., Okawai, Y., Ishii, S., Saito, K., Kojima, S., Sugiyama, T., Ono, T., Okumura, K., Nagai, K., Sugano, S. and Isogai, T., Sugano, S. and Isogai, T., Sugano, Trap in silico for Selection of Full-Length Human cDNAs Encoding Secretion or Membrane Proteins Erom Oligo-Capped cDNA Libraries
DNA Res. 12, 117-126 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
   Mammalia, Butheria, Buarchontoglires, Primates; Catarrhini;
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Mismatches:
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Clone distribution: clone distribution information can be found at:
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Hashimoto, K., Kusuda, J. and Sugano, S.
Hashimoto, K., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku-ku, Tokyo, 162-8640, Japan (E-mail: khashimohih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)
The International consortium for macaque cDNA sequencing and analysis consists of: Department of Virology and Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan; Division of Genetic Resources, National Health Research Institute, Taipei, Taiwan; Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan; Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA; Center for Information Biology, National Institute of Genetics of Japan, Mishima, Japan.
                                                                                                                                                                                                                                                                       AFSGSNASVSAPSPLVBLILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
SNHFLYLPRDVLAQLPSLRH.DLSNNSLVSLTYVSFRNLTHLBSLHLEDNALKVLHNG
TLABLQGLPHIRVFLDNNPWCDCHMADMYTMLKETEVVQGKDRLTCAYPEKMRNYL
LELNSADLDCDPILPPSLQTSYYFGIVLALIGAIFLLUXLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTYLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB168308 2714 bp mRNA linear PRI 18-JUN-2005 Macaca fascicularis testis CDNA clone: QtsA-11109, similar to human trophoblast glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 International consortium for macaque cDNA sequencing and analyais. DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications
                                                                                                                                                                                                                         APFLASAVSAQPPLPDQCPALCECSBAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
LAVLPAGAFARRPPLABLAALMLSGSRLDBVRAGAFEHLPSLRQLDLSHNPLADLSPP
                                                                                                                                                                                                    translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSPSSS
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
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                                              /codon_start=1
/product="5T4 oncofetal trophoblast glycoprotein"
/protein_id="AAH37161.1"
/db_xref="G1:22713383"
/db_xref="GeneID:7162"
/db_xref="GeneID:7162"
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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R. Sitel: Drail! (CACTGTG)

R. Sitel: Drail! (CACTGTG)

R. Site2: Drail! (CACTGTG)

Bescription: late strand cDNA was primed with an oligo(dT) primer lates: brail! (CACCATGTG)

Description: late strand cDNA was primed with a synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct Drail! sites of pME18S-FL3. Xho! sites just outside the Drail! sites can be used to isolate the CDNA insert. Libraries were constructed by oligo-capping method. Libraries were made from: QCCB: Cerebellum cortex

QnpA: pemporal lobe

QtrA: temporal lobe right

QflA: frontal lobe right

QflA: frontal lobe left

QflA: frontal lobe left

QmA: medial ablongata
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LAVLPAGAFRRPPLALAINLSGSRLDSWGGAFREILPSRGLDLSHGDLPLYTSPR
LAVLPAGAFRRPPLALINGSREILDSWGGAFREILPSRGLDLSHGLDLSHTBLALBLA
SNHFLYLPRDVLAQLPSLYLLINH IVPPDDKRQNRSFEGWYAAALVAGRALGALHLELLA
SNHFLYLPRDVLAQLPSLRYLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
TLAELGGLPHYRVFLDNNPWVCDCHAADWTWLKQTGVVGGKDRLTCAFPEKWRNYL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLGAIFLKFDAC
RDHWGGYHYRXEILDDPLTNLSSNSDV*
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glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3"
/codon start=1
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5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Homo eapiens (human)
Homo eapiens
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/dev_stage="adult"
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                                                            pME18S-FL3 (Acc.No. AB009864)
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OorA: occipital lobe right
OtsA: testis
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/db_xref="G1:67967900"
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/db_xref="taxon:9541"
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                                                                                                                                         Direct Submission
Submitted (13-0CT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                            King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine tissues
Biochim. Blophys. Acta 1445 (3), 257-270 (1999)
10366710
2 (bases 1 to 5551)
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Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, honore:OSJNBb0035N08.
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LELASADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLUVLYLNRKGIKKWMENIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
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Oryza sativa (japonica cultivar-group)
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                                                           109639. .116836
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VERSION
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. Benail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Dec 15, 2000 this sequence version replaced gi:11558491.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm:, EMBL; Sw:, SWISSPROT; Tr:, TREWBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group.

Http://www.sanger.ac.uk/HGP/Chr6

RP3-432P14 is from the library RPCI-3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                       HSJ492P14

121909 bp DNA linear PRI 18-MAY-2005

Human DNA sequence from clone RP3-492P14 on chromosome 6413-15

Contains a single stranded DNA binding protein pseudogene, the TPBG

gene for trophoblast glycoprotein (574-AG) and a CPG island,
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| Jours Laga RP3-492P14.2-001"
| Inotes Team Resch: proteins: P81877 Q99LX9 Q9BWW6 Q9CYZ8 Q9D6L4
| Q9P038 Q944T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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complement (10004. 10982)
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US-10-774-176-12 (1-9) x AP008208_073 (1-110000)
                                                                     37749 AATTTGTTTTTAACTGGTAACCAGCTA 37775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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                                               AsnLeuPheLeuThrGlyAsnGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP3-492P14"
/clone_lib="RPCI-3"
100
                                                                                                                                                                                                                                                                                                                                   AL121977.11 GI:11863678
HTG; CpG island; TPBG.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 121909)
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                                                                                                                                                                                                                                                                              complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barner, E
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                                                                                                                                                                 HSJ492P14
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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misc_feature
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                                                                                                                                                                                                                                                                                                                        Augustica (18-289-2002) Taxuil Sasaki, Mational institute of the States (18-202) Taxuil Sasaki, Mational institute of the States (18-202) Taxuil Sasaki, Mational institute of the States of the States of Japan

2-1-2, Tankuba, Ibaraki 305-8662, Japan

(Banil: teasakidanias affrc. 209-jp, URL: http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7449.

On Jun 39, 2004 this sequence version replaced gi-42627749.

Gense were predicted from the integrated results of the following: GENSCAN (http://com.) GeneWark. html), FGENESH (http://www.ioftcherr.com/) GeneWark. html), Google in Giber (http://www.ioftcherr.com/) GeneWark. html), Google in Giber (http://www.ioftcherr.com/) GeneWark. html), Google in Giber (http://globin.cse.psu.cdu/html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.html/doors/and.htm
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complement (join(157. .256,518. .608,645. .687,1665. .1820))
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                                                                                                                                                                                                                                             Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
Submitted (18-SEP-2002) Takuji Sasaki, National Institute of
                                                 Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC clone:OSJNBb0035N08
Published Only in Database (2002)
Sabaki. The Database (2002)
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| Mol type="genomic DNA"
| cultivar="Nipponbare"
| db_xref="taxon:39947"
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    included in IRGSP standard"
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complement(11805. .13042)
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predicted by GENSCAN
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/gene="OSJNBb0035N08.2"
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this category is not i
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AUTHORS
TITLE
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/trānslation="MPAVLLVIVVVTVVAAVLILVPVLVVGRRGLGLAGSAHSLHRR
RAGGGAESAAPVPLHHRIRCHRSFPPPDPPLSDPCGRWPPRLPTVGSATTRLTIVGSV
TAVASLLRPLPLPEPSTASGGRRGERRSGGEBEBAVVVALARRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGSPEBEBEAHPPPATGNNALASNNNGCPQTRSPSTPVVGWPPVRTFRRNLATSSKASL
ELONGKKABTRBIRRAPFIKINMOSVPIGRKIDLNAPDSYBKLSLAVDKLFRGILAA
GRDPLTAGAROCQQEDVAISGLLLOGTGBYTLVYBDYBGDKVLVGDVPWGMFVSSVKRL
RVLKTSDLSSSLITSGRKRTAAEC"
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Lglpqggwraacrdkgtttkhslaaaaaadddgdgkssmlslgystlvshsqgkankn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //oce="supported by full-length cDNA(s): AK121870"

complement (join(20211. .20252,20345. .20405,20630. .20777,

21029. .21282,22175. .22283,22950. .23238);

//ope="costNbB0035N08.7"

//noce="contains EST(s): AU100805(C51513),C27285(C51513)

contains full-length cDNA(s): AK121870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join[19965, .20252,20345, .20405,20630, .20777,
21029, .21282,22175, .22283,22950, .23497))
/gene="OSJNBb0035N08.7"
                                                                                                                                                                                                         probably inactive due to no initiation codon in CDS" complement (13420. .1366)
/gene="OSJNBb0035N08.4"
complement (13420. .13668)
/gene="OSJNBb0035N08.4"
/note="hypothetical ORF
                                                                 /note="supported by full-length cDNA(s): AX111070"
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this category is not included in IRGSP standard"
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complement (join(<11805. .12148,12855. .>13042))
/gene="OSJNBb0035N08.3"
                                                                                                                                                                                                                                                                                                                                                                                          predicted by GlimmerM
this category is not included in IRGSP standard
complement (14428 ... 14868)
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complement (14428 ... >14868)
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/note="Start and end point are not identified"
complement (14428 ... 14868)
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/note="predicted by GeneMark.hmm etc."
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/protein_d="BAD26156.1"
/db_xref=GI:49388936"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product=hypothetical protein"
/protein id="BAD26155.1"
db_xref="GI:49388935"
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/gene="OSJNBb0035N08.7"
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/gene="OSJNBb0035N08.9"
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/gene="OSJNBb0035N08.6"
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predicted by GlimmerM
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                                                                                                                                                                                          non-coding transcript
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PAT 15-SEP-2000
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                        MILES WILLIAM CARROLL, KEVIN ALAN MYERS
C115/90,461K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,C07K19/00,
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CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB)
                                                                                                                                                                                                                                                                                                                                                                              ce 1. .1281
/organism='Mus musculus (mouse)'.
Location/Qualifiers
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                                                                    OXFORD BIOMEDICA LTD
OS Mus musculus (mouse)
PN JP 2002530060-A/2
PD 17-SFP-2002
PP H8-NOV-1999 JP 2000582415
PR 18-NOV-1998 GB 9825303.2,27-JAN-1999 GB
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11281
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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                                                   Patent: JP 2002530060-A 2 17-SEP-2002;
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1. 1281
/organism="Mus musculus"
/mol type="unassigned DNR"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .1281
/organism="Mus musculus"
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Sequence 2 from Patent WO0029428.
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                                                                                                                                                                                                                 9917995.4
    Carroll, M.W. and Myers, K.A. Polypeptide
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PN JP 20025300
PD 17-SFP-20025
PF 18-NOV-1999
PR 18-NOV-1999
PR 18-NOV-1999
PC C12N15/09, A
PC C12N15/00, PC C12N15/00, PC C12N15/00, PC C12N15/00, PC PP PF Key
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Best Local Similarity:
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AX025012
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bummalia, Eutheria, Euarchontoglires, Glires, Rodentia,

Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 1281)
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/note...predicted by PGENESH etc."
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/protein id="BAD26158.1"
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contains full-length cDNA(s): AK058248"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                            product="hypothetical protein"
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JP 2002530060-A/2.
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Strausberg, L. Peingold, B.A., Grouse, L.H., Derge, J.G.,
Kausner, R.L., Peingold, B.A., Grouse, L.H., Derge, J.G.,
Atausner, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casvant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Norley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wazny, D.M., Sodergren, B.J., Hulyk, S.W.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Kodrigues, S.,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
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                                     5'UTR
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AUTHORS
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                                                                                                                                         PAT 14-DEC-2001
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Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Rattus norvegicus
Bukaryota; Metazos; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Buthazos; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 2333)
Ninkina,N.N. and Buchman,V.L.
                                                                                                                                                                                                                                                                                                                                                                             5t4 tumour-associated antigen for use in tumour immunotherapy Patent: BP 1160323-A 2 05-DBC-2001; Oxford Biomedica (UK) Limited (GB) Location/Qualifiers
                                                                                                                                         linear
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                             Carroll, M.W. and Myers, K.A.
                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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                                                                                                 RESULT 27
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ROD 13-DEC-2004

PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. Sciuler, G. Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G. Schuler, G. D., Altschul, S. F., Zoeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuti, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., McKernan, K. J., Mullahy, S. J., Boask, S. A., McZwan, P. J., McKernan, K. J., Malek, J. A., Gaunaratne, P. H., Richards, S. W., Woilalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, Y., Helton, E., Ketteman, M., Madan, A., Rodrigues, S. Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y. S., Kzzywinski, M. I., Skalska, U., Smallus, D. E., Schnerch, A., Schein, J. B., Jones, S. J. and Marra, M. A., Schein, J. B., Wann, J. Jones, S. J. and Marra, M. A., Schein, J. M. A., Mann, J. M. Mann, J. M. J. Mann, J. M. Mann, J. M. J. Mann, J. M. J. Mann, J. M. J. Mann, J. M. M. Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,R., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiallo,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                       2423 bp mRNA linear ROD 21-OCT-2003 Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 BCGS:5353871), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (15-582-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl.)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                 BC058198.1 GI:34849573
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RESULT 30
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                                                                                                                                                                                                                                                                                                        WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center. Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24
This clone was elected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143.

Location/Qualifiers
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HELLASNIFLYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHLBSLHLEDNAL
KVLHNSTLAEWQGLAHVYRTDNNPWYCDCTMADMVSMLKETEVVPDKARLTCAFPEK
MRNRGLDLTSSDLDCDATLPQSLQTSYVPLGIVLALIGAIFLLVLTLNRKGIKKMMI
NIRDACRDHMRGYHYRYEINADPRLTNLSSNSDV"
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paaplasgsagpppaercpaacecseaartvkcvnrnllevpadlppyvrnlflugwq
mtvlpagapargppladlavlnlsgwhlkevgagafehlpglrrldshmpltnlsaf
                                                                                                                                                      Submitted (02-DEC-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
Mol type="mRNA"
/db Aref="texon:10116"
/clone="MGC:9332 IMAGE:7193411"
/tissue type="Heart, rat (Brown Norway)"
/clone_lib="NHH MGC_234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnLeuPheLeuThrGlyAsnGlnLeu 9
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/gene="Tpbg"
                                           2 (bases 1 to 2361)
Director MGC Project.
Direct Submission
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gene

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FEATURES

Pred. No.:

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DRIGIN

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VPAGSNASVSAPSPLEELILNHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
TRLELASNHFLFLRPDLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KTHNSTLAEWQGLAHVYRPIDNNPWYCDCYMADMVAWLKETEVVPDKARLTCRFPEK
MRNRGLIDINSSDLOCDAVLPOSLOTSYVFGIVULALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
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WYLDRAGFRARDPELADLESHINELTWICAGPFRILLEGERRLDLERRBLITHSAP
VPAGSNASVBARPPLEBLI LINHI VPPEDQRONGSFEGHVAFEGHVAALIKSGAF
VFAGSNASVBARPELEBLI LINHI VPPEDQRONGSFEGHVAFEGHVAALIKSGIALRGI
TRLELASNHFILFLPRDLIAQLPSLRYLDLRNNSLVSLITVASFRNITHLESLHIEDNAL
KVLHNSTLASMGGLAHVKVFLDNNPWVCDCYMADMVAMLKETRVVPDKARLTCARPEK
MRNRGILDLNSSDLORSLTYLQSLGTYSVFLGIVLALIGAI FLLVLYLNRKGIKKWMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /proteIn id="CAP06466.1"
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/translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSVPSSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                     /note="unnamed protein product"
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Patent: WO 03104277-A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2557 bp DN Sequence 125 from Patent W003104277. AX961914
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        'organism="Mus musculus"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                           /translation="MCGAGSGGSGGSAGSTELARLALVLLGWVSASAPSSSVPSSSTS
PAAFLAGGSAQPPPAACBCBAARTVKCVNRNLLEVPADLPPYVRNLFTTGNQ
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APAGSNASVSAPSPLEELILMHIVPPEDOROMGSFEGWAPAFREGWAAALRSGIALRGI
TCLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLBSLHLENDAL
KVLHNSTLAERGGLAHTKVFLDNNPRWCDCYWADWYAMLKETEWVDKARLTCAFPER
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NIRDACRDHWEGYHYRYEINADPRLTNLSSNSDV"
                                      /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
(clone lib="NOT (GAP_Mam6"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="COG4886; Region: COG4886, Leucine-rich repeat (LRR)
proctin [Function unknown]"
/db.xref="CDD:COG4886"
1299..1415
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Mukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LRRCT; Region: Leucine rich repeat C-terminal
domain"
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Conservative:
Mismatches:
Indels:
/db_xref="taxon:10090"
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Patent: WO 03104277-A 123 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
1. 2557
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                                                                                                                                                                                                                                                                                                   /product="Tpbg protein"
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/db_xref="GeneID:11983"
/db_xref="ReneID:11983"
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/db_xref="GeneID:21983"
/db_xref="MGI:1341264"
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/gene="Tpbg'
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Best Local Similarity:
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DB:
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PAT 14-JAN-2004

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Length:
Matches:
Conservative:
Mismatches:
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                                                          /gene="5T4"
3866. .5056
/gene="5T4"
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5759. .5764
/gene="514"
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1 (bases 1 to 85624)
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Best Local Similarity:
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                                                                               mat_peptide
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Mus musculus 5T4 oncofetal trophoblast glycoprotein gene.
AJ012160
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/db_xref="InterPro:IPR000483"
/db_xref="InterPro:IPR000483"
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PADFLASGSAQPPPAERCEGSRAARTVKCVNRNLLEVPADLPPYVRNLFITGNO
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YAGGANAYCASAFEKLBELI LIMHIVPPEPDCROMGSFEGWYAFEGWYAAALRSGLARGGI
TRIELASHHFLFL PRDILAQUPSELRYLDLRNSLVSLTYASFRALTHLESILHEDNAL
KVIHNGTLARMGLAHVKVFLDNNPWVCDCYMADMVAMIKGTEVVPDKARLTCAPPEK
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Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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/product="574 oncofetal trophoblast glycoprotein"
                                                                                                                                                                                                                                                                                                        5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Mus musculus (house mouse)
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   Mismatches:
Indels:
Gaps:
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/db_xref="GI:3805949"
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/mol_type="genomic DNA"
/strain="129/Sv"
                                                                                                                                       838 AACCTTTTCCTTACCGGCAACCAGATG 864
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/clone_lib="Lambda Dash"
                                                                                                                  1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                               US-10-774-176-12 (1-9) x AX961914 (1-2557)
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/bound_moiety="Sp1"
3124. 5779
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3152. .3450
/gene="5T4"
3451. .5779
/gene="5T4"
3779. .5059
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     88.9$
95.7$
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Best Local Similarity:
Query Match:
DB:
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Human DNA sequence from clone RP3-428116 on chromosome 6q26-27 Contains part of a novel gene and the 5' end of the MAP3K4 gene for mitogen-activated protein Kinase kinase kinase 4 (MTK1, MEKK4, MAPKKK4, KIAN0213, homolog of yeast SSK2/SSK22 MAP kinase ki
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Bm:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
MRNRGLLDINSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMBGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a MAC.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="5T4 oncofetal trophoblast glycoprotein"
5713. .5718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
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/locus
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RP3-428L16 is from the library RPCI-3 constructed by the group Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VBCTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jocus tag="RR3-428L16.1-001"

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AL591045.5:2668. :25767, AL109942.13:3336. :2485)
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PKSYDNVMHVGLRKVTPKWQRGNKIGEGQYGKVYTCI SVDTGELMAMKEIRFQPNDHK
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AC015984 187098 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 6 clone RP11-570D18, WORKING DRAFT SEQUENCE, 14 unordered pieces.
as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotghun may have been used to obtain the consensus sequence. Shotghun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest. This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                 If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC015984.5 GI:8568939
HTG; HTGS_PHASE1; HTGS_DRAFT.
HTGmo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product of genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Sequence derived from one plasmid subclone."
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/note="Sequence derived from PCR product of 31565. ..31779
/note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46721. .46808
/note="Unresolved simple sequence repeat."
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Matches:
Conservative:
Mismatches:
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP24-511A23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142336. .142347
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44.00
100.0$
88.9$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC158516 167046 bp DNA linear ROD 21-JUN-2005
Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-JUN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Pubmitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Pubmitted (19-MAR-2005) WO 63108, USA
(Dases 1 to 167046)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality
       AL591045.5:9626. .9704, AL591045.5:12933. .13029, AL591045.5:17745. .17845, AL591045.5:18522. .18632, AL591045.5:22367. .22558, AL591045.5:224596. .24712, AL591045.5:224596. .24712, AL591045.5:25608. .25767, AL109942.13:2336. .24782, AL109942.13:3168. .3274, AL109942.13:7350. .7370)
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Center code: WUGSC
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On May 4, 2005 this sequence version replaced gi:61656412.
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Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
                                                                                                                                                                                                                                                                                                           85624
                                                                                                                                                     /gene="MAP3K4"
/locus_tag="RP3-473J16.4-002"
/standard_name="CTTHUMP0000017560"
/note="match: proteins: Q9P1M2"
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Matches:
Conservative:
Mismatches:
Indels:
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Contact: submissions@watson.wustl.edu
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Drafting center: WIBR
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Submitted (04-MXY-2005) Genome Sec
Parkway, St. Louis, MO 63108, USA
4 (Dases 1 to 167046)
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AC158516.2 GI:63025421
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95.7%
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TITLE
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AUTHORS
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Conservative:
Mismatches:
Indels:
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129363. .129462
/estimated_length=unknown
129463. .187098
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estimated length=unknown
12464. .18289
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1414. 2545
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30568. 40583
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    1313
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                                                                                                                                                         estimated_length=unknown
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                                                                                                                                                                                                                                                                                          length=unknown
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                        clone="RP11-570D18"
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      chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                          596. .12363
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                                                                                  Direct Submission
Submitted (17-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:6855230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the condigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; 77%
Sequencing vector: plasmid; 21%
Chemistry: Dye-primer E1; 77% of reads
Chemistry: Dye-primer E1; 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 176778 bases at least Q40
Consenus quality: 180123 bases at least Q20
Consenus quality: 182248 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 185799; sum-of-contigs
Quality coverage: 5.05 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
Center code: WUGSC
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contig of 4768 bp in length
gap of unknown length
contig of 5826 bp in length
gap of unknown length
contig of 7178 bp in length
gap of unknown length
contig of 4800 bp in length
contig of 4800 bp in length
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gap of unknown length
contig of 1132 bp in length
contig of 1132 bp in length
contig of 1353 bp in length
gap of unknown length
contig of 1043 bp in length
contig of 1043 bp in length
gap of unknown length
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contig of 57636 bp in length
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gap of unknown length
contig of 24986 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                       contig of 2254 bp in length
gap of unknown length
Hominidae; Homo.

1 (bases 1 to 187098)
Waterston, R.H.
The sequence of Homo sapiens clone
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                          Genome Center
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The Genome Sequencing Consortium.

Shat Genome Sequencing Consortium.

Direct Submission

Direct Submission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this asequence version replaced gi:23265004.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.nec.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 0.990329
Consensus quality: 201781 bases at least Q40
Consensus quality: 20321 bases at least Q30
Consensus quality: 205310 bases at least Q30
Bstimated insert size: 205531; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 210.37; contig of 210.27 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GZGV
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Center code: BCM
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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clone end:T7"
2177. .144799
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/note="wgs_end_extension
clone_end:Sp6"
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complement (206062. .206
/note="clone boundary
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clone_end:T7
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Pred. No.:
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18 I LDasses 1 to 21023
18 I LDASSES 2 T
                                                                                                                                                     ACI28294 210237 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE.
ACI28294
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                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                          AC128294.3 GI:25083347
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                   57962 AACATTTTTCTAACTGGCAATCAGTTG 57936
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Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
  84000
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                 Conservative:
Mismatches:
Indels:
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  Matches:
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                                                                                                                                              US-10-774-176-12 (1-9) x AC128294 (1-210237)
                                                                                                                                                                                            1 AsnLeuPheLeuThrGlyAsnGlnLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
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44.00
100.0%
88.9%
95.7%
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                                                                                                                                                                                                                                                                                                                                                                                                unordered pieces.
                    Percent Similarity:
Best Local Similarity:
                                                                  Query Match:
DB:
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AC106962/c
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON NOV 20, 2002 this sequence version replaced gi:22857070.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecs/rat/). Each contrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                           Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 239076)

Rat Genome Sequencing Consortium.
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Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
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Center clone name: GH230-87110
Center clone name: CH230-87110
Assembly program: Phrap; version 0.990329
Consensus quality: 228642 bases at least Q40
Consensus quality: 23266 bases at least Q30
Consensus quality: 234041 bases at least Q20
Estimated insert size: 231522; sum-of-contigs estimation
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234810: gap of unknown length
23524: contig of 1114 bp in length
236024: gap of unknown length
237114: contig of 1290 bp in length
237114: gap of unknown length
239076: contig of 1662 bp in length.
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Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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/db_xref="taxon:10116"
/clone="CH230-87110"
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                                                                                                                                                                                      Worley, K.C.
Direct Submission
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Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 39113 27-SEP-2001;
PR Corporation (NY) (US)
Location/Qualifiers
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Sequence 39113 from Patent WO0171042.
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/mol_type="unassigned
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  'note="Longest
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Submitted (18-DBC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley CA 94720, USA

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley Drosophila Genome From Collection 1 (Rubin et al.,
Berkeley, CA 94720

This clone was sequence has been subjected to integrity checks
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyh tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accuracity prisers with the generation of CDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcription that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
Location printing that the property of the process of the process
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/db_xref="FLYBASE:FBGN0039845"
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guartin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidde, Drosophilidae, Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                 AIV/1256 1673 bp mRNA linear
Drosophila melanogaster RB29447 full length cDNA.
AY071256
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Drosophila melanogaster (fruit fly)
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PAT 02-FEB-2004

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In Gases 1 to 68862)

Is (bases 1 to 68862)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguelavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gorde, S., Gorde, B., Gorden, L., Hanne, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, K., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Malorin, J., Nahova, T., Manga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68862 bp DNA linear HTG 23-NOV-2001
Mus musculus clone RP24-428H10, LOW-PASS SEQUENCE SAMPLING.
AC101828
PAT 02-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 68862)
                                                                                                                                                                                                      Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.
Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 1711042-A 39112 27-SEP-2001;
PR Corporation (NY) (US)
                                                                                                            Drosophila sp.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Mismatches:
                 Sequence 39112 from Patent WO0171042.
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Location/Qualifiers
1. 5278
/ organism="Drosophila sp."
/mol_type="unassigned DNA"
/db_xref="taxon:7242"
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Mus musculus (house mouse)
                                   CQ611354
CQ611354.1 GI:41662882
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for Genome
                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
         Viel.R., Vo.A., Wilson, B., Wu.X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submission
Submission
Submission
Submission
Submission
Submission
Submission
Submission
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Popham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.
                                                                                                                                                                                                                                                                                       * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads * and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will * be preserved.
                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L17490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
1 of 686 bp in length
2 100 bp
3 of 6696 bp in length
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g of 665 bp in length

g of 682 bp in length

f 100 bp

g of 675 bp in length

g of 676 bp in length

g of 693 bp in length

f 100 bp

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Drosophila melanogaters

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 77707)

Adams, M. and Venter, J.C.

Direct Submission

Lineat Submission

Lineat Submission

Lineat Submission

Lineat Submission

This sequence was identified as CDM:10212133 by the submitter.

Rockville, MD, USA

Por further Information on this sequence e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced

* This sequence will be preserved.

* Location/Qualifiers

I. 77707

| Location/Qualifiers
| Location/Qualifiers|
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
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Drosophila melanogaster
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AUTHORS
TITLE
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AsnLeuPheLeuThrGlyAsnGln

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musculus (house mouse)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AC123802/c DEFINITION Mus musculus

REFERENCE

(bases 1 to 121242)

Wilson, R.

AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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COMMENT

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The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CS7BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                This sequence is the entire insert of the clone. Location/Qualifiers
                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                   'organism="Mus musculus'
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rpt_family="MBR1_type"

2291. .2244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7642. .27731
rpt_family="MBR2_type"
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/rpt_family="MBR1_type"
10970. .4125.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .22449
family="MER2_type"
                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:10090"
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rpt_family="MER2_type"
4481. .24963
                                                                                                                                                                                                                                                                                                                                                                             /clone="RP24-398M15"
/clone lib="RPCI-24"
12662.12817
/rpc.family="L1"
1567. .15796
/rpc.family="L1"
16029. .16238
/rpc.family="L1"
18731. .18918
/rpc.family="MIR"
18943. .19017
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26851. .27088
/rpt_family="B4"
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33119. .33890
/rpt_family="L1"
33876. .33937
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rpt_family="BRV1"
5742. .35788
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5762. .35812
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rpt_family="BRV1"
6331. .36579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="ID"
20445. .20F.*
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38180.38274
/rpt_family="L1"
40027.40124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MER2"
27782. .27913
-/rpt_family="L1"
27917. .28708
/rpt_family="L1"
28887. .28975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3938. .34227
rpt_family="MalR'
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42964. .43810
/rpt_family="L1"
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_family="L1"
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42225. .42371
                                                                                                                                                                                                                                                                                                                                        chromosome="3"
  http://genome.wustl.edu
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Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
                                                                                                                                                                                ROD 05-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing of Mus musculus
Unpublished (2001)
3 (bases 1 to 121242)
birect Submission
Submitted (01-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-UUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (20-UUN-2002) S. (bases I to 121242) MCPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to a sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 121242)
                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1. (bases 1 to 121242)

Goyea, B., Meyer, R. and Schatzkamer, K.

The sequence of Mus musculus BAC clone RP24-398M15
                                                                                                                                                                           AC123802 121242 bp DNA linear ROD 05-NC
Mus musculus BAC clone RP24-398M15 from 3, complete sequence.
AC123802. GI:22539238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Aug 29, 2002 this sequence version replaced gi:21307495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
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US-10-774-176-12 (1-9) x AC014787 (1-77707)
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Genome Center

Center code: WUGSC

restriction digest

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US-10-774-176-12 (1-9) x AC123802 (1-121242)
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Direct Submission
                                                                                                                                                                               AC083918 15-JAN-2001
Homo sapiens chromosome 3 clone RP11-333B8 map 3, *** SEQUENCING IN
PRGRESS ***, 62 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-007-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 15, 2001 this sequence version replaced gi:10697455.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
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174: gap of 100 bp
915: contig of 741 bp in length
1015: gap of 100 bp
1513: contig of 498 bp in length
1613: gap of 100 bp
2371: contig of 758 bp in length
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1 (bases 1 to 129302)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 3, clone RP11-333B8
Unpublished
                                          103292 AATCTTTTTTAACCGGCAACCAA 103269
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Center clone name: 333_B_8
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Homo sapiens (human)
Homo sapiens
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AC083918
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AUTHORS
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Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   57444
60017
62461
62461
62565
64479
64479
64206
66306
69317
7676
74219
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84274
87820
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31759 AACCITITCCTGACTGGAAACCAA 31782

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AC021486.10 GI:17223358
                                                                                                                                                 (bases 1 to 144356)
                                                             Homo sapiens (human)
                                                                         Homo sapiens
                      ACCESSION
VECESSION
VERYWORDS
SOURCE
ORGANISM
                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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JOURNAL
RESULT 46
       AC021486
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project ness: L5353
Center clone name: 73_1_6
                                                                                                                                                                                                                                                                    clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt family="AT rich"
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/rpt family="LIMD3"
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complement(18385. .18434)
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8602. .18638
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complement(12422. .12550)
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complement(20595. .20733)
rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (21009. .21196)
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complement (5586. .5998)
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complement(7748...8468)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="(TG)n"
8936. .18981
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713. .4736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family="(TG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .16047
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                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MIR"
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/rpt_family="MIR"
3532. .3565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="L2"
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                                                                                                AC021486 144356 bp DNA linear PRI 01-DEC-2001
Homo sapiens chromosome , clone RP11-7316, complete sequence.
                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 144356)
Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome, clone RP11-7316
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Diages 1 to 161674)

Birren, B., Linton, L., Nusbaum, C., Lander, B., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boquelavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Colangelo, M., Collins, S., Collymore, A., Coke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forrest, C., Thuke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Supramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasslilev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Lister Submission

Lister Submission

Submisted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 312 Ocharles Street, Cambridge, MA 02141, USA

On May 13, 2001 this sequence version replaced gi:9864762.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:html
                        ACUISS67 161674 bp DNA linear HTG 13-MAY-2001
Homo sapiens chromosome 18 clone RP11-398L3 map 18, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center Cloud Hammer Statistics
Sequencing vector: M13; M77815; 95% of reads
Sequencing vector: Plasmid; n/a; 5% of reads
Sequencing vector: Plasmid; n/a; 5% of reads
Chemistry: Dye-primer-amersham; 6% of reads
Chemistry: Dye-terminator Big Dye; 94% of reads
Assembly program: Phrap; version 0.660731
Consensus quality: 155516 bases at least Q30
Consensus quality: 155516 bases at least Q30
Insert size: 170000; agarose-fp
Insert size: 170000; agarose-fp
Insert size: 3.9 in Q20 bases.
* NOTE This is a 'working draft' sequence. It currently
consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * arbitrary, Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10093: contig of 10093 bp in length
10193: gap of 100 bp
11784: contig of 1591 bp in length
11884: gap of 100 bp
113970: contig of 2086 bp in length
14070: gap of 100 bp
                                                                                                                                                                                                                                                                Hominidae; Homo.
1 (bases 1 to 161674)
1 'Erren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-398L3
                                                                                                                           AC015567.5 GI:14029904
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 398 L 3
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        Unpublished
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11785
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RESULT 47
AC015567
LOCUS
DEFINITION
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                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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Matches:
Conservative:
Mismatches:
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complement (22833. .22909)
/rpt_family="MIR"
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38382. .38410
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complement (39539. .39719)
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complement (39880. .40035)
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/rpt_family="Ar_rich"
complement(27119. .27412)
/rpt_family="L1MA9"
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complement (26283. .26392)
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/rpt_family="L2"
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complement(40842. .41141)
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2821. 33059
rpt family="L2"
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/rpt_family="L2"
36619. 36650
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Query Match: DB:

Pred. No.: Score:

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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS AUTHORS AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL COMMENT

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M. Submitted (21-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA

3 (Dases 1 to 173819)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Blarelland, C., Daviel, Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Conem, B., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Chang, J., Bloom, J., Bagos, B., Hall, J., Horderson, M., Hages, B., Hall, J., Horderson, M., Hages, B., Hall, J., Horne, M., Hages, D., Hages, D., Hages, B., Hall, J., Horne, J., Marthews, C., Lui, A., Mabbitt, R., Indblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., Indblad-Toh, K., Liu, G., Liu, A., Mathews, C., Nacdonald, P., Major, J., Manning, J., Matthews, C., Nacdonald, P., Major, J., Manning, J., Matthews, C., Nacdonald, P., Major, J., Manning, J., Matthews, C., Nacdonald, P., Malor, J., Schauer, S., Schupback, R., Stes, C., Poronnell, P., Najor, J., Schauer, S., Schupback, R., Stes, C., Kagov, P., Roman, J., Schauer, S., Schupback, R., Stes, C., Kogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfape, S., Theodore, J., Toworte, M., Wallson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Talamas, J., Young, G., Zainoun, J., Zembek, L., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Chongelly, Y., Dodes, S., Perreira, P., Stoges Ito 175819

Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, M., Anderson, M., Anderson, M., Anderson, M., Bastien, V., Bastien, V., Bastien, V., Bastien, V., Gardyna, S., Gardham, E., Collymore, A., Collymore, A., Collymore, A., Collymore, A., Collymore, M., Collymo
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1 (bases 1 to 175819)

Birren, B., Nusbaum, C. and Lander, R.

Mus musculus chromosome 3, clone RP24-35977
                                                                                          Mus musculus (house mouse)
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AC102290.7 GI:53793859
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eamily="HAL1"
ement (Ann)
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/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (42151. .42512) /rpt family="MLT1A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (42646. .43090) /rpt_family="MLTIC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_fami., 37613
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/rpt_family="MER65B"
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rpt_family="MIR"
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AUTHORS

AC102290 175819 bp DNA linear ROD 05-OCT-2004 Mus musculus chromosome 3, clone RP24-359J7, complete sequence.

RESULT 49
AC102290/c
LOCUS
DEFINITION

US-10-774-176-12 (1-9) x AC019239 (1-165591)

REFERENCE

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repeat_region
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Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlaga, V., Murphy, T., Major, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stanga, S., Severy, P., Sanith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Zimmer, A. and Zody, M., X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                         Submitted (05-0CT-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 5, 2004 this sequence version replaced gi:51699743.
All repeats were identified uning RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
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/rpt_family="IAPLTR2_MM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833. . . 868 / rpt family="(GA)n"

complement (1909. . 2010)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="genomic DNA"
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632...831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o452. .6493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TA)n"
055. .407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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rpt_family="L1M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="Lx6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
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                                                                                                                                                                                                                                                       TITLE
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AC008287 melanogaster, chromosome 3R, region 100C-100C, BAC clone BACR02G16, complete sequence.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                     rpt family="RSINB1"
9167. :19197
                                                                                                                                                                                                                                                                                                                                                                                      rpt family="ORR1A3"
1128. 21172
                                                                                                                                                                                                                                     17253, .17298
rpt family="(TA)n"
complement (17299, .17357)
rpt_family="Lx4"
                                                                                                                                                                                                                                                                           rpt family="ux"
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/rpt family="Bl_MM"
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24119. .24280
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complement(15383. .15663)
rpt_family="Lx4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .23446)
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                                                                                             /rpc_fami.y-
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11134. 11155
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13239. 11331
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13851. 13878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-12 (1-9) x AC102290 (1-175819)
                                                                                                                                                                                                                                                                                                                           rpt_family="AT_rich"
complement(17751..17
                                                                                                                                                                                                                                                                                                                                                                              rpt family="AT rich"
omplement (1942]. .19
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                                                                                                                                                                                                                                                                                                                                                                                                                            rpt family="(TG)n"
2412. .22508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="ORR1D"
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                                                                        rpt family="(A)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(A)n"
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25337. .25360
                                                                                                                                                                                                                                                                                                                                                                                                                                                        family="MIR"
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24965. .25336
                                                                                                                                                                                                                                                                                                                .17587
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Atthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Metazoa, Atthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera Brachycera; Muscomorpha;
Rphydroidea; Drosophilae, Drosophila.

1 (bases 1 to 177480)
1 (bases 1 to 177480)
1 (caliker, S.B., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
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Saveri, J.S., Smith, H.O., Ruinin, G. M. and Vencer, J. C.
Saveri, J.S., Santh, H.O., Ruinin, G. M. and Vencer, J. C.
Saveri, J.S., Smith, H.O., Ruinin, G. M. and Vencer, J. C.
Saveri, J. S., Sinth, H.O., Ruinin, G. M. sand Vencer, J. C.
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Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
CON or before Feb 24, 2011 this sequence version replaced
gi:6806808, gi:6630504, gi:6630510.
Sequence submitted by:
Berkeley Drosophila Genome Project
Berkeley, CA 94720
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Celniker, S.E., Abbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Celniker, S.E., Abbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.B., Galle, R., George, R.A., Harris, N.L., Hosking, R.A., Houston, K.A., Hunuston, K.A., Houston, K.A., Houston, K., Houston, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sechi, H., Snir, B., Svirskas, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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Gaps:

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Search completed: April 25, 2006, 20:41:36 Job time : 3090.7 secs

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03-JUN-2003; 2003US-0475872P.

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Adb72422 Human DUS
Ade9532 Human DUS
Acn44214 Human gen
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Differential expression; diagnosis; therapy; drug screening; cancer; neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;
                                                                              Human colon cancer differentially expressed polynucleotide, SEQ ID:2281.
                  ACLS6146 standard; cDNA; 505 BP.
                                                           24-MAR-2005 (first entry)
                                        ACL56146;
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Homo sapiens.

13-MAY-2004; 2004WO-US015421. 06-JAN-2005

WO2005000087-A2

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The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which are differentially expressed in colon cancer cells. The invention also celates to vectors and host cells comprising a differentially expressed polynucleotide of the invention; a method for detecting a cancerous cell by detection of a gene product of the polynucleotides; a method for inhibiting a gene product of the polynucleotides; a method of treating an individual with cancer by administration of a modulator of a gene product of the polynucleotides; and an isolated antibody that specifically binds to a polypeptide encoded to the diagnosis, prognosis and management of cancer; for the antibodies, and methods are useful for the detection of cancerous cells; for the diagnosis, prognosis and management of cancer; for the identification of agents that modulate the phenotype of cancerous cells; for the identification of therapeutic targets for cancer chemotherapy; and for the treatment of cancer, specially colon cancer and metastasized colon cancer, but also breast or pancreatic cancer. The polynucleotides are also useful as a source of probes or primers for use in diagnostic methods. The differentially expressed polynucleotides or their encoded proteins can additionally be used as vaccines to modulate primary immune response for the prevention or treatment of cancer. The present secuence represents a specifically claimed polynucleotide which is differentially expressed in colon cancer. Note: The sequence data for this patent did contraction of the printed specification, but was obtained in
                                                                                                                                                            New isolated polynucleotides, which are differentially expressed in colon cancer cell, useful for treating cancer, e.g. colon cancer, breast
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                Escobedo J,
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                                        (CHIR ) CHIRON CORP.
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a blological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or preast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-cresolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                           Detecting a breast cancer-associated transcript in a patient's cell, useful for disagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids.
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                                                                             24-JAN-2001; 2001US-0263965P.
02-FEB-2001; 2001US-0265928P.
09-APR-2001; 2001US-0282698P.
04-MAY-2001; 2001US-0282698P.
29-MAY-2001; 2001US-0288590P.
                                                                                                                                                                                                                                       (EOSB-) EOS BIOTECHNOLOGY INC
                                      24-JAN-2002; 2002WO-US002242
                                                                                                                                                                                                                                                                                  Mack DH, Gish KC, Afar D;
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N-PSDB; ABJ05564.
01-AUG-2002
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2001US-0339245P. 2001US-0350666P. 2001US-0334370P.

13-NOV-2001; 29-NOV-2001;

12-APR-2002;

2002US-0372246P

2001US-0290492P

18-APR-2001; 10-MAY-2001; 09-NOV-2001;

18-APR-2002; 2002WO-US012476

WO200286443-A2

31-OCT-2002

Unidentified

(EOSB-) EOS BIOTECHNOLOGY INC

WPI; 2003-093161/08. P-PSDB; ABU56604. Aziz N, Murray R;

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Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antinflammatory; autiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancervous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                927
                                               Conservative:
Mismatches:
                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                              Lung cancer-associated polynucleotide #197.
                                                                               Indel8:
                                                                                                                                                                                  AATCTGACCGAGGTGCCCACGGACCTG 267
                                                                                                 Gaps:
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                                                                                                                                                              1 AsnLeuThrGluValProThrAspLeu
                                                                                                                              US-10-774-176-11 (1-9) x ABT07721 (1-927)
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               4.21
46.00
100.0%
100.0%
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                                                                Similarity:
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gnment Scores:
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                                                                Best Local
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in cased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polymeleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell cor treating lung cancer, non-small cell cor treating lung cancer, such as small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchhectasis. The genes, polymucleotides and polymeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                                                                                                                                                                                             Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynuclectide that exhibits increased or decreased expression in lung cancer.
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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                               cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
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 Ovarian cancer-associated transcript #34.
                                                                                                                                         Location/Qualifiers
1. .927
/*tag= a
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                                                                                                                                                                                                                                                                                                                                      27-AUG-2001; 2001UG-0315287P.
05-88P-2001; 2001UG-0317544P.
13-NOV-2001; 2001UG-035666P.
12-APR-2002; 2002UG-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (EOSB-) EOS BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                         2001US-0299234P
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P-PSDB; ADB80504.
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

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927
     Length:
Matches:
Conservative:
Mismatches:
Indels:
             46.00
100.0%
100.0%
                            Best Local Similarity:
Query Match:
DB:
                     Percent Similarity:
Alignment Scores:
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US-10-774-176-11 (1-9) x ADB80503 (1-927)

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1 AsnLeuThrGluValProThrAspLeu 9
            241
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ADN38723 standard; cDNA; 927 BP ADN38723 ADN38723

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Human, differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                        Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41
                                                                                                                                                                                                                     2001US-0340376P.
2002US-0347211P.
2002US-0347349P.
2002US-0355250P.
2002US-0356714P.
2002US-0356714P.
                                                                                                                                                                                             2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
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2002US-0386614P.
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                                                                                                                                                                                                                                                                                                                                      2002US-0409450P
        (first entry)
                                                                                                                                 WO2003042661-A2
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                                                                                                                Homo sapiens
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       17-JUN-2004
                                                                                                                                                  22-MAY-2003
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Hevezi PA; A; Gish KC, Glynne R, Wilson KE, Zlotnik Aziz N, Ginsburg WM, Murray R, Watson SR, D, DH, Mack Afar

(EOSB-) EOS BIOTECHNOLOGY INC

WPI; 2003-468649/44. P-PSDB; ADN38724.

Claim 8; SEQ ID NO 41; 1385pp; English

Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

whose expression is upregulated or downregulated in specific cancers or other diseases such as anglogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The nucleic acid of the invention, antibodies which specifically bind a nucleic acid of the invention; use of such antibodies for drug targeting, and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and nucleic acids. The nucleic acids, polypeptides, and nucleic acids. The nucleic acids, polypeptides, and nucleic acids of the invention such as psoriasis, ischaemia, heart disease, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atterosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention. The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

ABV99349 standard; DNA; 1156

RESULT 7 ABV99349

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(first entry)

27-JAN-2003

ABV99349;

8

US-10-774-176-11 (1-9) x AAD56198 (1-973)

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nuclei caid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                              927
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human LRRCAPS related DNA #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-2002; 2002WO-US033540.
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46.00
100.0%
100.0%
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                                                                                              Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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AMD56198

AMD56198

AMD56198

AMD70

AMD7
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Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinfinglammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; Ertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; des
                                                                                                                                                                                                                                                                                                                                 2001US-0274849P
2001US-0275235P
2001US-0275578P
2001US-0275601P
2001US-027600P
2001US-027600P
2001US-027694P
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2001US-0277833P
2001US-0278894P
2001US-027899P
2001US-0279036P
2001US-0279036P
2001US-0279995P
2001US-0280233P
2001US-0280233P
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2001US-0277321P.
2001US-0277327P.
2001US-0277338P.
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2001US-0283675P.
2001US-0287424P.
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                                                              Human NOV8a coding sequence.
                                                                                                                                                                                                                            WO200272771-A2.
                                                                                                                                                                                                                                                                                                                                                          13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
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28-MAR-2001
30-MAR-2001
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973

Length: Matches: Conservative: Mismatches: Indels:

4.45 46.00 100.0% 100.0%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

Gaps:

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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli RA, Vernet CAM; Benda CRA, Burgess CB, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CB; Taupier RJ, Pedigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 114-115; 619pp; English.
30-MAY-2001; 2001US-0294485P.
31-MAY-2001; 2001US-0294899P.
31-MAY-2001; 2001US-0294899P.
18-JUN-2001; 2001US-0299303P.
19-JUN-2001; 2001US-0299303P.
19-JUL-2001; 2001US-0299310P.
10-JUL-2001; 2001US-039198P.
31-JUL-2001; 2001US-03189F.
16-AUG-2001; 2001US-0318462P.
12-SEP-2001; 2001US-0318462P.
                                                                                                                    77-SEP-2001; 2001US-0325430P.
27-SEP-2001; 2001US-0325681P.
18-OCT-2001; 2001US-0333308P.
14-NOV-2001; 2001US-0332172P.
14-NOV-2001; 2001US-0332172P.
14-NOV-2001; 2001US-0333184P.
14-NOV-2001; 2001US-0333184P.
14-NOV-2001; 2001US-03332094P.
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04-DEC-2001; 2001US-0337185P.
03-JAN-2002; 2002US-0345705P.
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                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-732824/79.
                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABP70071
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New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any under from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disquences and proteins are useful for treating, preventing or disguences, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's cancer, neurodegenerative diseases, Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, cardiovasquiar disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with chonic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods

Seguence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

Indels:

Percent Similarity: Best Local Similarity: Query Match: DB:

Gaps:

241 AATCTGACCGAGGTGCCCACGGACCTG 267

1 AsnLeuThrGluValProThrAspLeu

US-10-774-176-11 (1-9) x AAA27058 (1-1263)

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Matches:
Conservative:
Mismatches:
 Length:
5.41
46.00
100.0%
                    Percent Similarity:
Best Local Similarity:
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The present sequence encodes the human 574 tumour-associated antigen (TAA). The TAA 574 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inculated with a virus expression vector containing the present sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                  Human, TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                     Human 5T4 tumour-associated antigen gene.
                                                                                                           181 AATCTGACCGAGGTGCCCACGGACCTG 207
                                                                             1 AsnLeuThrGluValProThrAspLeu 9
                                             US-10-774-176-11 (1-9) x ABV99349 (1-1156)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 78; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98GB-00025303.
99GB-00001739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99GB-00017995.
                                                                                                                                                                        AAA27058 standard; DNA; 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB003859
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46.00
100.0%
100.0%
                                                                                                                                                                                                                                      22-AUG-2000 (first entry)
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-387735/33.
                                                                                                                                                                                                                                                                                                                                                                                              WO200029428-A2.
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2000
                                                                                                                                                                                                         AAA27058;
Query Match:
DB:
                                                                                                                                           RESULT 8
                                                                                                                                                           AAA27058
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Human cDNA differentially expressed in MYCN activated cells SeqID 105

human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; 88; MYCN activated cell.

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent blased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway—modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                               pathway; Leucine rich repeat capricious related protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1331
9
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 75-76; 99pp; English
                                                                                                                                              LRRCAPS; cancer; gene therapy; ds.
             AADS6199 standard; DNA; 1331 BP.
                                                                                                                                                                                                                                                                                             22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                  Human LRRCAPS related DNA #6.
                                                                                                                                                                                                                                                                 21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                                                                                     Belvin M, Schleithoff L, P
Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.35
46.00
100.0%
100.0%
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                          (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-421410/39.
                                                                                                                                                                                                       WO2003035831-A2
                                                                                                                                                                             Homo sapiens
                                                                      07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                    01-MAY-2003
                                                                                                                                Human; p53
                                          AAD56199;
AAD56199
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particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the

cancer.

genes regulated by MYCN activation, useful in gene therapy,

Shohet JM;

Plon SE,

Nuchtern JG,

SG,

Stuart

WPI; 2003-635698/60.

23-FEB-2001; 2001US-0270784P. 25-FEB-2002; 2002US-00084817.

JS2003119009-A1

Homo

26-JUN-2003.

(STUA) STUART S G. (NUCH/) NUCHTERN J G. (PLON/) PLON S E. (SHOH/) SHOHET J M.

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expressed in MYCN activated cells. Specifically, it refers to polymucleotide sequences that exhibit differential expression patterns in polymucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a proto-concogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these CDNA molecules is useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the CDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the US Patent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to novel isolated cDNAs that are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.segdata.uspto.gov/sequence.html?DocID=20030119009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AATCTGACCGAGGTGCCCACGGACCTG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 105; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-774-176-11 (1-9) x ADJ56299 (1-2020)
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46.00
100.0%
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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271

ADJ56299 standard; cDNA; 2020 BP

06-MAY-2004 (first entry)

ADJ56299;

RESULT 10
ADJ56299
ID ADJ5
XX
AC ADJ5
XX
DT 06-M

1 AsnLeuThrGluValProThrAspLeu 9

x AADS6199 (1-1331)

US-10-774-176-11 (1-9)

Gaps:

Percent Similarity: Best Local Similarity:

Query Match DB:

ung cancer-associated polynucleotide #196.

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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient. The method comprises that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancerassociated proteins given in ABR48146 to ABR48145. Bladder cancerassociated proteins given in ABR48146 to have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancerassociated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ಗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynuclectide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
                                                                                88
                                                                            Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                       Human bladder cancer associated cDNA sequence SEQ ID NO:192,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 296; 307pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                           03-JUL-2001; 2001US-0302814P.
03-MG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-MOV-2001; 2001US-0350666F.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                        03-JUL-2002; 2002WO-US021338
  12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-201532/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mack DH, Aziz N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABR48236
                                                                                                                                                          WO2003003906-A2
                                                                                                                       Homo sapiens
                                                                                                                                                                                                 16-JAN-2003
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Length:
Matches:
Conservative:
Mismatches:
                                      Indels:
                                               Gaps:
10.4
46.00
100.0%
100.0%
                   Percent Similarity:
Best Local Similarity:
                                      Query Match:
DB:
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US-10-774-176-11 (1-9) x ACC51052 (1-2053)

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325 AATCTGACCGAGGTGCCCACGGACCTG 351
σ
1 AsnLeuThrGluValProThrAspLeu
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ABX76332; RESULT 12
ABX76332
ID ABX76
XX
AC ABX76
XX
DT 02-AP

ABX76332 standard; DNA; 2053

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(first entry)
02-APR-2003
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325 AATCTGACCGAGGTGCCCACGGACCTG 351

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in creased or decreased expression in lung cancer samples. Lung cancer samples in Lung cancer compound that modulates a lung cancer-associated polymeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell corrections cancer in operations, contact by cancer or other benign or precancerous lesions, e.g. ateleotasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polymucleotides and polymeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polymucleotides of the Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesson; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis. Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased Claim 22; Page 335; 453pp; English. 10-MAY-2001; 2001US-0290492P. 09-NOV-2001; 2001US-0339245P. 13-NOV-2001; 2001US-035066EP. 29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P. (BOSB-) EOS BIOTECHNOLOGY INC 18-APR-2002; 2002WO-US012476 expression in lung cancer. 2003-093161/08. Aziz N, Murray R; P-PSDB; ABU56603 WO200286443-A2. Unidentified 18-APR-2001; 31-OCT-2002 

C; 499 G; 491 T; 0 U; 0 Other; 2053 0 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1 AsnLeuThrGluValProThrAspLeu 9 US-10-774-176-11 (1-9) x ABX76332 (1-2053) BP; 461 A; 602 10.4 46.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Sequence 2053 Alignment Scores: Query Match: Š Human; p53 pathway; Leucine rich repeat capricious related protein; LRRCAPS; cancer; gene therapy; ds.

Human LRRCAPS DNA #12

21-OCT-2002; 2002WO-US033540.

Homo sapiens. WO2003035831-A2

01-MAY-2003

22-OCT-2001; 2001US-0338733P. 15-FEB-2002; 2002US-0357600P. 01-MAR-2002; 2002US-0361196P.

```
The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capriclous related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in
                                                                                                                                                                                                                                                                                                                                                                     Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                 Human; p53 pathway; Leucine rich repeat capricious related protein;
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                                                                                                                                                                                                                                                                                                                 Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                Plowman GD, Punke RP,
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 73-74; 99pp; English.
                                                                                                                             LRRCAPS; cancer; gene therapy; ds.
                      AAD56197 standard; DNA; 2053 BP
                                                                                                                                                                                                                                          22-OCT-2001; 2001US-0338733P.
15-FKB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                      21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                              Schleithoff L, 19 H, Friedman
                                                                     (first entry)
                                                                                          Human LRRCAPS DNA #11
                                                                                                                                                                                                                                                                                          EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-421410/39.
                                                                                                                                                                                                                                                                                                                              Francis-Lang H,
                                                                                                                                                                         WO2003035831-A2.
                                                                                                                                                     Homo sapiens
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Pred. No.:
                                                                   07-AUG-2003
                                                                                                                                                                                                01-MAY-2003
                                                                                                                                                                                                                                                                                                                 Belvin M,
                                              AAD56197;
RESULT 13
AAD56197
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Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent

Disclosure; Page 76-77; 99pp; English.

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Plowman GD, Funke RP, Lioubin MN,

Belvin M, Schleithoff L, P. Francis-Lang H, Friedman L;

WPI; 2003-421410/39.

(EXEL-) EXELIXIS INC

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capticious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent blased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
inflammatory disease, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39.
                                                                                                                                                                                                                                                                                 Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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9
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATCTGACCGAGGTGCCCACGGACCTG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AsnLeuThrGluValProThrAspLeu 9
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46.00
100.0%
100.0%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN38721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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Length: Matches: Conservative: Mismatches: Indels:

10.4 46.00 100.0% 100.0%

> Percent Similarity: Best Local Similarity:

Query Match: DB:

BP

DNA; 2053

AAD56200 standard;

AAD56200;

RESULT 14
AADS6200
ID AADS
XX
AC AADS
XX
DT 07-A

07-AUG-2003 (first entry)

US-10-774-176-11 (1-9) x AAD56197 (1-2053)

8 8

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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                      Gish KC, Glynne R, Hevezi PA;
Wilson KB, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 39; 1385pp; English.
                                                                                                                                                                                                                                                                                                                       Ginsburg WM,
2, Watson SR,
                                                                                                 13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0335393P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-035530P.
13-FEB-2002; 2002US-0355714P.
29-MAR-2002; 2002US-0356809P.
29-MAR-2002; 2002US-0356809P.
                                                                                                                                                                                                                                                                                                   (BOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                             12-APR-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
                                                                                13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                                                                         22-JUL-2002; 2002US-0397775P
                                                                                                                                                                                                                                                                               09-SEP-2002; 2002US-0409450P
                                                                                                                                                                                                                                                                                                                       Aziz N, Gir
Murray R,
                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-468649/44.
P-PSDB; ADN38722.
                                         WO2003042661-A2
                                                            22-MAY-2003
                                                                                                                                                                                                                                                                                                                       , HD
                                                                                                                                                                                                                                                                                                                                Mack
                                                                                                                                                                                                                                                                                                                       Afar
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attended necesclerosis, inflammatory diseases, autoimmune diseases, retinal necowascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention. The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

2053 9 0 0

Length: Matches: Conservative: Mismatches: Indels: Gaps:

10.4 46.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

325 AATCTGACCGAGGTGCCCACGGACCTG 351

RESULT 17

AsnLeuThrGluValProThrAspLeu

US-10-774-176-11 (1-9) x ADLO6473 (1-2053)

	2053						
		Matches: 9	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 0	
		46.00				11	
lignment Scores:	red. No.:	Score:	ercent Similarity:	est Local Similarity:	Query Match:	DB:	

US-10-774-176-11 (1-9) x ADN38721 (1-2053)

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The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polymucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for diagnosing or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or
                                                                                                                                                                                                                    Human; tumour-associated antigenic target; TAT; cell death; tumour;
                                                                                                                                                                                      Human tumour-associated antigenic target (TAT) cDNA sequence #53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillan KJ, Polakis P, Polson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                 325 AATCTGACCGAGGTGCCCACGGACCTG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 53; 319pp; English.
1 AsnLeuThrGluValProThrAspLeu
                                                                                                                                                                                                                                                                                                                                                                                       ; 2002US-0404809P.
; 2002US-0405645P.
; 2002US-0413192P.
; 2002US-0419008P.
; 2002US-0426847P.
                                                                                              ADL06473 standard; cDNA; 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frantz G, Hil
u TD, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                            19-AUG-2003; 2003WO-US025892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003US-0484959P
                                                                                                                                                                                                                                    cancer; cytostatic; gene; ss
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desauvage RJ, Frant:
Spencer SD, Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-257144/24.
P-PSDB; ADL06552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide, use
treating cancer.
                                                                                                                                                                                                                                                                                                 WO2004016225-A2
                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-2002;
21-AUG-2002;
23-SEP-2002;
                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2002;
15-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2003;
                                                                                                                                                                                                                                                                                                                               26-FEB-2004
                                                                                                                            ADL06473;
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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
                                                                                                                                                                                                                                                     Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1305; 226pp; English
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                                                                                                                 ROSETTA INPHARMATICS LLC. NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN38510 standard; cDNA; 2053
                                                                            15-JAN-2003; 2003US-00342887.
                                    15-JAN-2004; 2004WO-US001100
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46.00
100.0%
100.0%
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                                                                                                                                                                                                                WPI; 2004-593473/57.
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Best Local Similarity:
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                                                                                                                   (ROSE-)
                                                                                                                                     (NECA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schoenfeld J, Williams PM,
                                                                                                                                                                            ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; breast cancer; prognosis; gene expression; diagnosis.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 355; 3069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnLeuThrGluValProThrAspLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-774-176-11 (1-9) x ADN03961 (1-2053)
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                                                                                                                                     Antipsoriatic cDNA sequence #180
                    ADN03961 standard; cDNA; 2053 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jackman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                    25-SEP-2003; 2003WO-US030907
                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2002; 2002US-0414006P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR25444 standard; DNA; 2053
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46.00
100.0%
100.0%
                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-305105/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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                                                                                                                                                                                                                                                     WO2004028479-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                  Homo sapiens
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                                                                                               01-JUL-2004
                                                                                                                                                                                                                                                                                               08-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         s,
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                                                        ADN03961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu TD;
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ADN 03961

ID ADN 03961

XX AC ADN 0377

XX ADN 0377

XX ADN 01-1

XX ADN 08-1

XX

2053 9 0 0 0

Indels:

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Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                          Tumour-associated antigenic target; TAT; human; overexpression; cr
tumour; diagnosis; cell proliferative disorder; breast cancer;
colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
325 AATCTGACCGAGGTGCCCACGGACCTG 351
                                                                                                                                                                                                                                                                                     therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-2003; 2003WO-US028547
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2002; 2002US-0414971P
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WO2004065545-A2

Homo sapiens

RESULT 1

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The invention relates to human tumour-associated antigenic target (TAT)

CC polypeptides, and their related nucleic acids. The TAT polypeptides are

coverexpressed in cancer tissues compared to normal tissues, and may thus

serve as effective tragets for the diagnosis and treatment of cancer in

cm ammals. The invention also relates to nucleic acid and polypeptide

sequences at least 80% identical to the TAT nucleic acids and

colypeptides, expression vectors and host cells comprising a TAT nucleic

cold, an antibody specific for a TAT polypeptide; a peptide or organic

molecule which binds to a TAT polypeptide; fusion proteins comprising a

CC TAT polypeptide; and methods and compositions for the treatment or

diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

antibodies, antagonists, binding molecules and compositions are useful

coloractal cancer, lung cancer, carricularly cancers such as breast cancer,

coloractal cancer, lung cancer, carrical cancer, liver cancer, bladder

coloractal cancer, nuls cancer, cervical cancer, inver cancer, bladder

concertal cancer, melanoma and leukaemia. TAT nucleic acids mapping, in

chromosome identification probes, in chromosome and gene mapping, in

chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2053 BP, 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   Claim 1, SEQ ID NO 2070; 7273pp; English
                                                                      Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                   prostate cancer or tumor.
                         (GETH ) GENENTECH INC.
                                                                                                                      WPI; 2004-347921/32.
P-PSDB; ABM80804.
                                                                      Wu ID,
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Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell

Example 6; SEQ ID NO 174; 39pp; English.

contacted with the test compound.

ñ Laeng

Hook D, Klimczak LJ,

Evans D,

Altar CA, Brockman JA, Palfreyman M, Rajan P; WPI; 2004-118903/12

(PSYC-) PSYCHIATRIC GENOMICS INC.

18-JUN-2001; 2001US-0299151P. 07-SEP-2001; 2001US-0317828P. 25-SEP-2001; 2001US-0325150P. 14-NOV-2001; 2001US-034393047P. 18-JAN-2002; 2002US-0349936P. 04-MAR-2002; 2002US-0361834P.

18-JUN-2002; 2002US-00175523.

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This invention relates to a novel screening method identified as a multicarameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals invention then describes the screening of candidate pharamecutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as including schizophrenia, bipolar affective disorder (BAD) and autism, as well as Parkinson's and Alzhaimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, nethod used in MPHTS will be automated, such that a large number of test method used in MPHTS will be automated, such that a large number of test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is differentially expressed in the presence of a therapeutic compound and represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #22979.
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AATCTGACCGAGGTGCCCACGGACCTG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnLeuThrGluValProThrAspLeu 9
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46.00
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DB:
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human; ss; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA of an exemplary efficacy gene for BAD SeqID174.
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Mismatches:
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Matches:
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10-PEB-2005 (first entry)

ADV35098;

US2003096264-A1 Homo sapiens

22-MAY-2003.

10.4 46.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

Query Match: DB:

325

셤 ò

RESULT 20

Alignment Scores:

ai T, Hayashi K, Ishii S, Kawai Y; Nagai K, Kojima S, Otsuki T, Koga H;

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830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                               Nishikawa T, Isogai T,
                                                                                                                                                                                                        11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765.
                                                                                                                                           07-JUL-2000; 2000EP-00114089
                                                                                                                                                                                                                                                                                                                                     Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAM93333
                     Homo sapiens
                                                                                                                                                                                  08-JUL-1999;
                                                          EP1130094-A2
                                                                                                   05-SEP-2001
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                                                                                                                                                                                                                                                                                                             Ota T,
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in adaptored and polymucleotide sequences have applications in the produce other types of data and products dependent on DNA and mino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                      New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 22979; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 AATCTGACCGAGGTGCCCACGGACCTG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                         31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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46.00
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                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
P-PSDB; ABG22988.
                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
DB:
                   WO200175067-A2
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Pred. No.:
                                                       11-OCT-2001
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1D AAK9

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this aptent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                          Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full length human cDNA clone SeqID 2864.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
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Best Local Similarity:
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Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

Human full-length cDNA, SEQ ID NO: 2864.

(first entry)

06-NOV-2001

AAK94253;

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                                                                                                                                                                                                        length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ trarget molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                   This invention relates to a novel primers useful for synthesising full
                                                                                                                                                New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
                                                                                           Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                              Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                          664 AATCTGACCGAGGTGCCCACGGACCTG 690
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                                                                          (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00194486.
2000JP-00118774.
2000JP-00183765.
                                    11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183865
07-JUL-2000; 2000BP-00114089
         07-JUL-2000, 2003EP-00025638
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                                                                                                                         WPI; 2004-204755/20.
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11-JAN-2000;
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                            08-JUL-1999;
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DB:
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830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                      The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers anable the production of the full length human cDNA of the invention. Note: The sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; human; signal transducer and activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding protein that promotes STAT6 activation #64.
                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
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Matches:
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2003UP-00137505.
2003US-0470836P.
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2002JP-00377326.
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                                                                                                                                                                                                    in genetic manipulation.
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                                                                                   WPI; 2001-524255/58
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Best Local Similarity:
                                                                                                                P-PSDB; AAM93334
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26-DEC-2002; 2
27-DEC-2002; 2
15-MAY-2003; 2
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for screening
                                                                                                                                                                                                                                       The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the trating a disease associated with STAT6 activation such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergic disease, inflammation, autoimmune diseases, diabetes, the prelipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STATS activation and/or prevention of Thi hyperactive disease. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATS compounds for treating and preventing disease associated with excessive activation or inhibition of STATS. The present sequence represents a human cDNA encoding a protein which promotes STATS activation.
                                                                                                          New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; medicine; signal transduction; glycoprotein; transcription;
                   Muramatsu S, Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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                                                                                                                                                                                                     Claim 4; SEQ ID NO 127; 1368pp; English
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                   Honda G,
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46.00
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                 Sugahara T, Matsuda A,
                                                       WPI; 2004-122214/12
                                                                                                                                                                    diabetes and cancer
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                                                                         P-PSDB; ADI26163
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DB:
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                               New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
                                                                                                            Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine BST associated with lactation/muscle/fat deposition #5770
                                                                                            ai T, Hayashi K, Ishii S, Kawai Y;
Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2361
9
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 AATCTGACCGAGGTGCCCACGGACCTG 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AsnLeuThrGluValProThrAspLeu
                                                                                              Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
             11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX40605 standard; cDNA; 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-2001; 2001US-00960352
                                                                                                            Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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46.00
100.0%
100.0%
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MATHIALAGAN N
TAO N.
                                                                                              Nishikawa T,
                                                                                                                                      WPI; 2004-204755/20.
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WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                    P-PSDB; ADL30834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS2002137139-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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(TAON/)
(WARR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                              Ota T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX40605
8
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The invantion relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising an electrically hybridise to a second complete acid molecule comprising an LMFD nucleic acid molecule comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising and the comprising a level or pattern of a molecule in a bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for breeding, preparation of complementary nucleic acid acid, where complementary nucleic acid acid, where the detection of the molecule. The LMFD nucleic acid is used for breeding, preparation of complementary nucleic acid is used for the gracefically improving cattle. The present sequence is one of the complement sequence was not shown in the specification but was obtained in preparation of expression or present sequence was not shown in the specification but was obtained in a power and an all and an addition and 
                                                                                                                                                         New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 343 BP; 40 A; 146 C; 108 G; 49 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html?DocID=20020137139
                                 Warren WC;
                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 5770; 245pp; English
                                 Tao N,
                                 Mathialagan N,
                                                                                             WPI, 2003-110599/10.
                                 Byatt JC,
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Length:
Matches:
Conservative:
Mismatches:
                            Indels:
      41.00
88.9%
88.9%
89.1%
            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-774-176-11 (1-9) x ABX40605 (1-343)

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131 AACTTGACCGAGGTGCCGGCCGACCTG 157
1 AsnLeuThrGluValProThrAspLeu 9
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ABK87175 standard; cDNA; 1260 BP 07-OCT-2002 (first entry) ABK87175, ABK87171
LID ABB
LID ABB
LID ABB
LID ABB
NXX A RESULT

cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.

Feline; cat; oncofoetal leucine-rich glycoprotein; 574; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunchherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.

gb. Pelis Location/Qualifiers Key

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in disgnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 tissues, and in cell culture media. Antibodies specific for the 574 incapation process may form part of a disgnostic method e.g. the foctal isolating foctal cells from maternal blood. The isolation process may form part of a disgnostic method e.g. the foctal section are useful for isolating foctal cells from maternal blood. The isolation process may form part of a disgnostic method e.g. the foctal section are useful for isolating fortal cells from maternal blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus (es) The present sequence encodes feline 514 protein
                        /product= "5T4 protein"
                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 68; 68pp; English
                                                                                                                                                                                                                                                                                                                                           Carroll M;
                                                                                                                                                                                                                                 13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-557449/59.
                                                                                                                                                                                                                                                                                                                                           fyers K, Drury N,
                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAU98694
                                                                            WO200238612-A2
                                                                                                                               16-MAY-2002
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 70.2 41.00 88.9\$ 88.9\$ Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-774-176-11 (1-9) x ABK87175 (1-1260) 1 AsnLeuThrGluValProThrAspLeu ð 238 AACCTGACCGAGGTGCCCGCGGACCTG 264 ADB97513 standard; DNA; 1260 BP. 04-DEC-2003 (first entry) Feline 5T4 antigen DNA. ADB97513; RESULT 29 ADB97513 윰

Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.

Unidentified

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The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 5T4 antigen. The invention further class I pervides a polypeltope string comprising the 5T4 epitope; a nucleic acid sequence encoding the 5T4 epitope or a polypepitope; a nucleic acid comprising the string of the 5T4 epitope or a polypepitope of the 5T4 epitope, a vector system capable of delivering the 5T4 epitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope, a polypepitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of molecile. The 5T4 epitope has cytostatic activity. The vaccine is method comprising the 5T4 epitope or its encoding nucleic acid and the vector of particularly cancer. The detection method is useful for diagnosing or particularly cancer. The detection method is useful for detecting the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or preventing a disease. This polynucleotide sequence represents the feline or preventing a disease. This polynucleotide sequence represents the feline or string the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New major histocompatibility complex class I peptide epitopes from human 5T4 tumor-associated antigen, useful for preventing and/or treating a
                                                                   /*tag= a
/product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                                                           Redchenko I;
                       Location/Qualifiers
1. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 67; 73pp; English
                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                   13-FEB-2002; 2002GB-00003419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, particularly cancer.
                                                                                                                                                                                                                       13-FEB-2003; 2003WO-GB000670.
                                                                                                                                                                                                                                                                                                                                                         Carroll M, Kingsman S,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-637141/60.
                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ADB97520.
                                                                                                                                 WO2003068816-A1.
                                                                                                                                                                             21-AUG-2003
                       Key
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other; 1260 Length: Matches: Conservative: Mismatches: Indels: 70.2 41.00 88.9% 88.9%

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Gaps:
                       Score:
Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                           Query Match:
DB:
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238 AACCTGACCGAGGTGCCCGCGGACCTG 264 US-10-774-176-11 (1-9) x ADB97513 (1-1260) AsnLeuThrGluValProThrAspLeu RESULT 30 ADB97452 셤

04-DEC-2003 (first entry)

B

ADB97452 standard; DNA; 1260

ADB97452;

The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polymucleotide sequence represents the DNA gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy. New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer. Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other; 1. 1260 /\*tag= a /product= "Feline 5T4 antigen protein" 80 Length: Matches: Conservative: Mismatches: Nucleotide sequence of canine 5T4 protein. Indels: 238 AACCTGACCGAGGTGCCCGCGGACCTG 264 σ US-10-774-176-11 (1-9) x ADB97452 (1-1260) 1 AsnleuThrGluValProThrAspleu Location/Qualifiers Disclosure, Page 49; 63pp; English coding for the feline 5T4 protein. Kingsman S; DNA encoding feline 5T4 protein. (OXFO-) OXFORD BIOMEDICA UK LTD. 13-FEB-2002; 2002GB-00003420. 13-FEB-2003; 2003WO-GB000618. AAF89736 standard; DNA; 1263 23-JUL-2001 (first entry) 70.2 41.00 88.9% 88.9% 89.1% Carroll M, Harrop R, WPI; 2003-663795/62. Similarity: P-PSDB; ADB97455 WO2003068815-A2. Percent Similarity: Unidentified Aliqnment Scores: 21-AUG-2003 AAF89736; Query Match: Best Local RESULT 31 Key AAF89736 셤 8

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The specification describes the use of a single chain antibody (SCFV), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The SCFV antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The SCFV antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, pariodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce SCFV of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
hypersensitivity; autoimmune disease; central nervous system disorder; Parkkinson's disease; pariodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bebbington CR,
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 26, 118pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                          /*tag= a
/product= "5T4"
                                                                                                                                                                                                                                                                                                                                             18-NOV-1999; 99WO-GB003859.
15-PEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                                                                                                                                                                                                                                                           13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsman A, Kingsman SM,
                                                                                                                                                        1. .1263
/*tag= a
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P-PSDB; AAB83839.
                                                                                                                                                                                                                                   WO200136486-A2
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                                                                                                                                     Key
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80400
    Length:
Matches:
Conservative:
Mismatches:
                              Indels:
      70.4
41.00
88.9%
88.9%
                              89.14
Alignment Scores:
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241 AACCTGACCGAGGTGCCGCGGACCTG 267
                                                                                                           AsnLeuThrGluValProThrAspLeu 9
                                                                           US-10-774-176-11 (1-9) x AAF89736 (1-1263)
                Best Local Similarity:
Percent Similarity:
                             Query Match:
DB:
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1263 8 0 1 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

70.4 41.00 88.9\$ 88.9\$

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

241 AACCTGACCGAGGTGCCCGCGGACCTG 267

1 AsnLeuThrGluValProThrAspLeu 9

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US-10-774-176-11 (1-9) x ABK87174 (1-1263)

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RESULT 33
ADN46845 12/c
Continuation (13 of 21) of ADN46845 from base 1200001 (Thermococcus kodakaraensis KOD1 g
                                                                       07-OCT-2002 (first entry)
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ABK87174 standard; cDNA; 1263 BP

ABK87174;

ABK87174
ID ABK
XX
AC ABK
XX
DT 07-

The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in disquestic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The solation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). encoding the Novel canine or feline 5T4 polypeptide and polynucleotides encodir polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat. Canine; dog; oncofoetal leucine-rich glycoprotein; 574; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss. cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4 Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other; The present sequence encodes canine 5T4 protein 1263
 tag= a
 product= "5T4 protein" Location/Qualifiers (OXFO-) OXFORD BIOMEDICA UK LTD Claim 1; Page 67; 68pp; English Carroll M; 13-NOV-2000; 2000WO-GB004317. 13-NOV-2001; 2001WO-GB005004. WPI; 2002-557449/59. Drury N, P-PSDB; AAU98693 WO200238612-A2 16-MAY-2002 Myers K, Canis sp. CDS 

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RESULT 36

ADN47209 08

Continuation (9 of 21) of ADN47209 from base 800001 (Thermococcus kodakaraensis KOD1 gen
WP Sequence split into 21 fragments LOCUS ADN47209 Accession Adn47209
WP ADN47209 01
WP ADN47209 01
WP ADN47209 03
WP ADN47209 04
WP ADN47209 04
WP ADN47209 05
WP ADN47209 05
WP ADN47209 06
WP ADN47209 06
WP ADN47209 06
WP ADN47209 07
WP ADN47209 07
WP ADN47209 06
WP ADN47209 06
WP ADN47209 07
WP ADN47209 11
WP ADN47209 12
WP ADN47209 12
WP ADN47209 13
WP ADN47209 13
WP ADN47209 13
WP ADN47209 14
WP ADN47209 15
WP ADN47209 15
WP ADN47209 15
WP ADN47209 16
WP ADN47209 16
WP ADN47209 17
WP ADN47209 17
WP ADN47209 18
WP ADN47209 19
                                                                                      from base 1200001 (Thermococcus kodakaraensis KOD1 LOCUS ADN46123 Accession Adn46123
                                                                                                                                                                                                                                                                                                                                                                              110000
7
2
0
0
                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                 30817 AATATCACCCAGGTGCCCACTGACCTC 30843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-774-176-11 (1-9) x ADN47591_08 (1-110000)
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310000
410000
510000
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21 fragments
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41.00
100.0%
77.8%
89.1%
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200001
300001
400001
500001
700001
1000001
11200001
11200001
11400001
11700001
11700001
11700001
11700001
11700001
11700001
11700001
                                                                          ADN46123 12/C
Continuation (13 of 21) on
WP Sequence split into 21
WP ADN46123 01
WP ADN46123 02
WP ADN46123 04
WP ADN46123 06
WP ADN46123 06
WP ADN46123 06
WP ADN46123 09
WP ADN46123 10
WP ADN46123 11
WP ADN46123 11
WP ADN46123 11
WP ADN46123 12
WP ADN46123 12
WP ADN46123 13
WP ADN46123 13
WP ADN46123 13
WP ADN46123 16
WP ADN46123 18
WP ADN46123 18
WP ADN46123 18
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                                                                  RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gen
                                                                                                                                                                                                                                                                                                                                                                                                                                              of ADN47591 from base 800001 (Thermococcus kodakaraensis KOD1
21 fragments LOCUS ADN47591 Accession Adn47591
Begin End
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ADN47591 08

Continuation (9 of 21) of

WP Sequence split into 21)

WP ADN47591 00

WP ADN47591 01

WP ADN47591 02

WP ADN47591 03

WP ADN47591 03

WP ADN47591 04

WP ADN47591 06

WP ADN47591 07

WP ADN47591 11

WP ADN47591 11
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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide for detecting cytosine methylation SEQ ID NO 29197.
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ID ABQ42606 standard; DNA; 792 BP.
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Continuation (9 of 21) of WP Sequence split into 21
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WP ADN47960 02
WP ADN47960 03
WP ADN47960 03
WP ADN47960 06
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and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, b); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention 8888888888

Seguence 792 BP; 119 A; 94 C; 297 G; 282 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 67.8 40.00 100.0% 77.8% 87.0% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: Score:

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208 AATCTAACCGAAATACCCACGAACCTA 182 AsnleuThrGluValProThrAspleu 9

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ABQ42607 standard; DNA; 792 40 RESULT 4 ABQ42607 

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(first entry) 12-JUL-2002 ABQ42607;

Oligonucleotide for detecting cytosine methylation SEQ ID NO 29198

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074

01-SEP-2000; 2000DE-01043826 05-SEP-2000; 2000DE-01044543

(EPIG-) EPIGENOMICS AG

ä Guetig Berlin K, Piepenbrock C, olek A,

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons diagnosis and prognosis, con from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (c) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonomic and of puppoints and the degree of hybridiseation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of This invention describes a novel method for determining the degree of

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

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methylation in genomic DNA, useful for selective hybridization of amplicons
       (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointeetinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, 9); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method disclosure of the invention
oligomers, the degree of methylation is calculated. The method is used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 29175.
                                                                                                                                                                          Sequence 792 BP; 282 A; 297 C; 94 G; 119 T; 0 U; 0 Other;
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05-SEP-2000; 2000DE-01044543.
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87.0%
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degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovoscular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, 8), and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ34121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention 

Sequence 795 BP; 132 A; 94 C; 313 G; 256 T; 0 U; 0 Other;

795 2 0 0 Length: Matches: Conservative: Mismatches: Indels: US-10-774-176-11 (1-9) x ABQ42584 (1-795) 68.1 40.00 100.0% 77.8% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

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BP ABQ42585 standard; DNA; 795

ABQ42585;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 29176.

Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens

WO200218632-A2

07-MAR-2002.

01-8EP-2001; 2001WO-BP010074

01-8EP-2000; 2000DE-01043826. 05-8EP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG.

Guetig Berlin K, Piepenbrock C, Olek A,

WPI, 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target c is amplified to form a labeled amplicon. ABGULT 4
ABG42585
ABG

The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nuclest acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP'S); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation catatus of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for the method of the method in the The invention relates to a method used for evaluating the toxicity of an agent comprising determining the expression of a rat toxic response gene(s) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and each with at least one member Bvaluating the toxicity of an agent, useful in drug development or in determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in Rat; toxicity study; rat toxic response gene; toxicological response; drug development; phase-1 rat CT gene; ds. Sequence 795 BP; 256 A; 313 C; 94 G; 132 T; 0 U; 0 Other; Length: Matches: Conservative: Mismatches: Indels: (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC. 498 AATCTAACCGAAATACCCACGAACCTA 524 Gaps: σ Disclosure; Page 108; 388pp; English. 1 AsnLeuThrGluValProThrAspLeu US-10-774-176-11 (1-9) x ABQ42585 (1-795) Phase-1 Rat CT gene SEQ ID No 10. 品 Farris G, Hicken SH, Farr SB 29-JAN-2002; 2002WO-US002935. 29-JAN-2001; 2001US-0264933P. 26-JUL-2001; 2001US-0308161P. disclosure of the invention ABT08922 standard; DNA; 691 response to the test agent 68.1 40.00 100.0\$ 77.8\$ 87.0\$ (first entry) WPI; 2002-674961/72. Percent Similarity: Best Local Similarity: WO200266682-A2. Alignment Scores: 05-DEC-2002 29-AUG-2002 Rattus sp. ABT08922; Query Match: DB: .. No:: **ABT08922**/ RESULT \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ 셤

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analysis before a new drug or compound is approved for human consumption or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention
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Sequence 691 BP; 168 A; 177 C; 157 G; 185 T; 0 U; 4 Other;

697 1100 Length: Matches: Conservative: Mismatches: Indels: Gaps: 95 39.00 88.9% 77.8% 84.8% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: .. 02

x ABT08922 (1-691) US-10-774-176-11 (1-9)

σ AsnLeuThrGluValProThrAspLeu -

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ADG30834/ RESULT

ADG30834 standard; DNA; 691 ADG30834; 

BP

(first entry) 26-PEB-2004

Liver toxicity predictive DNA 14.

liver toxicity; Norway rat; 24 hour combo All; ds.

Unidentified

WO2003085083-A2

16-OCT-2003.

01-APR-2003; 2003WO-US010141.

01-APR-2002; 2002US-0369287P

(PHAS-) PHASE 1 MOLECULAR TOXICOLOGY.

Derbel M; Nolan TD, Sankar U, Kier L,

WPI; 2003-804300/75.

ina Predicting the liver toxicity of an agent to an individual by using test expression profile with a set of reference expression profiles Predictive Model to determine whether the agent will reduce liver toxicity in the individual.

Claim 2; Page 150; 379pp; English.

The invention relates to a novel method for predicting the liver toxicity of an agent to an individual comprising obtaining a biological sample from an individual treated with the agent, measuring the expression of one or more liver toxicity predictive genes in the sample and using the test expression profile with a set of reference expression profiles in a predictive model to determine whether the agent will reduce liver toxicity in the individual. The method of the invention may be useful for predicting the liver toxicity of an agent to an individual. The current sequence is that of the liver toxicity predictive DNA of the invention which represents a 24 hour combo All gene

Sequence 691 BP; 168 A; 177 C; 157 G; 185 T; 0 U; 4 Other;

691 7 1 Length: Matches: Conservative: 95 39.00 88.9% Percent Similarity: Alignment Scores: Pred. No.: Score:

Predicting the liver toxicity in an individual to an agent by measuring the expression of one or more liver toxicity predictive genes in the sample from the individual treated with the agent. liver, liver toxicity, liver toxicity predictive gene; liver inflammation predictive gene; inflammation; gene; ds; rat Liver inflammatory predictive gene related DNA sequence -00 Mismatches: Indels: (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC. Gaps: Derbel M; AsnLeuThrGluValProThrAspLeu US-10-774-176-11 (1-9) x ADG30834 (1-691) ADG45384 standard; DNA; 691 BP Sankar U, 09-MAY-2003; 2003WO-US014832 10-MAY-2002; 2002US-0379831P. 26-FEB-2004 (first entry) 77.8% 84.8% WPI; 2004-042456/04. Nolan TD, Rattus norvegicus. Best Local Similarity: WO2003095624-A2. 20-NOV-2003 ADG45384; Н Kier L, Query Match: RESULT 45 ADG45384, 8 셤 

Claim 7; Fig 4; 336pp; English.

The present invention describes a method for predicting the liver toxicity in an individual to an agent. The method comprises: (a) obtaining a biological sample from the individual treated with the agent; (b) measuring the expression of one or more liver toxicity predictive corners in the sample; and (c) using the test expression profile with a set of reference expression profiles in a Predictive Model to determine whether the agent will induce liver toxicity in the individual. Also described: (1) predicting the liver toxicity of an agent using an individual, in vitro cell cultures or explants to an agent via a programmable machine; (3) a computer program product for enabling a computer to perform Predictive Model analysis for liver toxicity on a projectal sample from an individual, in vitro cell cultures or explants to an agent; (4) a computer system adopted to predict liver toxicity in a biological system from an individual, in vitro cell cultures or explants to an agent; (5) a computer program product for predictive of from a test sample expression profile; (6) mining genes predictive genes. The method is useful for predicting the liver toxicity in an individual to an agent. The present sequence represents a liver toxicity predictive gene agent. The present sequence represents a liver toxicity predictive gene agent. The present sequence represents a liver toxicity predictive gene agented that represents a liver toxicity in an individual to an agent. The presents a liver confocity predictive gene agented that represents a liver toxicity in an individual to an agent. The present sequence represents a liver toxicity predictive gene agent. The present sequence represents a liver toxicity predictive gene agent. sequence that represents a 24 hour combo 3 gene, which i claimed in the exemplification of the present invention.

Sequence 691 BP; 168 A; 177 C; 157 G; 185 T; 0 U; 4 Other

95 Alignment Scores:

Length:

691

altered expression; toxic response; spleen; toxicity; lymphoid; gene; ss.

Spleen necrosis predictive cDNA sequence, SEQ ID No 9.

16-DEC-2004 (first entry)

ADR91053;

AATCTTAGAGAGATTCCTACAGATCTT 404

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ADR91053 standard; cDNA; 691

RESULT 47 ADR91053,

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1 AsnLeuThrGluValProThrAspLeu

US-10-774-176-11 (1-9) x ADH22691 (1-691)

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This invention relates to novel isolated kidney toxicity predictive genes and methods of using such genes in the field of toxicology. Specifically, it refers to novel genes that can be used for generating predictive models, which in turn are useful for predicting the in vivo toxic response to one or more agents. The present invention describes obtaining a gene expression profile from a biological sample and using the predictive model to determine whether an agent will induce kidney toxicity in the individual. As such, it can be used to detect any toxic effects that may be manifested as long lasting or chronic consequences including irreversible toxicity or carcinogenesis. Furthermore, the predictive genes can be considered as therapeutic targets for toxic damage or to ameliorate specific disease conditions such as kidney tubule necrosis or acute renal failure, as well as for additional screening assays. This polynucleotide sequence is the partial gene sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting kidney toxicity in an individual to an agent, useful for predicting toxic responses to one or more agents comprising measuring the expression of one or more kidney toxicity predictive genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kidney toxicity; toxicology; predictive model; gene expression profile; toxic damage, kidney tubule necrosis; acute renal failure; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial DNA segeunce of a rat kidney toxicity predictive gene (19).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat kidney toxicity predictive gene of the invention.
74400
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                   Derbel M;
                                                                                                                                                                                                                                                                                                 1 AsnleuThrGluValProThrAspLeu 9
                                                                                                                                                                                                                         US-10-774-176-11 (1-9) x ADG45384 (1-691)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH22691 standard; DNA; 691 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kier L, Nolan TD, Sankar U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003; 2003WO-US006196
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84.8%
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                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH22691;
                                                                                                          Query Match:
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ADHI22691/1

ADHI2691/1

ADHI269
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New composition comprises cDNAs useful for detecting altered expression of genes in a toxic response of the spleen or for predicting toxic responses to one or more agents including lymphoid tissue types or other

Claim 1; SEQ ID NO 9; 249pp; English.

species.

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

17-MAR-2004; 2004WO-US008371 17-MAR-2003; 2003US-0455443P

WO2004083402-A2

30-SEP-2004

Unidentified.

Nolan

Derbel M,

WPI; 2004-691048/67. Sankar U, Kier L,

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The invention relates to a novel composition comprising cDNAs for use in detecting the altered expression of genes in a toxic response of the spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348) or their complements The invention further comprises:

CC spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348) or their complements The invention further comprises:

CC spleen toxicity in an individual to an agent; predicting the spleen toxicity in an individual to an agent; predicting the spleen toxicity from an expression profile of nucleic acids from a sample under test, comprising a computer program product for predicting spleen toxicity from an expression profile of nucleic acids from the cDNAs, and a predictive model for causing a general purpose computer to predict the spleen toxicity of the sample based upon the crahing data set, the list of genes selected from the CDNAs, and the composition profiles of spleen toxicity, comprising means for measuring system for predicting spleen toxicity, comprising means for measuring compression profiles of spleen predictive model. The composition comprising compassion profiles of spleen predictive model. The composition comprising compass is useful for detecting altered expression of genes in a toxic response of the spleen or for predicting toxic responses to one or more agents including lymphoid tissue types or other species. The predictive agents and models of the invention are useful for identifying and an expension of genes and models of the invention are useful for identifying and and models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes and models of the invention are useful for identifying and evaluating various in vitro systems that can be used to accurately predict in vivo toxicity. This polynucleotide sequence represents the genes predictive for spleen necrosis of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 168 A; 177 C; 157 G; 185 T; 0 U; 4 Other;
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Length: Matches: Conservative:

95 39.00 88.9**\*** 

Percent Similarity:

Sequence 691 BP; 168 A; 177 C; 157 G; 185 T; 0 U; 4 Other;

Length: Matches: Conservative: Mismatches: Indels:

95 39.00 88.94 77.84 84.84

Alignment Scores:
Pred. No.:
Scores:
Percent Similarity:
Best Local Similarity:
Query Match:

Alignment Scores:

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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus clausii genomic sequence tag (GST) #2241.
Mismatches:
Indels:
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                                                                                                                                                                                                         430 AATCTTAGAGAGATTCCTACAGATCTT 404
                                                         Gaps:
                                                                                                                                                                          AsnLeuThrGluValProThrAspLeu
                                                                                                                   US-10-774-176-11 (1-9) x ADR91053 (1-691)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
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77.8%
84.8%
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Best Local Similarity:
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                              Query Match:
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MAR(7938

MAR(79
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in cother Bacillus cells, comprising hybridising labelled mucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus isolated from Bacillus cells to a substrate containing array of Bacillus celerated from Bacillus cells an observed hybridiation reporter signal of a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for monitoring contain or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new companion problem of genes in one copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions.

Cup characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available.

Chis sequence represents a genomic sequence information is available.

Chis sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form to part of the printed specification, but was obtained in electronic format correctly from NIPO at ftp. hubblished\_pct\_sequences

Sequence 933 BP; 267 A; 219 C; 235 G; 212 T; 0 U; 0 Other;

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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the captocoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or core genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in Kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic effects of compounds or the progression of these toxic determining the changes in gene expression in tissues or cells the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                                                                                                                       Rat sequence differentially expressed in response to a hepatotoxin #1422.
                                                                                                                                                                                                                                                                                                                                                                   Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
differential expression; centrilobular necrosis; steatosis.
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933
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                Matches:
Conservative:
Mismatches:
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 Length:
                                                                                                                                                             669 AACTIGACTGAATGTCCCACTGACATC 695
                                                                              Gaps:
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                                                                                                                                          1 AsnLeuThrGluValProThrAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson KR,
                                                                                                            US-10-774-176-11 (1-9) x ABK79398 (1-933)
                                                                                                                                                                                                                                       ABK63515 standard; cDNA; 2977 BP
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2001US-029023P.

2001US-0292336P.

2001US-0295798P.

2001US-0295798P.

2001US-0297657P.
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              39.00
88.9$
77.8$
84.8$
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                       Percent Similarity:
Best Local Similarity:
Query Match:
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11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
13-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2000;
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                                                                                                                                                                                                        RESULT 49
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expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and statosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent comprising a database containing information identifying the \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$**\$** 

Sequence 2977 BP; 765 A; 717 C; 747 G; 748 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 39.00 88.9 77.8 84.8 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-10-774-176-11 (1-9) x ABK63515 (1-2977)

2373 AATCTTAGAGAGATTCCTACAGATCTT 2399 σ 1 AsnleuThrGluValProThrAspLeu

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ADB58652 standard; DNA; 2977 BP 

(first entry) 04-DEC-2003 ADB58652;

Toxicity-related gene, SEQ ID 3678.

Toxic; toxin; gene expression profile; hepatotoxicity; liver; drug screening; toxicity assay; ds.

Unidentified

WO2003064624-A2

07-AUG-2003.

31-JAN-2003; 2003WO-US003194. 31-JAN-2002;

31-JAN-2002; 2002US-00060087. 15-MAR-2002; 2002US-0364055P. 15-MAR-2002; 2002US-0366435P. 30-DEC-2002; 2002US-0436643P.

GENE-) GENE LOGIC INC

Castle A, Elashoff M; Higgs B, Johnson K, Mendrick D, Porter M, WPI; 2003-689530/65. Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to :he compound

Claim 1, SEQ ID NO 3678; 1156pp; English.

The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile

gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in sequence data for this patent ding screening and toxicity markers in sequence data for this patent din electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. 

Sequence 2977 BP; 765 A; 717 C; 747 G; 748 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches: 500 39.00 88.94 77.84 84.84 Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-774-176-11 (1-9) x ADB58652 (1-2977)

1 AsnLeuThrGluValProThrAspLeu 9 ઠે 용

Search completed: April 25, 2006, 12:33:51 Job time : 340.3 secs

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protein

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Sequence:

Title: Perfect

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BX571773 Zebrafish
AC011264 Homo sapi
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AC15596 Xenopus t
CR933001 Zebrafish
AC026799 Homo sapi
AC127247 Mus muscu
AL591106 Homo sapi
AC118419 Rattus no
AC151872 Lemur cat
CR933526 Danio rer
AC108394 Mus muscu
AC025964 Mus muscu
AC025910 Mus muscu
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AC166203 Oryctolag
AC092341 Homo sapi
AC092347 Homo sapi
AC166207 Oryctolag
AC166469 Pan trog1
CR388209 Danio rer
BV090626 RPAMMSEQ0
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AX55489 Homo sapi
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AX074786 Homo sapi
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CQ78272 Sequence
AX0961916 Sequence
AX04730 Homo sapi
BC037161 Homo sapi
AX07163 Homo sapi
AX07163 Homo sapi
AX07164 Homo sapi
AX121977 Human DNA
AX467373 Sequence
AX821533 Sequence
AX21548 Sequence
AX467371 Sequence
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AX16953 Sequence
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AX4653 Sequence
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                                         BD127282

ACO782724

ACO782726

BD127283

CQ782726

AXO61916

AXO61916

AXO7790

BC037161

ABL68308

HSG492P14

AX467373

AX821533

AX821548

AX149553

AX447371

AX67371

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-Q=/abss/ABSSWEB =ppool/US10774176/runat_24042006_165114_19197/app_query.fasta_1
-Q=/abss/ABSSWEB =ppool/US10774176/runat_24042006_165114_19197/app_query.fasta_1
-Q=/abss/ABSSWEB =ppool/US10774176/runat_24042006_165114_19197/app_query.fasta_1
-DB=GenEmbl -QFWT=fastap -SUPFIXE-p2n.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -TRR SCORE=pct -THR MAX=100 -TRR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-NORMEN=D10774176 GCGN 1 1 6765 GNUNA 24042006 165114 19197 -NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES_0 -WĀIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPEXT=7
-YGAPEXT=7
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76.1 178225 5 BX005286 76.1 178230 8 AC018828 76.1 178500 14 AL355926 76.1 178006 5 ALGEATAR	76.1 179165 14 AC140289 76.1 179192 14 AC122632 76.1 179296 14 BC649297 76.1 179396 14 BC649297 76.1 179396 14 AC165520 76.1 179576 1 BX294156	76.1 179741 14 AC116815 76.1 180042 14 CR388184 76.1 180353 8 AC07926	76.1 180481 5 BAXESYOL 76.1 180816 14 AC110395 76.1 180861 14 CR391970	76.1 181133 14 AC073478 76.1 181168 5 BX293540 76.1 181942 9 AC165145 76.1 190032 5 BY303544	76.1 182223 14 CR790384 76.1 182325 14 AC121193	76.1 182948 9 76.1 183229 5 76.1 183298 14 76.1 183374 14	76.1 183626 14 AC026648 76.1 183804 14 CR854989 76.1 183804 14 CR854989	76.1 183817 14 AC117137 76.1 183847 5 AC117137 76.1 183847 5 AC145510	76.1 184232 5 CR381684 76.1 184254 9 AL773566	76.1 185134 8 AC007064 76.1 185134 8 AC024878 76.1 185388 9 AC122483	76.1 185626 5 BX530068 76.1 185657 14 AC125630 76.1 185849 5 BX005073	76.1 185990 14 76.1 186820 5 76.1 187795 14	76.1 188066 14 ACIGO427 ACIGO33 ACIGO338 PG. 188681 8 ACIGO339 ACIGO333 ACIGO333 PG. 188716 14 ACI47323 PG.	76.1 189215 9 AC124490 AC124490 Mu	ALIGNMENTS	AX829164 927 bp DNA linear PAT 12-DEC-2003	GI:39838931	Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;		Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer Patent: WO 02059377-A 57 01.AUG-2002;	's Biorechnology, inc. (US) Location/Qualifiers 1927 /organism="Homo sapiens"
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PAT 03-FEB-2004

linear

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Myers, K. A.
Direct Submission
Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer
Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                             Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 2053)

Myers, K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J.
and Stern, P.L.
1solation of a cDNA encoding 5T4 oncofetal trophoblast
glycoprotein. An antigen associated with metastasis contains
leucine-rich repeats
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                         Patent: WO 02068579-A 17612 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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5T4 gene; 5T4 oncofoetal antigen.
Momo sapiens (human)
Homo sapiens
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DB:
                              CQ731678
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5t4 tumour-associated antigen for use in tumour immunotherapy Patent: BP 1160323-A 1 05-DEC-2001; Oxford Biomedica (UK) Limited (GB) Location/Qualifiers
                                                                                                                                                                                                            ; OXFORD
                                                                                                                                                                          POLYPEPLIGE
PATENT: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB)
BIOMEDICA LTD (GB)
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AX025011
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                                                                                                                                                             Carroll, M.W. and Myers, K.A.
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                                                                 Homo sapiens (human)
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Query Match:
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Query Match:
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PRI 18-APR-2005

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LAVLPAGAFARRPPIABLAALNISGSRIDEVRAGAFEHILPSIRQLDISHNPIADLSPP
AFSGSNASVSAPSPIVELIIAHIVPPEDBRQNRSFEGWVAALLAGRALQGILRRIELA
SHRFYLPROVIAQLPSLIAHIDLSNNSLVSITYVSFRULTHLESLHIEDNALKVIHNG
TLABLQGLPHIRVPLINNPWVCDCINADMYTWIKETEVVQGXORLTCAYPEKWRRYV
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLARRGIKK"
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APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
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                                                                                                                                                                                                                               10, cl2P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualiflers
        07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                           C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                  YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
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Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
424_.1575
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Location/Qualifiers
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     PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, T.
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOX
SHINICHI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC

    .2359
    /organism="Homo sapiens"
    /mol type="genomic DNA"
    /db_xref="taxon:9606"

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/db_xref="GI:45502668"
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Best Local Similarity:
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CQ782724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="transmembrane peptide"
/standard name="transmembrane region"
/function="Anchorage of the protein to the cell membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Desel to 2359)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
clone lib="lambda gtll library of J. Milan"
12. .372
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product="Leucine rich repeat region"
'label=LRRs
                                                                                                                                       /codon_start=1
/evidence=experimental
/product=5T4 oncofoetal antigen"
/protein_id="CAA82324.1"
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Matches:
Conservative:
Mismatches:
Indels:
                                                               'product="LRR N-terminal flank"
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                                                                                                                                                                                                                                                                              /db_xref="GOA:Q13641"
/db_xref="InterPro:IPR000372"
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JP 2002017375-A/2713
22-JAN-2002
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JP 2002017375-A/2713.
Homo sapiens (human)
Homo sapiens
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                                                                                        /label=N-flank
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RESULT 9 AK074786

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2361 bp DNA linear PAT 18-SEP-2002 full-length cDNA and use thereof.
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JP 2002017375-A/2714
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                       Hominidae, Homo.

1 (Dases 1 to 2361)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI YURI KAWAI,AI WAKAWATSU,TOMOYASU SUGIYAWA,KEIICHI NAGAI,
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
                                                                                                                                                                                                                                                                                                                                                                 Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2714 22-JAN-2002; HELIX RESEARCH INSTITUTE
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Matches:
Conservative:
Mismatches:
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Sequence 2866 from Patent BP1396543.
CQ782726. GI:45502669
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Location/Qualifiers
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664 AATCTGACCGAGGTGCCCACGGACCTG 690
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002017375-A/2714.
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                                                                                                                                                                                                                                                                               AK074786 2359 bp mRNA linear PRI 03-SEP-2002 Homo sapiens CDNA FLJ90305 fis, clone NT2RP2000694, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene. AK074786
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Wibbo human cDNA sequencing project
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Isogai, T. and Otsuki, T.
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Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,

AUTHORS

1 AsnLeuThrGluValProThrAspLeu 9

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Unpublished

13 (bases 1 to 2361)

14 Segai, T. and Otsuki, T.

15 Isogai, T. and Otsuki, T.

16 Direct Submission

17 Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,

18 Genomics Laboratory; 1532-3 Yans, Kisarazu, Chiba, 292-0812, Japan

19 Senome, Trade and Industry of Japan; Chiba, 1995, Fax:81-438-52-3986)

10 NEDO human CDNA sequencing project supported by Ministry of

18 E-mail:genomics@hri.co.jp, Tal:81-438-52-3975, Fax:81-438-52-3986)

19 NEDO human CDNA sequencing project supported by Ministry of

10 Research Association for Biotechnology; CDNA full insert sequencing:

11 Research Association for Biotechnology; CDNA library construction:

11 Institute of Medical Science, University of Tokyo, Laboratory of

12 Genome Structure, Human Genome Center; CDNA 5'- £ 3'-end one pass

13 Sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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DNA Res. 12, 117-126 (2005)
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oligo capping, fis (full insert sequence).
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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                             Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2866 10-MAR-2004;
Research Association for Biotechnology (JP)
     Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Patent: WO 03104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov Series: TRAL Plate: 26 Row: m Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717. Location/Qualifiers

i. 2379
/organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
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/lab host="NHIH MGC_17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trainiation="MPGGCSRGPAACDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
APFLASAVSAGPPLPDCPALCECSEAARTVKCVRRNLTFBYPTDLAYYTRULFLTGNO
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TLABLQGLPRITNYFALDNNWWYCDCHRADMYTWLKETEVVGGKDRLTCAYPERGRRNYL
LELNSADLDCDPILPPSLQTSYVFLAIJUALIGAIFLLVLYLYLNRGGIKKWHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masillo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Young, A., Zhang, L.-H. and Green, E.D.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="ST4 oncofetal trophoblast glycoprotein"
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AB168108.1 GI:679678899
AB168108.1 GI:679678899
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="TPBG"
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/gene="TPBG"
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Pred. No.:
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butch, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Maruslana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M. B., Banaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317
IMARS:4138906), complete cds.
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1 (bases 1 to 2379)
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Submitted (03-SEP-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web Bite: http://www.niac.nih.gov/
Contact: niac_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., BeckBtrom-Sternberg,S.M., Benjamin,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
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On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Matches:
Conservative:
Mismatches:
Indels:
     retinoic acid (RA) induction"
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Tissue Procurement: ATCC
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BC037161.2 GI:33872201
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AUTHORS
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TITLE
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BC037161
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COMMENT
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TLABLĄGLPHYRVFLDNNPWVCDCHMADMYTWLKQTGVVQGKDRLTCAPPEKMRNRVL
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RDHMEGYHYRYBINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (23-0CT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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protein id="CAA09930.1"
db_xref="G1:3805947"
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AJ012159
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Homo sapiens (human)
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Matches:
Conservative:
Mismatches:
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|db_xref="InterPro:IPR000483"
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/organism="Homo sapiens"
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2698. .2703
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2704. .2709
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/gene="5T4"
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/gene="5T4"
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Best Local Similarity:
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Bubmitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku-ku, Tokyo, 162-8640, Japan (E-mail: khashimohin.go.) p. URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)

The International consortium for macaque cDNA sequencing and analysis consists of: Department of Virology and Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan; Division of Genetic Resources, National Institute of Infectious Diseases of Japan, Tokyo, Japan; National Health Research Institute, Taipel, Taiwan; Institute of Molecular Biology, Academia Sinica, Taipel, Taiwan; Department of Roology & Evolution, University of Chicago, Chicago, IL, USA; Center for Information Clone distribution information can be found at: http://www.nih.go.jp/yoken/genebank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 International consortium for macaque cDNA sequencing and analysis. DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Custom primers were used for 5' and 3'-end sequencing. The full-insert sequencing was done by primer-walking method using ABI DNA sequencer.
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/note="unnamed protein product; Homo sapiens trophoblast
glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3"
                                                                                                                      Osada, N., Hirata, M., Tanuma, R., Kusuda, J., Hida, M., Suzuki, Y., Sugano, S., Gojobori, T., Shen, J.C.-K., Wu, C.I. and Hashimoto, K. Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="macaque cDNA library QtsA"
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                                                                                                                                                                                                      Unpublished
                                                                                    Unpublished
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PRI 15-APR-2005

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complement(10004. .10982)
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TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKMRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRGIKKMMHNIRDAC
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LAVLPAGAPFARPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPP
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                                                                        This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 300); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="trophoblast glycoprotein"
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AL544610 AW471072 AW662538 BE260089 BP306457 BF306926
BF314984 BI196133 BI562387 BW069633 BM670613
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/chromosome="6"
  Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 184, UK. B-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Dec 15, 2000 this sequence version replaced gi:11558491.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SWISSROT; Tr:, TREMBL: Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group.

Http://www.sanger.ac.uk/HGP/Chr6

RP3-492P14 is from the library RPC1

RP3-492P14 is from the library RPC1

RP3-492P14 is from the library RPC1

Http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA sequence from clone RP3-492P14 on chromosome 6q13-15 Contains a single stranded DNA binding protein pseudogene, the TPBG gene for trophoblast glycoprotein (5T4-AG) and a CpG island, AL121977
                                                                                                                           AFSGSNASVSAPSPLVELILMHTVPPEDERQNRSFEGMVVAALLAGGERELGELA
SNHEVYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHHEDNALKVLHNG
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                       /product="5T4 oncofetal trophoblast glycoprotein" 5331. .5336
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Matches:
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HTG; CpG island; TPBG.
Homo sapiens (human)
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1 (bases 1 to 121909)
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3517. .4690
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Best Local Similarity:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
                                                                                                                                                                                                                                                                                                                                                           PAT 10-DEC-2003
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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synthetic construct
other sequences; artificial sequences.
Patent: WO 03068816-A 1 21-AUG-2003;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers

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Sequence 1 from Patent W003068815.
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Sequence 14 from Patent W00136486.
AX149553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AACCTGACCGAGGTGCCCGCGGACCTG 264
                                                                                                                                                                                                                                                                                       238 AACCTGACCGAGGTGCCCGCGGACCTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1260
/organism="Felis catus"
                                                                                                                                                                                                                                                                          1 AsnLeuThrGluValProThrAspLeu 9
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                                                                                                                                          56.9
41.00
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Best Local Similarity:
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                                PEATURES
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis:
                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae;
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WHC class I peptide epitopes from the human 5t4 tumor-associated
antigen
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                             /note="Clone_right_end: RP3-492P14"
                                                                                     Length:
Matches:
Conservative:
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/locus_tag="RP3-492P14.1-001"
121909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide
Patent: WO 0238612-A 3 16-MAY-2002;
Patent: WO 0238612-A 3 16-MAY-2002;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX821533 1260 bp
Sequence 1 from Patent WO03068816.
AX821533
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AX467373
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Felis catus
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                                                                                                              Percent Similarity:
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Best Local Similarity:
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Felis sp.
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AX467373
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AP006878_09

AP006878_11

AP006878_13

AP006878_14

AP006878_15

AP006878_16

AP006878_17

AP006878_18

AP006878_18

AP006878_18

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AP006878_19
  AP006878_04
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AP006878_07
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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                                                                                                                                                                                                                                                                                                                                                                                        linear
Ellard, F.M. and Myers, K.A.
Antibodies
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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/note="574"
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Matches:
Conservative:
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002,
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 1 from Patent WO0238612.
AX467371
                                                                                                                                                                                                                                                                                                                   241 AACCTGACCGAGGTGCCCGCGGACCTG 267
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AP006878 01
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AP006878 03
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Scillagorani, muriolace; murinae; karcus.

Ruzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,

Anjale, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Barastead, M., Benahmed, F.,

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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

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Clackeland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D., Soura, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Drum, A., Durbin, K., Duval, B., Baves, K.,

Egan, A., Escottco, M., Eugene, C., Evans, C., Palls, T., Fan, G.,

Fernandez, S., Finley, M., Flaggi, N., Forbes, L., Foster, M., Guevara, M.,

Gabregeorgis, E., Geer, K., Gall, R., Garcia, A., Garner, T., Garza, M.,

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Harvey, Y., Havlak, P., Hawes, A., Hadun, S.L., Hodgson, A., Hogues, M.,

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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Rattus.
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HTG; HTGS PHASEL; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Matches:
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Mismatches:
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COMMENT

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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mavhiney, G., McCedd, M. P., Morell, T. Z., Mentenn B.,
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Direct Submission
Nidethausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Direct Submission
Nidethausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Melnstock, G. and Gibbs, R.A.

E. (bases I to 187783)

E. Basses I to 187783)

E. Basses I to 187783

B. Basses I to Sooties and there may be sequence of Molecular and Human Genome Sequencing reads assembled using a caffold in the feature table below represents a scaffold in the Sequence
Dysider Submission

Meller, M.W
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Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Center project name: CH210-unknown

Center project name: CH210-unknown

Assembly program: Phrapp version 0.990329

Consensus quality: 149999 bases at least Q40

Consensus quality: 149999 bases at least Q30

Consensus quality: 155975 bases at least Q30

Consensus quality: 155975 bases at least Q30

Consensus quality: 150322 bases at least Q30

Consensus quality: 160322 bases at least Q30

Consensus quality: 160322 bases at least Q40

Consensus quality: 160322 bases at least Q40

Consensus quality: 160322 bases at least Q40

**NOTE: Estimated insert size: 153789; sum-of-contigs estimation

**NOTE: Estimated insert size: may differ from sequence length

**NOTE: Estimated insert size may differ from sequence length

**NOTE: This is a "working draft' sequence It currently

**Consists of contigs. The true order of the pieces

** is not known and thair order in this sequence record is

** arbitrary. Gaps between the contigs are represented as

** runs of N, but the exact sizes of the gaps are unknown.

** This record will be updated with the finished sequence

** as soon as it is available and the accession number will

** be preserved.
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40744: contig of 40744 bp in length 40844; gap of unknown length 180556: contig of 139712 bp in length 180656: gap of unknown length

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

I (bases 1 to 225405)

Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Angalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barth, P., Brown, M., Biswaho, K., Blatr, J., Blark, P., Brown, M., Brancho, K., Blatr, J., Blark, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burcell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Clacko, J., Chan, C., Coyle, M., Cree, A., D'Souza, L., Caveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
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225405 bp DNA linear HTG 01-JUL-2005

Bos taurus clone CH240-53E16, *** SEQUENCING IN PROGRESS ***, 26

unordered pieces.
182042: contig of 1386 bp in length 182142: gap of unknown length 143 183473: contig of 1331 bp in length 144 185573: gap of unknown length 574 185310: contig of 1737 bp in length 11 185410: gap of unknown length 11 18783: contig of 2373 bp in length 11 197783: contig of 2373 bp in length Location/Qualifiers
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8
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1
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0
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:

    187783
    organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /estimated length=unknown
182043. .182142
/estimated length=unknown
183474. .183573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /estimated_length=unknown
185311. .185410
/estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                   /estimated length=unknown
76822. .80300
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                                                                                                                                                                                                              /mol_type="genomic DNA'
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                                                                                                                                                                                                                                 /db xref="taxon:10116"
/clone="CH230-unknown"
                                                                                                                                                                                                                                                                                                                                                                            /note="wgs contig"
107643. .109294
/note="wgs contig"
147795. .149099
                                                                                                                                                                                                                                                                        36541. .37777
/note="wgs_contig"
40745. .40844
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_contig"
169577. .171056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169577. .171056
/note="wgs_contig"
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88.9%
88.9%
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183474
183574
185311
185411
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Best Local Similarity:
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AC158075/c
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KEYWORDS
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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Bragado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Bgan, A., Escotto, M., Rugene, C., Bvans, C.A., Falls T., Fang, G., Franser, C.M., Falls, T., Falls, T., Fangene, C., Brans, C.A., Falls, T., Fangene, C., Brans, C.A., Falls, T., Garza, M., Garcia, A., Garcia, T., Garza, M., Gabisi, B., Gerk, G. Gill, R., Garcia, A., Garcia, T., Garza, M., Gaursence, P., Harland, W., Hamil, C., Hamilton, C., Hamilton, K., Harnandez, R., Harlas, S., Hladum, S.L., Hodgeon, A., Hogues, M., Harland, S., Hladum, S.L., Hodgeon, A., Hogues, M., Hollins, B., Howells, S., Hladum, S.L., Hodgeon, A., Hogues, M., Jackson, L., Jang, H., Johnson, B., Johnson, R., Jolivet, N., Karger, C., Kraft, C.L., Labow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., Longare, S., Loger, S., Loger, S., Loger, M., Malloy, K., Mangum, A., Mahleshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Marchod, W., Liu, Y., London, P., Longare, S., Logez, J., McLeod, M. P., McNeill, T. Z., Mennen, E., Mann, P., Mann, P., Mann, P., Mann, P., Martinez, E., Mander, S., Hall, W., Martin, R., Mann, P., Martinez, E., Mander, S., Mander, M., Martinez, E., Mander, S., Parke, K., Pasternak, S., Pall, H., Perez, A., Perez, L., Pfann, C., Raifs, R., Parke, K., Pasternak, S., Pall, H., Perez, A., Perez, L., Pfann, M., Parke, K., Pasternak, S., Pall, H., Perez, A., Perez, L., Pfann, M., Parke, K., Pasternak, S., Pall, H., Perez, A., Perez, L., Pfann, S., Sander, M., Savery, G., Scheter, S., Scott, G., Shateman, S., Sand, H., Sander, M., Savery, G., Scheter, S., Scott, G., Shateman, S., Sander, M., Savery, G., Scheter, S., Scott, G., Shateman, S., Sander, M., Streng, R., Wang, S., Wangor, Y., Vallsen, M., Streng, R., Wang, S., Watch, M., Streng, R., Wang, S., Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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shotgun sequence only contigs will be indicated in the feature
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------ Project Information
Center project name: FDBK
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Cow Genome Sequencing Consortium.
Direct Submission
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Center: Baylor College of
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Worley, K.C.
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html). NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                    Assembly program: Atlas 3.0;
Consensus quality: 212622 bases at least Q40
Consensus quality: 214515 bases at least Q30
Consensus quality: 214515 bases at least Q30
Consensus quality: 216171 bases at least Q30
Estimated insert size: 215649; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4233: contig of 4233 bp in length 8770: gap of 1336 bp 7744: contig of 2175 bp in length 8770: gap of 526 bp in length 11091: gap of 526 bp in length 11091: gap of 526 bp in length 13977: contig of 2796 bp in length 13977: gap of 50 bp in length 25870: gap of 1369 bp in length 3959: contig of 1369 bp in length 4663: gap of 1324 bp in length 4663: gap of 1324 bp in length 4663: gap of 1324 bp in length 49277: gap of 1324 bp in length 49277: gap of 50 bp in length 10536: contig of 31069 bp in length 10536: contig of 2470 bp in length 10536: gap of 1328 bp in length 10536: contig of 18633 bp in length 112651: contig of 18633 bp in length 113922: contig of 1922 bp in length 13021: contig of 1922 bp in length 13021: contig of 1922 bp in length 13021: contig of 192 bp in length 13021: contig of 192 bp in length 13177: gap of 50 bp in length 16162: contig of 18495 bp in length 16162: contig of 18495 bp in length 16162: gap of 50 bp in length 16762: gap of 50 bp in length 16778: contig of 1068 bp in length 1778: gap of 50 bp in length 16778: contig of 1068 bp in length 1778: gap of 50 bp in length 16778: contig of 1068 bp in length 1778: gap of 50 bp in
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Center clone name: CH240-53E16
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/organism="Bos taurus"
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Eggal, A., Escotto, M., Eugen, C., Evane, C.A., Falls, P., Fanga, P., Franciez, S., Finley, M., Elaggi, N., Forbes, L., Foster, M., Gebregeorgis, S., Gels, A., Garcia, A., Garcer, M., Guraara, M., Guraaran, C., Handlan, S., Garcia, A., Garcia, A., Garcia, A., Garcia, M., Guraaa, M., Guraaa, M., Handlan, C., Handlton, K., Harley, P., Havlak, P., Hawe, A., Henderson, A., Hogues, M., Handlan, S.L., Hodgen, A., Hogues, M., Henlins, B., Howells, S., Hulby, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kaelly, S., Khan, Z., King, L., Kovar, J., C., Lebow, H., Levan, J., Leavis, L., Li, Z., Liu, J., Liu, W., Martin, K., Martin, R., Reige, R., Reger, R., Reige, R., Reder, R., Reige, R., Reige, R., Reige, R., Reige, R., Reige, R., Ride, R., Sodery, G., Scherz, S., Soct, G., Shateman, S., Shen, H., Scherz, S., Sort, G., Shatek, A., Sodersten, R., Sodersten, R., Song, X.-Z., Sorelle, R., Sola, J., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Treige, Z., Usu, M., Williams, G., Milleon, R., Wale, S., Swatek, A., Tabor, P., Taylor, T., Williams, G., Wille, R., Wu, J., Yakub, S., Dunn, D., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., Yon, W., Williams, C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 241280)
Rat Genome Sequencing Consortium.
Evans, C.A., Falls, T., Fan, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
Center code: BCM
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Center clone name: CH230-171M15
  ., Eugene, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- Genome Center
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TITLE
JOURNAL
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AUTHORS
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, M. Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, R., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bulary, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., D'Souza, L.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Dersmo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus clone CH230-171M15, *** SEQUENCING IN PROGRESS
***, 7 unordered pieces.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACIISIS8.5 GI:25072995
HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                   /estimated length=315
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39560. 39609
/estimated length=50
43340. 44663
/estimated length=1324
/9228. 49577
estimated length=50
6811mated length=50
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130822. .130911
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     /mol_type="genomic DNA"
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/clone="CH240-53816"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AsnLeuThrGluValProThrAspLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /estimated_length=1552
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/estimated length=526
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143068. .143117
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Best Local Similarity:
Query Match:
DB:
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AC115158
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AC115158/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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AL Submitted (19-VMOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON Nov 19, 2002 this sequence version replaced gi:23321705.
The sequence in this assembly is a combination of BAC based reads and whole genome shortun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Esch contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Levisis by DNA linear HTG 10-MAY-2003 Cattus norvegicus clone CH230-111N19, *** SEQUENCING IN PROGRESS AC095339
217408 AACCTAACTAGGGTACCTACTGACTTG 217382
                                                                                                                                                                                         AC095339.6 GI:30522597
                                                             RESULT 27
AC095339/c
LOCUS
                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                            DEFINITION
                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Assembly program: Phrap; version 0.990329
Consensus quality: 144835 bases at least Q40
Consensus quality: 155713 bases at least Q30
Consensus quality: 157747 bases at least Q20
Estimated insert size: 147852; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                      197836: contig of 197836 bp in length
1837 197956: gap of unknown length
1828 232627: contig of 34591 bp in length
1828 233677: contig of 1040 bp in length
1828 233677: contig of 1040 bp in length
1837 234899: gap of unknown length
1890 234899: gap of unknown length
1890 234899: gap of unknown length
1897 236876: contig of 1987 bp in length
1897 236876: gap of unknown length
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1898 239939: contig of 1983 bp in length
1899 236876: gap of unknown length
1890 236876: gap of unknown length
1890 241280: contig of 2241 bp in length
1891 241280: contig of 2241 bp in length
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Matches:
Conservative:
Mismatches:
Indels:
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/mol type="genomic DNA"
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159135. .160674
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197837. .197936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234790. .234889
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Best Local Similarity:
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Gaps:

US-10-774-176-11 (1-9) x AC115158 (1-241280)

Query Match:

1 AsnLeuThrGluValProThrAspLeu 9

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Schurographi, Muroadea, Murinae; Martine; Kattus,
Stilurographi, Muroadea, Murinae; Martine;
Schurographi, Muroadea, Murinae; Martine;
Manyle, Martie, Merzker, M. Lee, Abramzon,S., Adame,C., Allen,T.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angulano,D.,
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Jackson,L., Jacob,L., Martin,R., Martin,R., Man,J.,
Mangum,B., Mapus,P., Martin,R., Martin,R., Martin,R., Man,J.,
Mangum,B., Mapus,P., Martin,R., Martin,R., Man,J., More,B., Rober,B., Martin,R., Man,J., Mortis,R., Man,J., Reves,R., Petankoch,C., Redie,R., Reves,R., Petankoch,C., Rodey,R., Mortis,R., Martin,R., Man,J., Martin,R., Martin,R., Man,J., Martin,R., Man,J., Martin,R., Man,J., Martin,R., Man,J., Martin,R., Martin,R., Martin,R., Martin,R., Man,J., Martin,R., Martin,R., Martin,R., Martin,R., Mang,S., Ritton,A., Savat,R., Rober,R., Mang,S., Man,J., Ratter,M., R
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Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                    Euteleostomi;
                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Unpublished
2 (bases 1 to 267375)
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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STS 09-APR-2005
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qgi26e11.bl Clint Pan troglodytes verus STS genomic, sequence
tagged site.
         25 263673: contig of 1379 bp in length
74 263773: gap of unknown length
74 265303: contig of 1430 bp in length
74 265303: gap of unknown length
74 265303: contig of 2072 bp in length.
75 267375: contig of 2072 bp in length.
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length
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Matches:
Conservative:
Mismatches:
Indels:
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12594. .12633
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12694. .14240
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/estimated length=unknown 248910. .249009
unknown
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                                                                                                                                                                                                 /clone="CH230-111N19"
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                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig"
240576. .240675
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/estimated lenge
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88.9%
88.9%
89.1%
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Best Local Similarity:
Query Match:
DB:
                               263674
263774
265204
265304
                                                                                                                                                                                                                   misc_feature
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LOCUS
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   Rat Genome Sequencing Consortium.

Breat Genome Sequencing Consortium.

Direct Submitsed (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, UGA

On May 10, 2003 this sequence version replaced gi:23269154.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Sstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Atlas 3.0;
Consensus quality: 242457 bases at least Q40
Consensus quality: 247377 bases at least Q30
Consensus quality: 250200 bases at least Q30
Consensus quality: 350200 bases at least Q30
Sstimated insert size: 248371; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 12593 bp in length
contig of 227882 bp in length
contig of 227882 bp in length
gap of unknown length
contig of 3560 bp in length
contig of 1036 bp in length
contig of 1036 bp in length
gap of unknown length
contig of 1177 bp in length
contig of 2161 bp in length
gap of unknown length
contig of 2161 bp in length
contig of 1823 bp in length
gap of unknown length
contig of 1823 bp in length
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contig of 2161 bp in length
gap of unknown length
contig of 1823 bp in length
gap of unknown length
contig of 1204 bp in length
contig of 1390 bp in length
gap of unknown length
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length
bp in length
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Baylor Plaza, Houston, TX 77030, USA
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gap of
contig
gap of
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gap of
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259007:
259107:
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260663:
262194:
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256003:
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240676
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              REFERENCE
AUTHORS
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87.0%
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    Query Match:
DB:
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                     RESULT 29
BV564129
                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to all pairs of overlapping reads to call NQS bases and SNPs. Alignments (between two reads) with less than 100 NQS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two
                                                                                      Pan troglodytes verus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                            Initial Sequence of the Chimpanzee Genome and Comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             troglodyřes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan
troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies of a single read, comparisons between two reads that share 95% of their genome
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(Gon, Unknown Chimp). Common names: Pan troglodytes verus is the
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Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
including Clint (Pan
                                                                                                                                                   Hominidae, Pan.
1 (bases 1 to 701)
Mikkelsen, T.S., Hillier, W.L., Bichler, B.B., Zody, M.C. and
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Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes verus"
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Mismatches:
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sub_species="verus"
/db_xref="texon:37012"
/clone_lib="clint"
<1. .>701
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mczody@broad.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
                           BV561288.1 GI:62452309
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                                                                      Pan troglodytes verus
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                                                                                                                                                                                                                                                                  Human Genome
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Best Local Similarity:
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Goo, Unknown Criding). Common names: Pan troglodytes verus is the western chimp and Pan troglodytes trogalodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must have phred calls must have phred scovers, a calls must have phred score >= 20, at least 30% of its base calls must have phred score >= 20, at least 30% of its base calls must have phred score >= 30, the surrounding 10 bases in the read have Phred score >= 30, the surrounding 10 bases in the read have Phred score >= 30, the surrounding 10 bases in bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were
                                                                                                                                                                                                                                                                                                                                                           STS 09-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Build 34 (hg16,7uly 2003). Chimp WGS reads were from 9 donors, including Clint (Pan
troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan
troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
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qxq68d12.g1 Clint Pan troglodytes verus STS genomic, sequence
tagged site.
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Hominidae, Pan.
1 (bases 1 to 804)
Mikkelsen,T.S., Hillier,W.L., Bichler,B.E., Zody,M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 Charles Street, Cambridge, MA 02141, USA Tel: 6172580933 Fax: 6172580903
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Broad Institute of MIT and Harvard
Indels:
                                    Gaps:
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Primer A: No sequence submitted
Primer B: No sequence submitted
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                                                                                             US-10-774-176-11 (1-9) x BV561288 (1-701)
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Pan troglodytes verus
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Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbi.nig.ac.jp/c-elegans/html/CB INDEX html) and The C. elegans ORFeeme cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using jim Kent's wABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The 5' clone is F26B1, 200 bp overlap; the 3' clone is ZG308, 600 bp overlap. Actual start of this clone is at base position 23932 of F26B1, actual end is at 4388 of ZC308.
                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-SEP-2004) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.wormbase.org/db/seq/sequence?name=K04F10;class=Sequence
                                                                                                Direct Submission
Submitted (15-UUN-2003) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Department of Genetics, Washington University
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: submissions@watson.wustl.edu and jes@sanger.ac.uk
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
8 (bases 1 to 35413)
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/note="SL1 trans-splice acceptor; see yk846a02.5"
/gene="bli-4"
/locus_tag="K04F10.4"
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/chromosome="1"
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Submitted (06-JUL-2001) Department of Genetics, Washington
Submiversity, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
4 (bases 1 to 35413)
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Submitted (01-AUG-2001) Department of Genetics, Washington
Submitted, Vol-AUG-2001) Department of Genetics, Washington
Louis, MO 63110, USA
5 (bases 1 to 35413)
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Submitted (19-NOV-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
7 (bases 1 to 35413)
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Direct Submitted (23-MAX-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
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Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
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                              /organism="Pan troglodytes verus"
/mol type="genomic DNA"
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Latreille, P. and Wamsley, P.
The sequence of C. elegans cosmid K04F10
Unpublished (2001)
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11237. .11554,11600. .11680,11790. .11966,12018. .12245,
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/product="Blistered cuticle protein 4, isoform d"
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BVGRTCPGGLLLTUDVDNMPHYDHGKCVBSCPPCLVADYESNLVGCTGGGGY
YINAVGKCDLCDSSCETCTAPGPMSCERCSKGSIGTGCRCKCASETKSWGCEDC
SKDPTLLIDSNKSSGFGELMFWIVVSLIAACGICGKCKCASETKSSNVETKSMCEDC
TGANTALAGANTDDBDBEDBUFVNPQIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(10252. .10332,10377. .10664,10772. .10915,10976. .11181, 11237. .11554,11600. .11680,11790. .11966,12018. .12245, 22.12461, .12660,13241. .13371,21787. .21859, 22715. .22893,22945. .23053,23096. .23247)
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OSTF153A12 1, OSTF088G71, OSTF090A51,
VK308A3.3, VK308A3.5, VK1995.3, VK1995.5,
VK308A3.3, VK208A3.5, VK218A9.3, VK21967.5,
VK308A3.3, VK208A3.5, VK218A9.3, VK319A7.5,
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VK408C4.5, VK408G9.3, VK53A0.3, VK13B4C0.5,
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PDPLYKDQWYLHGGAVGGYDMNVRQAWLQGYAGRNVSVSILDDGIQRDHPDLAANYDP
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PRPIVGREQLNFTLDVNGCESGTPVLYLLEHVQVHATVRYLKRGDLKLTLFSPSGTRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG 28-JUL-2005
LASTDINDHDDDPTPQNNGDNKHGTRCAGEVAALAGNNQCGVGVAFKAKIGGVRMLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Pan.
1 (bases I to 106590)
Xu, W., Hua, A. and Roe, B.A.
Pan troglodytes BAC Clone rp43-149k8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, W., Hua, A. and Roe, B.A.
Direct Submission
Submitted (14-OCT-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OK 73019, USA

3 (bases 1 to 106590)

Xu,W., Hua,A. and Roe,B.A.

Direct Submission

Submission

Submission

Submission

OK 73019, USA

OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ncibles 106590 bp DNA linear HTG 28-JU Pan troglodytes clone rp43-149k8, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OK 73019, USA
On Jul 28, 2005 this sequence version replaced gi:71067220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTB: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2128: contig of 2128 bp in length 2228: gap of unknown length 4366: contig of 2158 bp in length 4486: gap of unknown length 6694: contig of 2208 bp in length 6794: gap of unknown length 8829: contig of 2035 bp in length 8929: gap of unknown length 11542: contig of 2613 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                         3887 AATTTGACACCTGTTCCTACAGATTTG 3913
                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                    1 AsnLeuThrGluValProThrAspleu 9
                                                                                                                                                                                                                                                                                                                                        US-10-774-176-11 (1-9) x AP039719 (1-35413)
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Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC151952.13 GI:71361787
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                                                                                                                                                                         2.29e+03
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2229
4387
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6695
6795
8830
8930
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                                                                                                                                                         Alignment Scores:
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KEYWORDS
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TITLE

CDS

COMMENT

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Leporidae; Oryctolagus.

1. (Dasses 1 to 16590)

S. Antonellis, A., Ayele, K., Bass, D., Benjamin, B., Bera, J.,
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G.,
Coleman, H., Engle, J., Franks, S., Fuksenko, T., Gestole, M.,
Greene, A., Guaran, X., Gutson, N., Haghighi, P., Han, J.,
Hansen, N., Ho, S.-L., Hu, P., Hunter, G., Hurle, B., Idol, J.R.,
Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R.,
Maddero, L., Maduro, Q.L., Magrulies, E.H., Masiello, C.,
Maskeri, B., McDowell, J., Modidi, H.A., Margulies, E.H., Masiello, C.,
Portnoy, M. E., Prasad, A., Puri, O., Rantz, K., Reddix-Dugue, N.,
Sante, A., Thomas, J.W., Thomas, P. J., Tsipouri, V., Ung, L., Vogt, J.L.,
Wetherby, K. D., Withers, T. R., Young, A. and Green, E.D.
ACLEGICAL

166980 bp DNA linear HTG 27-JUL-2005
Oryctolagus cuniculus clone LB1-115F14, WORKING DRAFT SEQUENCE, 4
UNDOCHERE PIECES.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Lagomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11862: contig of 11862 bp in length 11962: gap of unknown length 23352: contig of 11330 bp in length 23462: gap of unknown length 87182: contig of 63730 bp in length 87282: gap of unknown length 166980: contig of 79698 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
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Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1 to 166980)
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11963
23353
23453
87183
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               LOCUS
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                                                                                                                          ORGANISM
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AUTHORS
TITLE
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                                                          ACCESSION
VERSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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2129. :2228
            106590
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
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Conservative:
Mismatches:
Indels:
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14665. 14964
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34715. 34814
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39113. 39212
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45069
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53900
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111643
114865
120402
220402
221082
221182
232294
344115
348115
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Best Local Similarity:
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DB:
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AC166203
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PEATURES

gap gap gap gap gap gag gap gap gag gap gap gap

DRIGIN

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ACU92347

Homo sapiens chromosome 16 clone RP11-285K4, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
                                  www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 173718 bases at least Q40
Consensus quality: 178005 bases at least Q30
Consensus quality: 178068 bases at least Q30
Consensus quality: 178648 bases at least Q30
Estimated insert size: 167000; agarose-fp estimation
Quality coverage: 8.05 in Q20 bases; agarose-fp estimation
Quality coverage: 8.05 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* Consists of contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC092347
AC092347.1 GI:14589536
AC1971471 HTGS PHASE1, HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                       1. .180623
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae, Homo
1 (bases 1 to 181161)
DOB Joint Genome Institute.
Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83580 CTCACAGAGGTCCCCACGGATCTC 83557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-774-176-11 (1-9) x AC092341 (1-180623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: RPCI-11_285K4
                                                                                                                                                                                                                                                                      /clone="RP11-260K13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LeuThrGluValProThrAspLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center Project Name: 516049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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AC092341 AC025926
AC092341.5 GI:29294031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUL-2002) Production Sequencing Facility, DOE Joint Submitted (08-JUL-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute.

Direct Submission Institute.

Direct Submission Sequencing Facility, DOE Joint Submitted (13-DEC-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (bases 1 to 180623)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 18623) DOE Joint Genome Institute.
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1 (base 1 to 180623)

DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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breed: New Zealand White"
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Conservative:
Mismatches:
Indels:
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2 (bases 1 to 180623)
DOE Joint Genome Institute.
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Best Local Similarity:
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misssemblishs, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/s; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 187747 bases at least Q20
Consensus quality: 187747 bases at least Q20
Consensus quality: 187744 bases at least Q20
Insert size: 187864; sum-of-contigs
Quality coverage: 9.31x in Q20 bases; sum-of-contigs
Taye, A., Thomas, J.W., Thomas, P.J., Tsipouri, V., Ung, L., Vogt, J.L., Wetherby, K.D., Withers, T.R., Young, A. and Green, B.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of S contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 18795 18894: captig of 18794 bp in length

* 18795 18894: captig of 37774 bp in length

* 56769 80795: cantig of 23627 bp in length

* 56769 80795: cantig of 23627 bp in length

* 169237 188254: contig of 18918 bp in length

* 169337 188254: contig of 18918 bp in length

* 169337 188254: contig of 18918 bp in length

* 169337 188254: contig of 18918 bp in length

* 169337 188254: contig of 18918 bp in length

* Accention/Qualifiers

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                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-AUG-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Aug 6, 2005 this sequence version replaced gi:71274277.
                                                                                                                                                                                        Submitted (27-JUL-2005) NIH Intramural Sequencing Center, 5625 Fishers Lane, Rockville, MD 20852, USA (bases 1 to 188254)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc zoo@nhgr1.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: 11w
Center clone name: 239102
                                                                                                             (bases 1 to 188254)
                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                  Green, E.D
                                                                                                                                            Green, B.D
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1 (bases 1 to 188254)

3 Antonellis A., Ayele, K., Bass, D., Benjamin, B., Bera, J., Chu, G., Blakesley, R., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H., Engle, J., Franks, S., Puksenko, T., Gestole, M., Greene, A., Gura, X., Gupta, J., Gurson, N., Haghighi, P., Han, J., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Marguiles, E. H., Masiello, C., Masteri, B., MoDowell, J., Mojdil, H.A., Mullikin, J.C., Park, M., Portnoy, M. B., Prasad, A., Schueler, M.G., Sison, C., Stantripop, S., Sante, A., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S.,
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     runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1282 7785: contig of 6404 bp in length
1382 7785: contig of 6404 bp in length
1385: gap of unknown length
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133 102028: contig of 27199 bp in length
133 102028: contig of 48796 bp in length
123 102128: contig of 48796 bp in length
129 181161: contig of 79033 bp in length
120 181161: contig of 79033 bp in length
120 181161: contig of 79033 bp in length
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Matches:
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HTG; HTGS PHASE2; HTGS DRAFT.
Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
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231264 bp DNA linear HTG 11-AUG-2005
Danio rerio chromosome 16 clone DKEY-25C4, WORKING DRAFT SEQUENCE,
5 unordered pieces.
                A (bases 1 to 191684)

Ku, W. and Roe, B.A.

Submitted (15-70L-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Jul 15, 2004 this sequence version replaced gi:47901752.

Center: Department Of Chemistry And Biochemistry
Che University Of Oklahoma
Center code:UOKNOR
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyptinidae; Danio.
1 (Sases 1 to 231264)
Phillimore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (10-A002-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests:
http://www.sanger.ac.uk/Projects/D rerio/fags.shtml#dataeight
On Aug 12, 2005 this sequence version replaced gi:68161913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGA64; version 4.5
Chemistry: Due-terminator; 100% of reads
Consensus quality: 230238 bases at least Q40
Consensus quality: 230512 bases at least Q30
Consensus quality: 230578 bases at least Q20
Insert size: 230864; sum-of-contigs
Insert size: 223468; 2.8% error; agarose-fp
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Danio rerio
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Mismatches:
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Center code: SC
Web site: http://www.sanger.ac.uk
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1. .191684
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Submitted (15-AUG-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 191684)
Xu,W. and Roe, B.A.
Birect Submission
Submitted (02-UNN-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
/note="BAC resource: http://bacpac.chori.org/
breed: New Zealand White"
1. .1013190
/note="clone overlaps with GenBank Accession Number
AC166203 clone LB1-115F14 (center project name llv)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      / 16937. ... 180354
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clone_end:T7
vector_side:right"
187910. ... 180354
/note="clone overlaps with GenBank Accession Number
AC165396 clone LB1-64D22 (center project name llx)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC146469 191684 bp DNA linear
Pan troglodytes clone rp43-45g24, complete sequence.
AC146469
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                            /estimated length=unknown
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80496. .169236
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169237. .169336
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                                                                                            1. .18794
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (chimpanzee)
                                                                                                                                       clone_end:SP6__
vector_side:left"
18795._.18894
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                                                                                                                                                                                                                                                                                                                                           30396. .80495
                                                                                                                                                                                                                                                                                                56769. .80395
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1 (bases 1 to 191684)
Xu, W. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 191684)
Xu, W. and Roe, B.A.
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77.8%
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VERSION
SEYWORDS
SOURCE
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AUTHORS
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JOURNAL
REFERENCE
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AUTHORS
TITLE
JOURNAL
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1. .394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Sukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroides; Muridae; Rattus.
                                                                                                                                                                                                                                                                                                                        different strains of mice (as of October 1, 2003). Those strains include
                                                                                                                                                                                                                                                                                                                                                              A/J, A/HeJ,
129/bd, ARKJ, B10.D2-H2/oSnJ, BALB/CByJ, BALB/CJ,
C3H/HeJ, CS7BL/GJ,
CAST/Ei, DBA/2J, WRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.
                                                                    3431 Hillytew Ave, Mailstop S3-1, Palo Alto, CA 94024, USA Tel: 650855807
Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farris,G., Hicken,S.H. and Farr,S.B.
Rat toxicologically relevant genes and uses thereof
Patent: WO 02066682-A 10 29-AUG-2002;
Phase-1 Molecular Toxicology Inc. (US)
Location/Qualifiers
                               Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     691 bp I
Sequence 10 from Patent WO02066682.
AX525488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
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                   Jonathan Usuka
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Query Match:
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AX525488/c
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VERSION
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AUTHORS
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ORIGIN
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394 bp DNA linear STS 15-OCT-2003
RPAMMSEQ0002525 Roche Palo Alto Mus musculus STS genomic, sequence
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Sciurcognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 394)
1 (bases 1 to 394)
McMcA,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A.,
McPherson,J.D., Poernzler,D. and Peltz,G.
Mus musculus SNPs
Unpublished (2003)
                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                      130645: contig of 130645 bp in length 130745: gap of 100 bp 223377: contig of 92632 bp in length 223477: gap of 100 bp 226256: contig of 2779 bp in length 226356: gap of 100 bp 229095: contig of 2739 bp in length 229195: gap of 100 bp 231264: contig of 2069 bp in length.
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Matches:
Conservative:
Mismatches:
Indels:
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// note * assembly fragment: 01232

fragment chain: I*

130746. .223377

/note * assembly fragment: 03846

fragment chain: I*

223478. .226256
 coverage: 9.70x in Q20 bases; agarose-fp
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226357. 229095
inote="assembly_fragment:00100"
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                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-774-176-11 (1-9) x CR388209 (1-231264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKEY-25C4"
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BV090626
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PAT 21-NOV-2002

linear

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db_xref="taxon:9031"
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                                                                                                                       PAT 28-JUN-2002
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Kwaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum, Institut fuer Molskulare Strahlenbiologie, Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caldwell, R. B., Kierzek, A.M., Arakawa, H., Bezzubov, Y., Zaim, J., Fiedler, P., Kutter, S., Blagodatski, A., Kostovska, D., Koter, M., Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M. Full-length cDMAs from chicken bursal lymphocytes to facilitate gene function analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2949 bp mRNA linear VRT 1
Gallus gallus mRNA for hypothetical protein, clone 16m20.
AJ720394
                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                       linear
                                                                                                                                                                                                                                                      Berka, R. and Clausen, I.G.
Methods for monitoring multiple gene expression
Patent: WO 0229113-A 6689 11-APR-2002;
Novozymes Biotech, Inc. (US) ; Novozymes A/S (DK)
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Seguence 6689 from Patent WO0229113.
AX438274
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                                             430 AATCTTAGAGAGATTCCTACAGATCTT 404
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                 1 AsnLeuThrGluValProThrAspLeu
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US-10-774-176-11 (1-9) x AX525488 (1-691)
                                                                                                                                                               AX438274.1 GI:21663082
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Caldwell, R.B.
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77.8%
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Best Local Similarity:
Query Match:
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SGRNILRKALLMCESCRVQQYPFSADQDIPEMDWBICLRETANAIVSQQSPQRLLEVRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 06-JUN-2002
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Sciurognathi; Muroidea; Muridae; Murinae; Rattus
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Blashoff, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Buarchontoglires; Glires; Rodent
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Matches:
Conservative:
Mismatches:
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Patent: WO 0210453-A 1422 07-FEB-2002;
Gene Logic, Inc. (US)
Location/Qualifiers

    .2977
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1422 from Patent WO0210453.
AX401746
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                                                                                                dev stage="2 weeks old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVAKFMAIYKKFMEDGLDDMMF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AsnLeuThrGluValProThrAspLeu 9
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Rattus norvegicus
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/clone_lib="NGT (GAP_Mam5" |
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk

Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Whe Batte: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 8 Row: m Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6680677.

Location/Qualifiers
                                                   3007 bp mRNA linear ROD 13-FEB-2004 Mus musculus aldehyde dehydrogenase family 3, subfamily A2, mRNA (CDNA clone MGC:6055 IMAGE:3490519), complete cds.
                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (28-F92-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse CDNA sequences
Proc. Warl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                          BC003797.1 GI:13277827
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                   RESULT 44
BC003797
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                                                                                                                                                                                                                                                              KALWAD 29-17 bp mRNA linear ROD 27-APR-1993
Rat microsomal aldehyde dehydrogenase mRNA, complete cds.
M73714
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J. Biol. Chem. 266 (29), 19536-19542 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Miyauchi, K., Masaki, R., Taketani, S., Yamamoto, A., Akayama, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Original source text: Rattus norvegicus (strain Sprague-Dawley) (library: lambda-gt10; lambda-gt11) liver cDNA to mRNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    M73714.1 GI:205265
aldehyde dehydrogenase; integral membrane protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="liver"
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Matches:
Conservative:
Mismatches:
Indels:
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124. .1578
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Mismatches:
Indels:
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                                              Gaps:
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77.8%
84.8%
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39.00
88.94
77.84
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Best Local Similarity:
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Best Local Similarity:
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DB:
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SOURCE
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FEATURES

COMMENT

AUTHORS

TITLE

REFERENCE

RESULT 43

È 셤 RATMAD

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Submitted (04-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: vega@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clon Jun 13, 2002 this sequence version replaced gi:20803600. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Bm: BME; Sw:, SWISSEROT; Tr:, TERMBL; Wp:, WORMPEP; Information on the WORMPEP Information at the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL672172 S2478 bp DNA linear ROD 09-FEB-2005 Mouse DNA sequence from clone RP23-133K20 on chromosome 11 Contains the Aldh3a2 gene for aldehyde dehydrogenase family 3 subfamily A2 and a CDG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; aldehyde dehydrogenase; Aldh3a2; CpG island.

Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.
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Peatures and Mapping of Sixty-six TAC clones which cover the 6.7
                                                                                                                                                                                     Direct Submission
Submitted (126-MR-2002) Yasukazu Nakamura, Kazusa DNA Research
Submitted (26-MR-2002) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1533-3, Yana,
Kisarazu, Chiba 292-0812, Japan (B-mail:yn@kazusa.or.jp,
URL:http://www.kazusa.or.jp, Tel:81-438-52-3935,
Location/Qualifiers
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8ynonym: Lotus japonicus"
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Matches:
Conservative:
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Contact: vega@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="LjT44L05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL672172
AL672172.7 GI:21425250
                                              Regions of the Genome
                                                                                                                       (bases 1 to 30916)
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39.00
88.9%
77.8%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Center
                                                                                        Unpublished
                                                                                                                                                  Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  romans, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL672172/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                             JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                            TITLE
JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //gcce="Aldedh; Region: Aldehyde dehydrogenase family. This family of dehydrogenases act on aldehyde substrates. Members use NADP as a cofactor. The family includes the following members: The prototypical members are the aldehyde dehydrogenase EC:1.2.1.3. Succinate-semialdehyde dehydrogenase EC:1.2.1.2. Benzaldehyde dehydrogenase EC:1.2.1.2. Methylmalonate-semialdehyde dehydrogenase EC:1.2.1.2. Methylmalonate-semialdehyde dehydrogenase EC:1.2.1.3. Delta-1-pyrroline-5-carboxylate dehydrogenase EC:1.2.1.9. Delta-1-pyrroline-5-carboxylate dehydrogenase EC:1.2.1.0. Glutamate-5-semialdehyde dehydrogenase EC:1.2.1.10. Glutamate-5-semialdehyde dehydrogenase EC:1.2.1.1. This family also includes omega crystallin, an eye lens protein from squid and octopus that has little aldehyde dehydrogenase activity."
                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GenelD:11671"

/db_xref="GenelD:11671"

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/db_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILPIVSVKAVDEAINPINDREKPLALYVPSRNNKLIKRVIDETSSGGVTGNDVIMHF
TVNSLPFGGVGASGMGAYHGKYSFDTFSHQRPCLLKGLKGESVNKLRYPPNSESKVSW
AKFFLLKQFNKGRLGMLLFVCLVAVAAVIVKDQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN 22-JUL-2003
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Lotus corniculatus var. japonicus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids I; Pabales; Pabaceae, Papilionoideae, Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko, T., Nakamura, Y., Asamizu, E., Kato, T., Sato, S. and Tabata, S. Structural Analysis of a Lotus japonicus Genome. I. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lotus corniculatus var. japonicus genomic DNA, chromosome 4, clone:LjT44L05, TM0162b, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2377 AATCTTAGAGAGATTCCTACAGATCTA 2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                           xref="MGI:1353452"
_xref="MGI:1353452"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="Aldh3a2"
                                                                                                                                                                                                                               gene="Aldh3a2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP004979.1 GI:21907997
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84.8%
                                              . .3007
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Best Local Similarity:
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Query Match: DB:

8 셤

Pred. No.:

Score:

ORIGIN

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

DEFINITION RESULT 45 AP004979/c

ACCESSION

VERSION

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TAUSILPEGOVGASGAMAINT MOUSEAN TAULAN TAURIST PERUNALIAN TAURIST 
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26742. .26908,29857. .29998,31859. .31976,35337. .35545,
37364. .37449,38182. .38413,39972. .40124))
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29857. .29998,31859. .31976,35337. .35453))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRNA
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                                                                                                                                          SOS
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complement (join (20645. . 21600, 21980. . 22215, 24061. . 24160, 26742. . 25908, 29877. . 29998, 31889. . . 31976, 35337. . 35545, 2661. . 37449. . 37449. . 38413, 39972. . 40303))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lhes_RPCG-23*

/clone_lhes_RPCG-23*

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BR100302.1 BF784081.1 BG1844.1 BQ179769.1 BQ712918.1
as compressions and repeats; all regions were covered by at least one subclone; and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgum may have been used to confirm this sequence. Sequence data from the whole genome shotgum alone has only been used where it has a phred quality of at least 30.

RP23-133K20 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (17971)
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26742. .26908,29857. .29998,31859. .31976,35337. .35545,
37364. .37449,38182. .38413,39972. .40303))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    match: cDNAs: AK079571.1 AK079639.1 AK086262.1 BC003797.1
M73714.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: proteins: P47740 Q99164 Q99PH3" (codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || Jocus tag="RP23-5512.7-002"
|standard name="OTTMUSP00000006018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Aldh3a2"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 300); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (71773. .71961), complement (69964. .70185), complement (21507. .21964))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Justic Complement (AL390866.14:119140...113401), complement (AL390866.14:119140...113401), complement (AL390866.14:119140...11340), complement (AL390866.14:1108064...109323, complement (AL390866.14:108064...108200), complement (AL390866.14:108064...105807...105803), complement (AL390866.14:95189...95334), complement (AL390866.14:93144...93239), complement (AL390866.14:69037...69183), complement (AL390866.14:69037...69183), complement (AL390866.14:68443...68652), complement (AL390866.14:68443...68652), complement (AL390866.14:68443...69037...69183), complement (AL390866.14:68443...68652)
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                                Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (21505)
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emi. EMBL, Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORNERP; Information on the WORNERP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chr10

RP11-69113 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. Rox further details see
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B7118 bp DNA linear PRI 18-MAY-2005

Human DNA sequence from clone RP11-691113 on chromosome 10 Contains
3' end of the gene for a novel protein (FLJ10817) (DKFZP434P1735),

Complete sequence.

AL355372

AL355372

BG127652621

Humon sapiens (human)

Homo sapiens (human)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mismatches:
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Center: Wellcome Trust Sanger Institute
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Matches:
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1 (bases 1 to 87118)
Lovell, J.
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| HOREAKEVPVBLEMNTSLAPSAFEGGYVVSETTVKSEKDINGOPLLELSCYPOITER |
| POPERAKEVPVBLEMNTSLAPSAFEGGYVVSETTVKSEKDNTMKENS I ALN I LGKT TRD |
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| POPERA I ENTED YER SHOCKRAP PURD I SELS HATVOKT COITER POPERAGORY I LOGAT TOLSTAN I SERVED YER ROGIS I VYNOVITER REGIS I VYNOVITER SENDEN PER ROGIS ENTED TRANSKLI SENDEN PER ROGIS SESTED BED POPERAGOSAT HTGKLEKPR PS VSHGRAQLLRKSABKI BETVSDS SESSEEDE P POPERAGASAD LPSE Y WOLGO KLYNYT LALCSKROPS SLAPCOLA I ROGISLELI I NILLET DEV KCKT GSLAKILKET SHIPPOTRON I VOLGOSI PLAND I LOSA PROSINCALARET DEV KCKT GSLAKILKET SHIPPOTRON I VOLGOSI PLAND I LOSA PROSINCALARET DEV KCKT GSLAKILKET SHIPPOTRON I VOLGOSI PLAND I LOSA PROSINCALARET LANDAKER RARRVVROHGGITKLIVET SHIPPOTRON I VALLED CALLAREN SCHATTN
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KSNDTNVHRATAQALYQLSEDADNCI TWHENGAVKLLLDMVGSPDQDLQEAAAGCI SN
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.21964))
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PRI 31-AUG-2000
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Submitted (23-MAR-2000) Production Sequencing Facility, DOE Joint
Benome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 108661)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-AVG-2000) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 31, 2000 this sequence version replaced gi:7711970.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                          ACO26736 108661 bp DNA linear PRI 31-AUK
Homo sapiens chromosome 5 clone CTD-2350M8, complete sequence.
ACO26736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 108661)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Ouality: Phrap Quality >=40 99% of Sequence;
Betimated Total Number of Errors is 1.
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Ab13323 Human imm
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Adv39405 Rat cardi
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Abk87174 CDNA enco
Aaa27059 Mouse 574
Adf56299 Human CDN
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Adr25444 Breast ca
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Adv35098 Human cDN
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Adn38723 Cancer/an
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Abk87175 CDNA enco
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Abt07721 Breast ca
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           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                     nucleic search, using frame_plus_p2n model
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ACD97670 standard;		ACD97670,		23-SEP-2003 (first		Human colon cancer		Open reading frame	breast cancer; popu	antibiotic resistan	agriculture, food c	influenza virus; eu	gene; ss.		Homo sapiens.	•	US2002155438-A1.		24-OCT-2002.	
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## ALIGNMENTS

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cell expressed cDNA #6082
CDNA; 108 BP.
                                                               entry)
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detection; genome sequencing; colon cancer; lation genome analysis; genetic shift; cancer; nce; antibiotic non-tolerance; congenital disease; rzcp genome; resistance gene; retrovirus; ukaryotic pathogen detection; trypanosome; Plasmodium;

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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (1) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (1), amplifying conditions and sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting much amplifying steps with different primers and sequencing resulting and amplifying steps with different primers and sequencing resulting and amplifying steps with different primers and sequencing resulting and amplifying steps with different primers and sequencing resulting and amplifying steps with different primers and sequencing recommend and amplifying steps with different primers and sequencing concluded and amplifying steps with different primers and sequencing concluded and amplifying sequence of an organism. mRNA is obtained from mammalian concluded and organism. mRNA is obtained from mammalian concluded with a pathological condition s.g. a colon cancer or breast cancer cell. The method is useful for analyses of colon cancer or breast cancer cell. The method is useful for analyses of large or small populations. further, it can be used to study living systems to determine if e.g. there have been genetic shifts which render an individual or populations for lass likely to be afflicted with the state of softh, the method can also be used in the study of the study of whether the conditions are likely to be passed to offspring the study of whether the conditions are likely to be passed to offspring through over or sperm. The analyses for pathological conditions can be crudied to the pathogens which integrate into the genome, such as the crudied in this way. Similarly, the method escential genomes and other integrating viruses such as influence retroviruses and other integrating viruse spream to the pathogens which in regrate into the method of setting the sequencing of the pathogens
                                                                                                                                                                                                                                                                                                  Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of
                                                                                                                                                                                                             Brentani RR;
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                                                                  98US-00196716.
                   99US-00406117.
                                                                                                                                                                                                             Simpson AJG, Neto ED,
                                                                                                                SIMPSON A J G.
                                                                                                                                                              (BREN/) BRENTANI R R.
                                                                                                                                                                                                                                                              WPI; 2003-182626/18.
                                                                  20-NOV-1998;
                   27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                 individual.
                                                                                                                (SIMP/)
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Sequence 108 BP; 18 A; 33 C; 22 G; 35 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	4.04	Length:	108
Score:	40.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-774-176-10 (1-9) x ACD97670 (1-108)

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ADU11677 standard; DNA; 475 BP RESULT 2 ADU11677 ID ADU1 00000

Conservative: Mismatches: Indels: Matches:

Gaps:

(1-475)

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WPI; 2004-804779/79
                            (AMHP ) WYETH.
(STRA/) STRAHS A.
                WO2004097052-A2
             Unidentified
                  11-NOV-2004.
 ADU11677;
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, ds, breast cancer; breast cancer-associated gene sequence; development; pharmacogenetics; biosensor development.
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09-APR-2001; 2001US-00829472.
09-APR-2001; 2001US-028698P.
04-MAY-2001; 2001US-02848590P.
29-WAY-2001; 2001US-0294443P.
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N-PSDB; ABJ05564.
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                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                           US-10-774-176-10 (1-9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method comprising comparing an expression to profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second classe of patients where coth the first and second classes of patients have the solid tumour, and each of the first and second classes of patients have the solid tumour, and each of the first class of patients has a first clinical outcome, and pority of the first class of patients has a second classe of patients has a second classe of patients has a second class of the majority of the second class of patients has a second claimical cutcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at class one reference expression profile of the gene, (ii) at least one reference expression profile to the reference expression profile, and (iv) a processor capable of executing the expression profile, and (iv) a processor capable of executing the expression profile, and (iv) a processor capable of executing the comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the connounclear cells of patients who have the solid tumour correlate with clinical outcomes of the patients who have the solid tumour prognosis genes, where each of the solid tumour prognosis genes is differentially expressed in EBMCs of a first class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to patients as each of content and the series of the patients as compared to patients as comparients as condend 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outcome, and the second class of patients has a second clinical outcome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slonim DK;
                                                                                                                                                                                    cytostatic; gene therapy; expression profile; solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds.
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                                                                                                                                  Solid tumour prognosis gene seqid 2116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-2003; 2003US-0466067P
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                                                                               27-JAN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strahs A, Trepicchio WI
Immerman F, Dorner AJ;
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a blological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cel, and for detecting genes that are method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761

represent the 69 breast cancer-associated gene sequences of the invention Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids. Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other; Claim 9; Page 372; 414pp; English.

Alignment Scores:

475

22.5

Alignment Scores:

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polymelectides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interetitial pulmonary disease, fibrosis, bronchiectasis. The genes, polymucleotides and polypeptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer-associated polynucleotide, gene, ds, cytostatic, emphysema, antiinflammatory, antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease, hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma, bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
927
0
0
0
 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                     cancer-associated polynucleotide #197.
                                                                            Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2001; 2001US-0284770P.
10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
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                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                              ABX76333,
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                                                                      Query Match:
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the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymuclectide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnoshing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule,
for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
                                                                        Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                                                                                                  927
                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-031544P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytoetatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids used for the detection method of the invention.
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Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                               Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
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Mismatches:
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Murray R, Watson SR,
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29-NOV-2001; 2001US-0332464P.
03-DRC-2001; 2001US-033334P.
14-DRC-2001; 2001US-034334P.
10-JAN-2002; 2002US-0347349P.
10-JAN-2002; 2002US-0347349P.
10-FRB-2002; 2002US-035250P.
13-FRB-2002; 2002US-0355077P.
20-FRB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0368809P.
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2002US-0386614P.
2002US-0396839P.
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Best Local Similarity:
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05-JUN-2002;
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DB:
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide and methods of screening for modulators of activity or expression of the polypeptides and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attended else and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attended else acetular and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attended reconsistivation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
                                                                    Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                              Claim 8; SEQ ID NO 41; 1385pp; English
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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Francis-Lang H, Friedman L;
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                   WPI; 2003-468649/44.
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                                    P-PSDB; ADN38724.
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New NOVX polypeptides and polymucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capridous related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, anti-HIV, cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; carebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoletic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopolesis; wound healing; angiogenesis; ds.
                                 Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                      Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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08-MAR-2001; 2001US-0274291P.
08-MAR-2001; 2001US-0274281P.
09-MAR-2001; 2001US-0274322P.
09-MAR-2001; 2001US-0275235P.
13-MAR-2001; 2001US-0275535P.
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           WPI; 2003-421410/39
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Best Local Similarity:
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DB:
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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli RA, Vernet CAM; Pena CRA, Burges CB, Liu X, Spytek RA, Gorman L, Spaderns SK; Voss BZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PP;
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2001US-0288666F
2001US-0288342P
2001US-0281342P
2001US-0291090P
2001US-0291090P
2001US-0294485P
2001US-0294889P
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2001US-029480P
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2001US-0312903P.
2001US-0318462P.
2001US-0318470P.
2001US-0325430P.
2001US-0335380P.
2001US-0333301P.
2001US-0333301P.
2001US-0332312P.
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2001US-0333272P.
2001US-0332094P.
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                               20-MAR-2001;
21-MAR-2001;
22-MAR-2001;
23-MAR-2001;
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28-MAR-2001;
30-MAR-2001;
30-MAR-2001;
02-APR-2001;
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18-JUN-2001;
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20-MAR-2001;
20-MAR-2001;
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27-MAR-2001;
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P-PSDB; AAU98694

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disgnosing diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, parkinson's disease, immune disease, anorexia, cancer, neurodegenerative diseases, Alzheimer's disease, parkinson's disease, immune disease, haematopoietic disorders, cardiovascular disorders associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of anti-cancer and immunespecifically to NOVX substances for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peline, cat; oncofoetal leucine-rich glycoprotein; 574; tumour; call proliferative disorder; infiammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
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Matches:
Conservative:
Mismatches:
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/product= "5T4 protein"
Claim 16; Page 114-115; 619pp; English.
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                                                                                                                                                                                                                                                                                                                                therapeutic or diagnostic methods
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40.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
Percent Similarity:
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(OXFO-) OXFORD BIOMEDICA UK LID Myers K, Drury N, Carroll M;

WPI; 2002-557449/59

13-NOV-2000; 2000WO-GB004317. 13-NOV-2001; 2001WO-GB005004

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the proposation of polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The composition may also be used in disgnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).
                           Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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/product= "Feline 5T4 antigen protein"
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Matches:
Conservative:
Mismatches:
Indels:
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1. .1260
/*tag= a
                                                                                                  Claim 4; Page 68; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB97513 standard; DNA; 1260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OXFO-) OXFORD BIOMEDICA UK LTD
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40.00
100.0%
100.0%
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Query Match:
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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further provides a polypelicope string comprising the 5T4 epitope; a nucleic acid capture ancoding the 5T4 epitope; a vactor system capable of delivering the 5T4 epitope; a uncleic acid to a cell, a cell pulsed with the 5T4 epitope, a polypelitope of the 5T4 epitope, its ancoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease of a specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the 5T4 epitope and/its encoding nucleic acid; a method comprising the 5T4 epitope has cytostatic activity. The vaccine inclear acid in a subject; and a T cell line or close capable of comprising the 5T4 epitope has cytostatic activity. The vaccine inclear acid and the vaccine of particularly cancer. The detection method is useful for diagnosing or system or cell is useful in the prevention and/or treatment of a disease, paresence of the 5T4 epitope or its nucleic acid and for detecting the prevence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a needcament for treating and/or treating and/or the feline and and acid and the feline and acid.
                                                                                                                                  New major histocompatibility complex class I peptide epitopes from human 5T4 tumor-associated antigen, useful for preventing and/or treating a disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5T4 antigen coding DNA of the invention.
  Redchenko I,
                                                                                                                                                                                                                                              Disclosure, Page 67, 73pp, English.
Kingsman S,
                                                 WPI; 2003-637141/60.
P-PSDB; ADB97520.
Carroll M,
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

Alignment Scores:

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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                            U8-10-774-176-10 (1-9) x ADB97513 (1-1260)
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                  Percent Similarity:
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ADB97452 standard; DNA; 1260 BP ADB97452; 

04-DEC-2003 (first entry)

DNA encoding feline 5T4 protein.

gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.

Unidentified

/\*tag= a /product= "Feline 5T4 antigen protein" Location/Qualifiers 1. .1260 /\*tag= a

WO2003068815-A2

21-AUG-2003

(OXFO-) OXFORD BIOMEDICA UK LTD.

99GB-00017995.

27-JAN-1999; 30-JUL-1999;

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The invention relates to a Major Histocompatibility Complex (MHC) class il peptide epitope of the 5T4 antigan. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for disapnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                                                                                                                                         New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-774-176-10 (1-9) x ADB97452 (1-1260)
                                                                                                                                                                                                                                         Disclosure; Page 49; 63pp; English.
                                                                                                      Kingsman S;
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                                                                         (OXFO-) OXPORD BIOMEDICA UK LTD
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              13-FEB-2003; 2003WO-GB000618.
                                           13-FEB-2002; 2002GB-00003420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA27058 standard; DNA; 1263
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40.00
100.0$
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                                                                                                      Harrop R,
                                                                                                                                 WPI; 2003-663795/62.
P-PSDB; ADB97455.
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Best Local Similarity:
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                                                                                                      Carroll M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA27058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
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8XCCCCCCCCCX8X4444X8XXXCCCCCCCCCCCCX8X4X4X4444
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The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metaatasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were incoulated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                              Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                        Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of canine 5T4 protein.
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                                                                                                                             Example 2; Page 78; 79pp; English.
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40.00
100.0%
100.0%
                                                                           Tumor associated antigen,
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                Carroll MW, Myers KA;
                                              WPI; 2000-387735/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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(OXFO-) OXFORD BIOMEDICA UK LTD.

99WO-GB003859. 2000GB-00003527. 2000GB-00005071.

18-NOV-1999; 15-PEB-2000; 02-MAR-2000;

13-NOV-2000; 2000WO-GB004317

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Length: Matches: Conservative: Mismatches: Indels:

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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a disease pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's diseases, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacter related diseases, and other immune disorders. The present sequence
                                                                                             associated
treating a
                                                                                                                                                                                                                                                                                                                                                                                   encodes a 5T4 protein, which is used to produce ScFv of the invention
Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                            Use of single chain antibody capable of recognizing a disease molecule for manufacturing a medicament for preventing and/or disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                            Disclosure; Fig 26; 118pp; English.
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/product= '
Kingsman A, Kingsman SM,
Myers KA;
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                                              WPI; 2001-343805/36.
P-PSDB; AAB83839.
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The present invention relates to the isolation of canine and feline oncofostal leucine-rich glycoproteins known as 574, and the proportion of polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell compositions for the prevention and/or preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes canine 574 protein
                                                                                                                                             Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                 Claim 1, Page 67; 68pp; English
                       Carroll M;
                                                                     WPI; 2002-557449/59.
                       Drury N,
                                                                                                    P-PSDB, AAU98693
                         Myers K,
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Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;

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Mouse, TAA, tumour-associated antigen, anti-tumour, cytostatic, immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer,
       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                         1072 TTCCTAGGTATTGTCTTAGCCCTGATA 1098
                                                                                                                                                                                                            Mouse 5T4 tumour-associated antigen gene.
                                                         Gaps:
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                                                                          US-10-774-176-10 (1-9) x ABK87174 (1-1263)
                                                                                                                                                    AAA27059 standard; DNA; 1281 BP
        69.9
40.00
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100.0$
                                                                                                                                                                                          22-AUG-2000 (first entry)
                           Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                                                                                                                                        AAA27059;
                                              Query Match
DB:
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(OXFO-) OXFORD BIOMEDICA UK LTD.

98GB-00025303. 99GB-00001739. 99GB-00017995.

27-JAN-1999; 30-JUL-1999;

99WO-GB003859

18-NOV-1999; 18-NOV-1998;

25-MAY-2000

WO200029428-A2 Mus musculus.

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TAA, The TAA 5T4 is a glycopoted which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were incoulated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                          Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li D;
                                                                                                                                                          The present sequence encodes the mouse 5T4 tumour-associated antigen
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
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                                                                                                                            Example 2; Page 78; 79pp; English.
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human LRRCAPS related DNA #6.
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              Myers KA;
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                                              WPI; 2000-387735/33.
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                Carroll MW,
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capricious related polypeptide or nucleic acid with a test agent
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-blased activity, where a difference between the test agent-blased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA Disclosure; Page 75-76; 99pp; English

Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;

00000 Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-774-176-10 (1-9) x AAD56199 (1-1331) 74.3 40.00 100.0\$ 100.0\$ Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: .. 9

PheLeuGlyIleValLeuAlaLeu11e 9 1102 ઠે 셤

ADJ56299 standard; cDNA; 2020 BP ADJ56299; ADJ5629 RESULT 

(first entry) 06-MAY-2004 Human cDNA differentially expressed in MYCN activated cells SeqID 105

human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss; MYCN activated cell.

Homo sapiens.

26-JUN-2003.

US2003119009-A1

25-FEB-2002; 2002US-00084817

23-FEB-2001; 2001US-0270784P

STUART S G. NUCHTERN J G. PLON S E. SHOHET J M. (STUA/) (NUCH/) N (PLON/) N (SHOH/) S

New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the WPI; 2003-635698/60

Shohet JM;

SE,

Plon

Stuart SG, Nuchtern JG,

Claim 1; SEQ ID NO 105; 27pp; English

cancer

This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to

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polymucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a proto-
concogene that is amplified in neuroblastoma cells and is common in small concogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bladder cancer associated cDNA sequence SEQ ID NO:192
                                                                                                                                                                                                                                                                      Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
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2001US-0310099P.
2001US-0343705P.
2001US-0350666P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC51052 standard; cDNA; 2053
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P-PSDB; ABR48236.
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08-NOV-2001;
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Claim 22; Page 335; 453pp; English.

contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in the undiscand sacreening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications 8X888888888888X**8** 

Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
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Best Local Similarity:
Alignment Scores:
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DB:
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ABX76332 standard; DNA; 2053 ABX76332, 셤

Lung cancer-associated polynucleotide #196. ВВ 02-APR-2003 (first entry) 

Lung cancer-associated polynucleotide, gene, ds; cytostatic; emphysema, antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease, hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

Unidentified

WO200286443-A2.

31-OCT-2002

18-APR-2002; 2002WO-US012476

18-APR-2001, 2001US-0284770P. 10-MAY-2001, 2001US-0290492P. 09-NOV-2001, 2001US-0339245P. 13-NOV-2001, 2001US-0350666P. 29-NOV-2001, 2001US-0334370P. (EOSB-) ROS BIOTECHNOLOGY INC

Aziz N, Murray R;

WPI; 2003-093161/08. P-PSDB; ABU56603. Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in cassed or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell corrections to other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, isothema and bypersensitivity pneumonitis, intersitial pulmonary disease, isothema and for treating to pulmonary disease, intersitial pulmonary disease, confortation in the patient and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences

MRY7614-ABX76474 represent lung cancer-associated polymucleotides of the
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15-PEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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                                                                                                                                                                                                                                                                                                                                                                    invention
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; p53 pathway; Leucine rich repeat capricious related protein; LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                  Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                5; Page 73-74; 99pp; English
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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Francis-Lang H, Friedman
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Pred. No.:
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                  Example
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Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

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test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                            Human; differential expression; cancer; anglogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                       Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39
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                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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2001US-033334P.
2001US-034339P.
2002US-034721P.
2002US-0347349P.
2002US-035250P.
2002US-0355714P.
2002US-0356714P.
2002US-035809P.
                                                                                                                                                                                                                                                                                                           ADN38721 standard; cDNA; 2053
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                                                                                                                                        Percent Similarity:
Best Local Similarity:
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09-SEP-2002;
                                                                                                     Alignment Scores:
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Mack DH,
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DB:
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Lioubin MN,

Plowman GD, Funke RP,

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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a polypeptide of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; polypeptides and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attencedlerosis, inflammatory diseases, autonimume diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                           Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a nucleic acid sequence of the invention
                                                                                                                                                         Claim 8; SEQ ID NO 39; 1385pp; English
P-PSDB, ADN38722.
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                       US-10-774-176-10 (1-9) x ADN38721 (1-2053)
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Best Local Similarity:
Alignment Scores:
Pred. No.:
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Human tumour-associated antigenic target (TAT) cDNA sequence #53 ADL06473 standard; cDNA; 2053 BP 20-MAY-2004 (first entry) ADL06473; 

Human; tumour-associated antigenic target; TAT; cell death; tumour; cancer, cytostatic, gene, ss

Homo sapiens

WO2004016225-A2

26-FEB-2004

19-AUG-2003; 2003WO-US025892

19-AUG-2002; 2002US-0404809P. 21-AUG-2002; 2002US-0405645P. 23-SEP-2002; 2002US-0413192P.

15-OCT-2002; 2002US-0419008P. 15-NOV-2002; 2002US-0426847P. 02-JUL-2003; 2003US-0484959P.

(GETH ) GENENTECH INC.

Smith V; Hillan KJ, Polakis P, Polson A, Desauvage FJ, Frantz G,

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The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a
                                                                 New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                         Claim 1; SEQ ID NO 53; 319pp; English.
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Zhang
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P-PSDB; ADN03962.
W TD,
                           WPI; 2004-257144/24
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Best Local Similarity:
                                          P-PSDB; ADLO6552
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Spencer SD,
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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
               treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
The invention relates to novel polynucleotide and polypeptides for
                                                                                                   Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; breast cancer; prognosis; gene expression; diagnosis.
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Matches:
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(NECA-) NETHERLANDS CANCER INST.
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                                                                                                                                                                                                                                                                                                                                                                                                             ADR25444 standard; DNA; 2053
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Best Local Similarity:
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                                                                                                                                  Alignment Scores:
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Alignment Scores: Pred. No.:

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; uson proteins comprising a TAT polypeptide; fusion proteins comprising a TAT polypeptide; fusion proteins comprising a TAT polypeptide; molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide, mucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, increased TAT expression, particularly cancers such as breast cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour-associated antigenic target, TAT; human, overexpression, citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
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                                                                                                        US-10-774-176-10 (1-9) x ADR25444 (1-2053)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-347921/32.
  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; 88; multi-parameter high throughput screening; MPHTS;
disease signature; neuropsychiatric; neurodegenerative; schizophrenia;
bipolar affective disorder; BAD; autism; Parkinson's;
Alzheimer's disease; neuroleptic; nootropic; antimenic; antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contacted with the test compound.
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                      Other;
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                    Sequence 2053 BP; 461 A; 602 C; 499
                                                                                                                                                                                                                                                                                                                                                                                                                             ADV35098 standard, cDNA, 2053 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2001; 2001US-0299151P.
07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-0335150P.
14-NOV-2001; 2001US-0333047P.
18-JAN-2002; 2002US-0349936P.
04-MAR-2002; 2002US-0361834P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-2002; 2002US-00175523
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Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-118903/12.
                                                                                                                                                         Best Local Similarity:
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                                                                                                                                  Percent Similarity:
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                                                                  Alignment Scores:
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                                                                                                                                                                  Query Match:
DB:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders
nootropic, antimanic and antidepressant. Purthermore, the screening method used in MPHTS will be automated, such that a large number of tes compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human CDNA sequence of a gene that is differentially expressed in the presence of a therapeutic compound and represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-774-176-10 (1-9) x ADV35098 (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PheLeuGlyIleValLeuAlaLeuile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS87175 standard; cDNA; 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG22988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of that length cDNA easily without any special methods. The present sequence is a full length human cDNA of the
              polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to primers for synthesising full length cDNA
 involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
                                                                                                                                                                                        Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                          1413 TTCCTGGGTATTGTTTTAGCCCTGATA 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human full-length cDNA, SEQ ID NO: 2864.
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                                                                                                                                                                                                                                                                                                                                                                 (1-2338)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK94253 standard; cDNA; 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                                                                                                                                                   x AAS87175
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                                                                                                                                                                                                                                              143
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P-PSDB; AAM93333.
                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                 US-10-774-176-10 (1-9)
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                                                                                                                                                                                                                                                                                                               Match
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polymucleotide sequence is a full length human cDNA clone of the invention.
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invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonuclectide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; medicine; signal transduction; glycoprotein; transcription;
                                                            C; 634 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                           Full length human cDNA clone SeqID 2864.
                                                                                                                                                                                 Gaps:
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                                                                                                                                                                                                                                                                                                                                  ADL30831 standard; cDNA; 2359 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligo-capping method; ss; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999; 99JP-00194486.
11-JMX-2000; 2000JP-00118774.
02-MAX-2000; 2000JP-001183865.
07-JUL-2000; 2000EP-00114089.
                                                            BP; 498 A; 692
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                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                              US-10-774-176-10 (1-9)
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                                                             Sequence 2359
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                                                                                           Alignment Scores:
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Pred. No.:
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830 Primers useful for synthesizing full length cDNA clones and their use
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K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                   Human full-length cDNA, SEQ ID NO: 2866.
                                                                                                                                                                               US-10-774-176-10 (1-9) x ADL30831 (1-2359)
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Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                      AAK94254 standard; cDNA; 2361 BP
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                              Percent Similarity:
Best Local Similarity:
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DB:
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AAK94254

AAK94254

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AAK542
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated ben molecules dequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the thrown construction. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.

Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;

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2361
9
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      Length:
Matches:
Conservative:
Mismatches:
      144
40.00
100.0$
100.0$
                    Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                 Query Match:
DB:
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No.:
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US-10-774-176-10 (1-9) x AAK94254 (1-2361)

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se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                    Human cDNA encoding protein that promotes STAT6 activation #64.
                                                                                                                                                                                                                                                                                                                                                                                                                               Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                              Muramatsu S,
PheLeuGlyIleValLeuAlaLeulle 9
                                                                                                                                                                                                                                                                                                                                                                                                                               Honda G,
                                                                 ADI26162 standard; cDNA; 2361
                                                                                                                                                                                                                                                                                                                                    06-UUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-00377326.
27-DEC-2003; 2002JP-00137505.
15-MAY-2003; 2003JP-00137505.
                                                                                                                                                                                                                                                                                                       05-JUN-2003; 2003WO-JP007123
                                                                                                             22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               Sugahara T, Matsuda A,
                                                                                                                                                                                                                                                                                                                                                                                                       (ASAH ) ASAHI KASEI KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-122214/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ADI26163.
                                                                                                                                                                                                                                                          WO2003104277-A2
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                             05-JUN-2002;
                                                                                                                                                                                                                                                                                 18-DEC-2003
                     1497
                                                                                       ADI26162;
                                            RESULT 32
                                                        ADI26162
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useful for the producing an antibody, which involves administering the protein of transcription 6 activation (97746). The protein is useful for the producing an antibody, which involves administering the protein in the nucleic acid is useful for disquesing a disease or antigen. The nucleic acid is useful for disquesing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for societivity of the composition. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions and antisense molecules are useful for the treating a disease associated with 67745 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, allergic diseases associated with 87745 activation and/or prevention of Thi hyperactive disease. Compositions are also useful in theumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AlDS. The protein has efficient promoting 57746 activation or inhibition of 577476. The present sequence represents a culturation or inhibition of 577476. The present sequence represents a culturation. The invention relates to a purified protein promoting signal transducer

Claim 4; SEQ ID NO 127; 1368pp; English.

Indels:

Query Match:

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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3th human cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human, medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
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K, Kojima S, Otsuki T, Koga
   638 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                                                                                          Length:
Matches:
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Mismatches:
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                                                                                                                                                                                                                                                         Gaps:
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Wakamatsu A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL30833 standard; cDNA; 2361 BP
   BP; 506 A; 684 C;
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-001183865.
07-JUL-2000; 2000BP-00114089.
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Sequence 2361
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                                                               Alignment Scores:
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Length: Matches: Conservative: Mismatches:

144 40.00 100.0% 100.0%

Score: Percent Similarity: Best Local Similarity:

Alignment Scores:

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STATē; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as antigen. The nucleic acid is useful for diagnosting a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening expressing the protein is useful for screening expressing the protein is useful for screening composition. A transformant compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as
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                                                                                                                                                                                                                                                                                                                                                             gene; human; signal transducer and activator of transcription
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                                                                                                                                                                                                                                                                                                                        Human cDNA encoding protein that promotes STAT6 activation #63.
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                     Gaps:
                                                                                           PheLeuGlyIleValLeuAlaLeuIle 9
                                                    US-10-774-176-10 (1-9) x ADL30833 (1-2361)
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2002JP-00377326.
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100.0%
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06-JUN-2002; 2
26-DEC-2002; 27-DEC-2002; 2
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activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a human cDNA encoding a protein which promotes STATE activation.
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Sequence 2557 BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;

60000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 158 40.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Pred. No.:

US-10-774-176-10 (1-9) x ADI26160 (1-2557)

1645 TTCCTAGGTATTGTTTTAGCTCTGATA 1671 0 PheleuglylleValleuAlaLeuile ઠે 셤

ADI26158 standard, cDNA, 2557 BP RESULT 35

ADI26158;

Human cDNA encoding protein that promotes STAT6 activation #62.

(first entry)

22-APR-2004

88; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

Homo sapiens.

WO2003104277-A2

18-DEC-2003

05-JUN-2003; 2003WO-JP007123

05-JUN-2002;

06-UUN-2002, 2002US-0385912P 26-DEC-2002, 2002JP-00377336. 27-DEC-2002, 2002JP-003773467P 15-MAY-2003, 2003JP-00137559. 16-MAY-2003, 2003US-0470836P.

(ASAH ) ASAHI KASEI KK

Muramatsu S, Ishizawa K; Honda G, Sugahara T, Matsuda A,

WPI, 2004-122214/12. P-PSDB, ADI26159 New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. diabetes and cancer

for

New nucleic acid encoding a Moraxella catarrhalis polypeptide, useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis.

Disclosure; SEQ ID NO 693; 429pp; English.

The invention relates to an isolated nucleic acid encoding an Moraxella catarrhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents DNA encoding a M. catarrhalis protein.

Claim 4; SEQ ID NO 123; 1368pp; English.

transducer The invention relates to a purified protein promoting signal transduces and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the AD126188

AD126188

XX
AD12

AD13

protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, the for treating disease associated with STAT6 activation and/or prevention for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 compounds for treating and preventing diseases associated with excessive activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation. Sequence 2557 BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other; 2557 9 0 0 0 0 Length: Matches: Conservative: Mismatches: DNA encoding a M. catarrhalis protein #693 ds; gene; Moraxella catarrhalis; infection 1645 Trccraggrafrerrragcrcraara 1671 Indels: Gaps: x ADI26158 (1-2557) 1 PheLeuGlyIleValLeuAlaLeuIle (GENO-) GENOME THERAPEUTICS CORP. 0007/c ADL03007 standard; DNA; 207 BP. 04-APR-2000; 2000US-00540236. 40.00 100.0% 100.0% 06-MAY-2004 (first entry) Moraxella catarrhalis. WPI; 2004-178127/17. P-PSDB; ADL04927. Percent Similarity: Best Local Similarity: US-10-774-176-10 (1-9) US6673910-B1 38-APR-1999; Alignment Scores: 06-JAN-2004 Breton GL; ADL03007; Query Match: RESULT 36 ADL03007, 8x88888888888888888 셤 ઠ

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The condition is unnecessary, when one spot on an array equals one copen reading frame, since sequence information is available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                          Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
             G; 58 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                              Bacillus clausii genomic sequence tag (GST) #1964.
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Matches:
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Mismatches:
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27-MAR-2001; 2001US-0279526P.
            68 A; 30 C;
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                                                 64.8
36.00
100.0%
77.8%
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                                                                         Percent Similarity:
Best Local Similarity:
            Sequence 207 BP;
                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus clausii.
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                                      Alignment Scores:
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                                                                                                   Query Match
DB:
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Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
This sequence represents a genomic sequence tag (GST) used in the method of the invortion. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer.
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Matches:
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AAS37087 standard; cDNA; 402
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36.00
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                     ..
No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                                                                                                       Plant DNA sequence which confers altered metabolic characteristic #1150.
                                                                                                                                                                                                                                                                                                                                                                                                                                              alcohol metabolism; fatty acid metabolism;
branched fatty acid metabolism; alkaloid metabolism;
amino acid metabolism; ester metabolism; glyceride metabolism;
phenolic metabolism; carbohydrate metabolism; sterol metabolism;
terpene metabolism; isoprenoid metabolism; alkene metabolism;
alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blakeslee B, Mccreary DA, Pell RJ;
Reddy AS, Shukla V, Larrinua I, Miller BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 575 BP; 181 A; 104 C; 140 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               metabolic characteristic; plant; acid metabolism;
      0000
      Conservative:
                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, SEQ ID NO 1150; 2576pp; English.
                                                                                                                                                                  238 TTTCTGGGGGTGCTTTTAGCCCTTATG 212
                                                                                                                                              1 PheLeuGlylleValLeuAlaLeuIle 9
                                                                                                      US-10-774-176-10 (1-9) x AAS37087 (1-402)
                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-2002; 2002WO-US027884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                                                                                                                  767/c
ADK53767 standard; DNA; 575
    100.0%
77.8%
90.0%
                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Crosley R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana benthamiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crosley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-313091/30.
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2003.
                                                                                                                                                                                                                                                                                                            ADK53767;
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                                                                                                                                                                                                                                                  ADK53767,
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Length: Matches:

212 36.00

Alignment Scores: Pred. No.: Score:

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The invention relates to human breast cancer expressed polymucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 689 BP; 219 A; 99 C; 116 G; 255 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     689
00 7 8 9
0000
                                                                                                                                                                                                                                                                                                                                                                                                       Human breast cancer expressed polynucleotide 12316.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; cell marker; cytostatic; ss.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                      TTTCTTGGAGTTGTAGTAGCTCTCATA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PheLeuGlyIleValLeuAlaLeuIle 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2176; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-774-176-10 (1-9) x AAL19859 (1-689)
                                                                                                      US-10-774-176-10 (1-9) x ADK53767 (1-575)
                                                                                                                                                                                                                                                                            BP
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24-MAR-2000; 2000US-019209P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-02930P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0220534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2001; 2001WO-US000798.
                                                                                                                                                                                                                                                                          AAL19859 standard; cDNA; 689
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36.00
100.0%
77.8%
90.0%
100.0%
77.8%
90.0%
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  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                    AAL19859;
                                                                                                                                                                                         413
                                Query Match:
DB:
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells. The method is useful for monitoring of a spot in the same genes in one or more second Bacillus cells. The method is useful for monitoring genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiclogical provocation. Extensive follow cup characterisation is unnecessary, when one spot on an array equals one environmental stress or other physiclogical provocation is available. This sequence represents a genomic sequence tag (GST) used in the method of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                             Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                      Bacillus clausii genomic sequence tag (GST) #2012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 6460; 200pp; English.
172 TTTTTGGTTTTGGTGCTGGCAATTATT 198
                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVOZYMES BIOTECH INC (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2001; 2001WO-US031437
                                                                               ABK79169 standard; DNA; 829
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berka R, Clausen IG;
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                                                                                                                                                                                                                                                                                                                                Bacillus clausii.
                                                                                                                                                                                                                                                                                                                                                                       WO200229113-A2
                                                                                                                                                            13-AUG-2002
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                                                                                                                       ABK79169;
                                        RESULT 41
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Length: Matches: Conservative: Mismatches: Indels:

> 36.00 100.08 77.88 90.08

> > Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
mucleic acid; (2) a host cell containing the vector; (3) an isolated
conclude acid; (2) a host cell containing the vector; (3) an isolated
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibited by the
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contisense nucleic acid; (4) an antibody capable of specification or
the proliferation or the activity of a gene in an operon required for
contisense product or that has an activity against a biological pathway
contained for proliferation-required gene or its gene product lies
contained a gene required for cellular proliferation of an
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound satiation is present in a culture or collection of
contents or (13) identifying the target of a compound that inhibits the
confidentifying proteins or screening for homologous nucleic acids required
for cellular proliferation in cells other than S. aureus, S. typhimurium,
confidentify or proliferation in cells other than S. aureus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                       Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto R,
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                                                                    σ
                                           1 PheLeuGlyIleValLeuAlaLeuIle
US-10-774-176-10 (1-9) x ABK79169 (1-829)
                                                                                                                                                                                                                                                                                                            Prokaryotic essential gene #20681.
                                                                                                                                                                          ACA39024 standard; DNA; 1833 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malone C,
, Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2002; 2002US-00072851, 06-MAR-2002; 2002US-0362699P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BLIT-) BLITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       Moraxella catarrhalis.
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                              drug design; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200277183-A2.
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                                                                                                                                                                                                                     ACA39024;
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Wall D,
                                                                                                                                                      ACA39024/c
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K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the transparent directly from WIPO at the print directly from wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody a specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense, ds; prokaryotic essential gene; cell proliferation;
                                                                                               U; 0 Other;
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Forsyth RA,
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                                                                                                                                            Length:
Matches:
Conservative:
                                                                                                Sequence 1833 BP; 538 A; 368 C; 424 G; 503 T; 0
                                                                                                                                                                                           Mismatches:
Indels:
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 9310; 1766pp; English.
                                                                                                                                                                                                                                                                                                         1720 TTTCTAGGGCTTGTTTTAGCTCTTCTT 1694
                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                         PheLeuGlyIleValLeuAlaLeuIle 9
                                                                                                                                                                                                                                                          US-10-774-176-10 (1-9) x ACA39024 (1-1833)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prokaryotic essential gene #3097.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-8EP-2001; 2001US-00948993.
25-OCT-2001; 2001US-00342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                  ACA21440 standard, DNA; 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
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100.0%
77.8%
90.0%
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-029926/02.
P-PSDB; ABU17570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus anthracis.
                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug design, gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200277183-A2.
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                                                                                                                              Alignment Scores:
Pred. No.:
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DB:
                                                                                                                                               Мо.:
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Wall
                                                                                                                                                                                                                                                                                                                                                    RESULT 43
                                                                                                                                                                                                                                                                                                                                                                      ACA21440
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cc proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway consequence for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; sativity; (11) a culture comprissing strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of product is overexpressed or underexpressed; (12) determining the extent of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in calls other than S. aureus, S. typhimurium, continually discovery programs, or for screening homologous nucleic acids captured corporated for proliferation in cells other than S. aureus, S. typhimurium, contour form part of the printed specification, but was obtained in celectronic format directly from WIPO at the present for this patent did contour form part of the printed specification, but was obtained in cells contour contour form part of homologous nucles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic library; bacteria; human upper airway; otitis media; sinusitis;
bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2271 BP; 826 A; 337 C; 537 G; 571 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF28548 standard; DNA; 96109
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90.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic fragment #35.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis and meningitis
   8888888888888888
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Sequence 96109 BP; 28783 A; 18910 C; 20341 G; 28075 T; 0 U; 0 Other;

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96109
7
2
0
0
        Length:
Matches:
Conservative:
Mismatches:
                                         Indels:
         8.01e+04
36.00
100.0%
77.8%
90.0%
                         Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
                                         Query Match:
DB:
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US-10-774-176-10 (1-9) x AAF28548 (1-96109)

PheLeuGlyIleValLeuAlaLeuIle 9 -4034 ઠે

ABD33266 standard; DNA; 168407 BP ABD33266; 

(first entry) 18-NOV-2004 Murine cancer-associated (CA) gene MD07-046.

Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene; de; cancer; cytostatic

Mus musculus.

WO2004058146-A2.

15-JUL-2004.

15-DEC-2003; 2003WO-US040081.

17-DEC-2002; 2002US-00322281.

(SAGR-) SAGRES DISCOVERY INC.

Malandro Morris DW,

WPI; 2004-499109/47

Novel human cancer associated protein encoded within open reading frame

cancer associated gene, useful as targets for diagnosing cancer

Disclosure; SEQ ID NO 305; 182pp; English.

associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample activity of a CAP protein capable of modulating the activity of a CAP protein capable of modulating the activity of a CAP protein of a CAP protein in a test cell sample activity of a CAP protein of a CAP protein in a capable of modulating the activity of a CAP protein of a CAP protein in a capable of modulating the capable of modulating the capable of modulating the capable of a CAP protein in a capable of modulating the capable of capable of capable of modulating the capable The invention relates to cancer-associated proteins (CAP) and the cancer

The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQB1842 and ABQB1843, or a sequence spiven in ABQB1842 and ABQB1843. Also described is a polynucleotide (II) encoding a tusion protein, comprising a sequence selected from 1097 sequences given in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of a probe) is useful for the detection and/or identification of activities and/or receving and/or treating diarrhoea brought about by pathogenic used for preventing and/or treating diarrhoea brought about by pathogenic bectow and and and an activities and and and an activities and and an activities. (I) the carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented creal based products, milk based products, infant formula, pet food or a pharmaceutical composition

Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum

30-JAN-2001; 2001EP-00102050. 30-JAN-2001; 2001EP-00102050.

31-JUL-2002

(NEST ) SOC PROD NESTLE

WPI; 2002-668397/72.

Claim 1; SEQ ID NO 1; 80pp; English.

in a biological sample.

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tissue. This sequence represents a murine CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                    Sequence 168407 BP; 46388 A; 34421 C; 36717 G; 50689 T; 0 U; 192 Other;
                                                                                                                                                                                                                                                                                                                             Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiartheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition; gene; ds.
                                                                                                                                                                                                                                                                                                         Bifidobacterium longum NCC2705 genomic sequence SEQ ID NO:1.
                                                                                  168407
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Matches:
Conservative:
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ID ABQ81842 standard; DNA; 349980
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36.00
100.0%
77.8%
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Query Match:
DB:
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                                                                        Alignment Scores:
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                                                                                   Pred. No.:
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supplement, wet oral supplement, dry tube feeding or wet tube feeding.

(I) is useful in DNA arrays or chips to carry out analysis of the expression of the Bifidobacterium sens. ABQ81844 to ABQ81850 represent Bifidobacterium related nucleocide sequences given in the Sequence Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information selected from tablets, liquid bacterial suspensions, dried oral 8888888888888

Sequence 349980 BP; 72540 A; 102738 C; 103221 G; 71481 T; 0 U; 0 Other;

349980 Conservative: Mismatches: Indels: Length: Matches: 3.52e+05 36.00 100.0\$ 77.8\$ 90.0\$ Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

PheLeuGlyIleValLeuAlaLeuIle 9 -

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(1-349980)

US-10-774-176-10 (1-9) x ABQ81842

147704 TTCCTTGGCCTTGTTCTTGCCCTTCTC 147678

ACF73669 standard; DNA; 666 RESULT

ВР.

(first entry) 20-NOV-2003 ACF73669;

Staphylococcus aureus DNA #1349.

gene therapy; infection; sepsis; diagnosis; enzymatic assay, antibiotic target, gene; ds Antibacterial; vaccine;

Staphylococcus aureus.

WO200294868-A2.

28-NOV-2002

27-MAR-2002; 2002WO-IB002637.

27-MAR-2001; 2001GB-00007661.

CHIR-) CHIRON SPA

Scarselli M; Masignani V, Mora M,

WPI; 2003-120786/11. P-PSDB; ABM72109.

New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.

6, SEQ ID NO 2697; 49pp; English. Claim

The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention ACP73669

LD ACP73669

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Sequence 666 BP; 257 A; 90 C; 110 G; 209 T; 0 U; 0 Other;
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                                   Matches:
Conservative:
Mismatches:
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35.00
100.0%
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US-10-774-176-10 (1-9) x ACF73669 (1-666)

0 PheLeuGlyIleValLeuAlaLeuIle

ABS63032/c

ABS63032 standard; DNA; 853

BP

ABS63032;

(first entry) 05-NOV-2002 Selected Interacting Domain (SID) polynucleotide #229.

Yeast; selected interacting domain; SID; gene; ds; antifungal; cancer; cytostatic; neuroprotective; Candida infection; gene therapy; neurodegenerative disease.

Saccharomyces cerevisiae.

WO200259255-A2.

01-AUG-2002

25-JAN-2002; 2002WO-EP001350. 

(HYBR-) HYBRIGENICS

26-JAN-2001; 2001US-0264577P.

Legrain P;

WPI; 2002-619165/66. P-PSDB; ABG77418. New complex between two interacting bait and prey Saccharomyces cerevisiae polypeptides, useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in a mammal.

Claim 7; Page 158; 196pp; English

The invention relates to a complex between two interacting Saccharomyces cerevisiae polypeptides, comprising two Selected Interacting Domain (SID) polypeptides as bait and prey proteins. A pharmaceutical composition comprising the complex is useful for preventing or treating Candida infection, cancer and neurodegenerative diseases in a human or animal, preferably in a mammal. This sequence represents DNA encoding a SID polypeptide of the invention

Sequence 853 BP; 309 A; 140 C; 152 G; 252 T; 0 U; 0 Other;

8833 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 35.00 100.0% 66.7% 87.5% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-10-774-176-10 (1-9) x ABS63032 (1-853)

RESULT

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 16667.
                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132484P.
99US-0132486P.
99US-0132487P.
99US-0132487P.
99US-0134256P.
99US-0134218P.
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9905-013421P
9905-013476PP
9905-0134941P
9905-0135124P
9905-0135629P
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9905-0123548P-
9905-0125788P-
9905-0126785P-
9905-0126785P-
9905-0128234P-
9905-0128234P-
9905-0130649P-
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9905-0130649P-
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              17-OCT-2000 (first entry)
                                                                                                             Arabidopsis thaliana
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25-MAR-1999;
29-MAR-1999;
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18-JUN-1999;
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1-APR-1999;
3-APR-1999;
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16-APR-1999,
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 New protein-protein complexes of Saccharomyces cerevisiae, useful in drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida infection or cancer).
                                                                                                                                                                         Yeast, protein-protein interaction, Selected Interacting Domain, SID (RTM); secretion yield; cancer, neurodegenerative disease; fungicide; cytostatic; neuroprotective; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of protein, and in gene therapy. The protein complexes, polypeptides and polynucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present sequence is a coding sequence of the invention
                                                                                                                                                  Yeast selected interacting domain coding sequence SEQ ID NO: 773.
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US-10-774-176-10 (1-9) x ABT11637 (1-853)
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                                                                          ABT11637 standard; DNA; 853 BP
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                                                                                                                                                                                                                             Saccharomyces cerevisiae
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RESULT 5(

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RR 22-7JW-1399 99JW-013991P

RR 23-7JW-1999 99JW-013991P

RR 23-7JW-1999 99JW-0140354P

RR 24-7JW-1999 99JW-0140354P

RR 10-7JW-1999 99JW-0140354P

RR 01-7JW-1999 99JW-014128PP

RR 01-7JW-1999 99JW-014128PP

RR 13-7JW-1999 99JW-014139P

RR 13-7JW-1999 99JW-0144062P

RR 13-7JW-1999 99JW-0144062P

RR 13-7JW-1999 99JW-0144062P

RR 13-7JW-1999 99JW-014432PP

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RR 13-7JW-1999 99JW-014433PP

RR 19-7JW-1999 99JW-014433PP

RR 22-7JW-1999 99JW-014431PP

RR 23-7JW-1999 99JW-014431PP

RR 05-AUG-1999 99JW-014431PP

RR 11-AUG-1999 99JW-014431PP

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RR 11-AUG-1999 99JW-014932PP

RR 11-AUG-1999 99JW-014932PP

RR 11-AUG-1999 99JW-014932PP

RR 12-AUG-1999 99JW-014932PP

RR 23-AUG-1999 99JW-014933PP

RR 23-AU
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-DB=GenEmbl -QFPMT=fastap -SUPFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITSE=bits -START=1 -END=-1 -MATRIXE-blosum62 -TRANS=human40.cdi -LiST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
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Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
Patent: WO 02059377-A 57 01-AUG-2002;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Sequence 2116 from Patent WC2004097052.
CQ920916
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Sequence 57 from Patent WO02059377.
AX829164

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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 32642 12-SEP-2002;
Chondrogene Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQ687716 290 bp DNA
Sequence 32642 from Patent WO02070737.
CQ687716
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AC156671
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AC123984
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AC112092
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AC129791
AC123080
AC087226
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AC107003
AB017305
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AC098609
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1. .290
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PAT 10-DEC-2003
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Pelinae, Pelis.
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Carroll, M.M., Kingsman, S.M. and Redchenko, I.M.
MHC class I peptide epitopes from the human 5t4 tumor-associated antigen
Patent: WO 03068816-A 1 21-AUG-2003;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1260
| organism="Felis catus"
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MHC class II peptide epitope of 5t4 antigen
Patent: WO 03068815-A 121-AUG-2003;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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JP 2002530060-A/1.
Homo sapiens (human)
Homo sapiens
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Felis catus
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AX821548
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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                             1. .927
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Patent: WO 0238612-A 3 16-MAY-2002, Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers

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Sequence 1 from Patent W003068816.
AX821533 1 GI:39724929
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Sequence 3 from Patent W00238612.
AX467373 GI:21900603
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    BOS Biotechnology, Inc. (US)
Location/Qualifiers
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Felis sp.
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Pred. No.:
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 4 AX467373 LOCUS

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REFERENCE AUTHORS TITLE JOURNAL

RESULT 5
AX821533
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PAT 08-JUN-2001
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 1 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W., Ellard, F.M. and Myers, K.A.
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Location/Qualifiers
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                                                                               1072 TTCCTGGGTATTGTTTTAGCCCTGATA 1098
                                                                                                                                          Sequence 14 from Patent W00136486.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (bases 1 to 1263)
Carroll,M.W. and Myers,K.A.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LID (GB)
Location/Qualifiers
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Location/Qualifiers
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AX025011

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PAT 15-SEP-2000
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
MILES WILLIAM CARROLL,KEVIN ALAN MYERS
C12N15/09,A61K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,
C07K19/00,
C12N15/00
Polypeptide
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                                                                                           /organism='Mus musculus (mouse)'
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Patent: WO 0029428-A 2 25-MAY-2000;
PATROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN
BIOMEDICA LID (GB)
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1. .1281
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                        1090 TICCTAGGTATTGTTTTAGCTCTGATA 1116
                                                                                                                                                                                                                                                                          Indels:

    .1281
    /organism="Mus musculus"
/mol_type="genomic DNA"
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Sequence 2 from Patent W00029428.
AX025012
AX025012.1 GI:10184933
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Sequence 2 from Patent BP1160323.
AX316087
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AX025012
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                                                                                                                                                                                                                                                         Canis sp.
Canis sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                           PAT 16-JUL-2002
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sclurognathi; Muridae; Murinae; Mus.
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JP 2002530060-A/2
17-SEP-2002
18-NOV-1999 JP 2000582415
18-NOV-1998 GB 9825303.2,27-JAN-1999 GB
UL-1999 GB 9917995.4
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Patent: JP 2002330060-A 2 17-SEP-2002;
PATENT: JP 2002330060-A 2 17-SEP-2002;
OXFORD BIOMEDICA LTD
OX Mus musculus (mouse)
PN JP 2002530060-A/2
PD 17-SEP-2002
PP 18-NOV-1999 JP 2000582415
PR 18-NOV-1998 GB 9917995.4
                                                                                                                                                                                           DNA
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002,
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers

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                                                                                                                          1072 TTCCTGGGTATTGTTTTAGCCCTGATA 1098
                                                                                                                                                                                          AX467371 1263 bp
Sequence 1 from Patent WO0238612.
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Carroll, M.W. and Myers, K.A.
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JP 2002530060-A/2.
Mus musculus (house mouse)
Mus musculus
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Polypeptide.
BD249732
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Best Local Similarity:
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                                                                                                                                                                                                                      AX467371
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BD249732
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LAVLPAGAFARRPPLAELAALMLSGSRLDBVRAGAFEHLPSLRQLDLSHNPLADLSPF
AFSGSNASVSAPSPLVELTLMHTVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
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LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
Location/Qualifiers
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/function="Anchorage of the protein to the cell membrane"
                                                                                                                                                                                            Hominidae, Homo.

1 (bases 1 to 2053)

Myers, K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.

Isolation of a CDNA encoding 5T4 oncofetal trophoblast elycoprotein. An antigen associated with metastasis contains leucine-rich repeats

J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="placenta"
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                                 HSST40A 2053 bp RNA linear Homo sapiens 5T4 gene for 5T4 oncofoetal antigen.
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/product="Leucine rich repeat region"
/label=LRRs
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="LRR N-terminal flank"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="LRR C-terminal flank"
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                                                                                      GI:435654
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Percent Similarity:
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Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                         5t4 tumour-associated antigen for use in tumour immunotherapy Patent: BP 1160323-A 2 05-DEC-2001; Oxford Biomedica (UK) Limited (GB) Location/Qualiflers
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PB Corporation (NY) (US)
Location/Qualifiers
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                                      Mus musculus (house mouse)
   GI:17899279
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Buchman, V.L.
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E [bases 1 to 2183]

E [Anaya, B., Ashurst, J.L., Bonfield, J.K., Croning, M.D.R., Davies, R.M., Francis, M.D., Garfham, D.V., McLaren, S.R., Papalopulu, N., Rogers, J., Smith, J.C., Taylor, R.G., Voigt, J. and Zorn, A.M.

Direct Submission

L Submitter (10:1004) Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST/CDNA project.

This sequence is from a Xenopus Gene Collection (XGC) library, from a library constructed by Aaron M. Zorn. cDNA was prepared from RNA extracted from gasterial embryos. Ecorl. CDNI was prepared from some constructed from gasterial embryos. Ecorl. CDNI was prepared from some constructed from gasterial embryos. Ecorl. Songer and NotI at the 3'
                                                                                                                                                                                                        VRT 03-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="TGas020h08"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stage 10.5-13 mixed)"
                                                                                                                                                                                   2183 bp mRNA linear
Xenopus tropicalis finished cDNA, clone TGas020h08.
CR855786.1 GI:55295318
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HORt: Bscherichia coli XL1-blue.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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    .2183
    /organism="Xenopus tropicalis"

     Mismatches:
                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:8364"
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                                                                    US-10-774-176-10 (1-9) x HS5T4OA (1-2053)
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AF063939
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PAAFLASGSAQPPPAERCPAACECSEAARTVKCVNRNILEVPADLPPYVRNLFITGNQ
MTVLPAGARNEQPPLADLAVINLSGRHIKEVGAGAFBHLPGIRRLDLEHNPITNISAP
TRAGSNVSVSTPSPLILELILHINHIVPPEDQRQNGSFEGWVAFEGWVAAALRSGLALRGI
HHERASNHFYILPRDLLDQLPSLKHLDLRNSLVSLTYASFRNITHLESLHEBNAL
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MRNRGLLDLTSSDLDCDATLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPSLTNLSSNSDV"
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                                                                                                                                                                               Direct Submission
Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
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/translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSLPSSSTS
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 2359)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciucognathi, Muroidea, Muridae, Murinae, Rattus.
1 (bases 1 to 2333)
Ninkina,N.N. and Buchman,V.L.
Structure and expression of the rat 5T4 gene
Unpublished
(bases 1 to 2333)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'codon_start=1
product="5T4 oncofetal antigen homolog"
protein_id="AAR21770.1"
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Mismatches:
Indels:
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/db_xref="taxon:10116"
/tissue_type="cerebellum"
/dev_stage="newborn"
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Matches:
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JP 2002017375-A/2713.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="5T4"
1.363
/gene="5T4"
364..1644
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2315. .2320
/gene="5T4"
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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- £ 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

1. .2359
| ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2359 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | ... .2350 | .
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKMRNVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRGIKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK074786 2359 bp mRNA linear PRI 03-SBP-2002 Homo sapiens cDNA FLJ90305 fis, clone NT2RP2000694, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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18ogal.T. and Orsuki.T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
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mRNA from NT2 neuronal precursor cells after 2-weeks
retinoic acid (RA) induction"
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AK074786.1 GI:22760460
Oligo capping; fls (full insert sequence).
Homo sapiens (human)
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/clone_lib="NT2RP2"
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APBGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALGGERRIELA
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
BY JP 2002017375-A/2713
PN JP 2002017375-A/2713
PD 32-JAN-2002
PP 77-JUL-2000 JP 2000253172
PP 77-JUL-2000 JP 2000253172
PT TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer for synthesizing full-length cDNA and use thereof PH Key Location/Qualiflers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
SHINICHI KOJIMA,
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Matches:
Conservative:
Mismatches:
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/organism="Homo sapiens"
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424. .1575
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Bequence 2864 from Patent EP1396543.
CQ782724
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/db_xref="taxon:9606"
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Best Local Similarity:
Query Match:
DS:
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CQ782724
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LAVLPAGAFARRPPLAELAALNISGSRLDEVRAGAFEHIPSIRQLDLSHNPLADISPF
AFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGWVVALLAGRALQGIRRLELA
STRHFYLLPROVLAGLESLRHDLSNNSLVSLTYVSFRMLTHLESLHTEDNALKYLHNG
TLAELQGLPHINVFLONNPWYCDCHMADMVTWLKETEVVQGKDRLTCAYPEKRNRVL
LELNSADLDCDPILLPSELQTSYPFLGTVLALIGAIFLLVLYLNRKGIRKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                               Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                              Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2866 10-MAR-2004;
Research Association for Bittechnology (JP)
Location/Qualifiers
1. .2361
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
426. .1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene
Stat6 activation gene
Patent: WO 03104277-A 127 18-DBC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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Matches:
Conservative:
Mismatches:
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/codon_start=1
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Seguence 127 from Patent WO03104277.
AX961916
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                                                          Hominidae; Homo.
     Homo sapiens
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SOURCE
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                                                                                                                                                                                                              FEATURES
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JP 2002017375-A/2714
22-JAN-2002
07-JUL-2000
JP 200253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bades 1 to 2361)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
                                                                                                                                                                                              ыл 27283 2361 bp DNA linear PAT 1
Primer for synthesizing full-length CDNA and use thereof.
BD127283
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2714 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Indels:
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CQ782726
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Location/Qualifiers
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   Indels:
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                         Gaps:
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                                                                                             PhereuglyllevalLeuAlaLeulle 9
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                                                        US-10-774-176-10 (1-9) x AK074786 (1-2359)
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JP 2002017375-A/2714.
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Homo sapiens
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Homo sapiens (human)
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Query Match:
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CQ782726
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BD127283
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PAT 14-JAN-2004

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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba, 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biorechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported
APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFITGNQ
LAVLPAQAPRRPPLANINGSBRENDGWASAPRENLESKQLDCENPRIADLSPP
APGGSRASVSARSPYVBLILMHIYPPEDBRORNSFEGWYVAALLAGGRALGGLSERELELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVILNG
THLELQGLPHIRVPLDNNPWYCDCHANDMYTRIKETEVVQGKORLTCAYPEKRRYL
IBLASADLDCDPILPRONDPWYCDCHANDMYTRIKETEVVQGKORLTCAYPEKRRNYL
IBLASDLDCDPILPROTGYTSVPLGIYLALIGAIPLLIGAYPKKORKMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK074790 2361 bp mRNA linear PRI 09-JUL-2005 Homo sapiens CDNA FLJ90309 fis, clone NT2RP2000903, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogal, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yanamoto, J., Wakanatsu, A., Nakamura, Y.,
Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
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Mammalla, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otsuki,T., Ota,T., Nishikawa,T., Hayashi,K., Suzuki,Y., Yamamoto,J., Wakamatsu,A., Kimura,K., Sakamoto,K., Hatano,N., Kawai,Y., Ishili,S., Saito,K., Kojima,S., Sugiyama,T., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Nagai,Y., Aotsuka,S., and Isogai,T. Signal Sequence and Keyword Trap in silico for Selection of Full-Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped CDNA Libraries
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens (human)
Homo sapiens
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Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AK074790
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Straueberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Riausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haish, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, R.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2361 bp mRNA linear ROD 13-DBC-2004 Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Bxpress Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
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Submitted (02-D02-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
/clome="NT2RP2000903"
/cell_line="NT2"
/cell_type="teratccarcinoma"
/clome_lib="NT2RP2"
/note="cloming vector: pME18SFL3
mRNA from NT2 neuronal precursor cells after 2-weeks
retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Rattus norvegicus
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Director MGC Project.
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Wagner, L., Shenmen, C.M., Schuler, G.D.

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Klausner, R.D., Collins, F.S.,
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                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHLELASNHPLYLPRDILDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KYATHSTLEAWGGLAHVRUPLDNNPWTOCYNADMYSWLKETEVVPDKARLTCAFPEK
MRNRGLIDLTSSDLDCDATLPSCOLOTSYVPIGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNBV"
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Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAAPLASGSAQPPPAERCPAACECSEAARTVKCVNRNILLEVPADLPPYVRNLFIJGNQ
WTVLPAGAPARQPPLADLAVINLSGNHLKEVGAGAFEHLPGIRRLDLSHNPLTNISAP
TPAGSNVSVSTPSPLLELILNHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSLPSSSTS"
                 Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 2379)
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
                                                                                                                                                                                                                                                                                                                                                     /tissue type="Heart, rat (Brown Norway)"
/clone Tib="NIH MGC 234"
/lab_host="DH10B"
/note="Vector: pExpress1"
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
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/db_xref="GeneID:83684"
/db_xref="RGD:621453"
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/db_xref="RGD:621453"
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BC037161.2 GI:33872201
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/gene="Tpbg"
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VERSION
KEYWORDS
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Altschul, S.P., Colling, F.D., magner, D., Schaefer, C.F., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaky, S.J., Bosak, S.A., McEwan, P.J., Peters, G.J., Worley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, R.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Butterfield, Y.S., Krzywinski, M.I., Skald Marra, M.A., Schmutz, J., Myers, M., Generation and initial analysis of more than 15,000 full-length human and mouse DNA sequences

D. 12477932
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help desk
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/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5T4-AG, 5T4"
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    .2379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .2379
/gene="TPBG"
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Best Local Similarity:
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8 (Tausner, R.D., Collins, P.S., Wagner, L.H., Derge, J.G., Altschul, S.F., Zoeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Carcia, M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Bouffard, G.G., Blakesley, R.W., Toung, A.C., Shevchenko, Y., Butterfield, Y.S., Ketteman, M., Madan, A., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myes, R.M., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, S., Karzywinski, M.I., Salska, U., Smailus, D.E., Butterfield, S., Karzywinski, M.I., Schein, J.S., and Marza, M.A., Schein, J. M. A., Schein, J. Schei
                                                                                                                                                                                                                                   ARSGSNASVSAPSPLVELILMHIVPPEDERQNRSFEGMVVAALLAGRALQGERELEA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTVVSFRALTHLBSLHHEDNALKVILMG
TLABLQGLPHIRVFLDNNPWCDCHPMADMVTMLKETEVVQGKDRLTCAYPEKMRNVI
LELNSADLDCDPILPSPSLQTSSYPKGIVLALIGAIFLLULYLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2423 DD mRNA linear ROD 21-OCT-2003 Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 RCGS:5353871), complete cds.
                                                                                                                                        /translation="Mpggcsrgpaagdgrlrlarlalvilgwvssssptssassfsss
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Submitted (15-SEP-2003) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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Best Local Similarity:
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DB:
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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BC058198
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Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),

Gaithersburg, Maryland;

Web sites http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Shkter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blakesley,R.W., Bouffard,G.G., Naren,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Gudn,X., Gupta,J., Haghighi,P.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrians,B.D., Legaspi,R.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tanrgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK plate: 123 Row: p Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854.
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/db
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TCLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KVHNSTLAEMQGLAHVVFPLDNNPWYCDCYMADMVAWLKETEVVPDKARLTCAFPEK
MRNRGLIDLNSSDLDCDAVLPQSLCTSYVPLGIVVLALIGAIFLLVLTLNRKGIKKWMM
NIRDACRDHMRGYHYRYEINADPRLTNLSSNSDV"
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/clone="MGC:68145 IMAGE:5353871"
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/mol_type="mRNA"
/strain="FVB/N"
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/db_xref="MGI:1341264"
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/gene="Tpbg"
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VPAGSNASVSARSPLEELIJMHIVPPEDQRQNGSFEGNVAFEGNVAALRSGLALRGL
TRLELASNHFPLPLPRDLLAQLPSLRYLDLRNNSIVSLTYASFRNLTHLESLHLEDNAL
KVLHNSTLAGGAHVKYPLDNNPWYCDCYMADMVAMLKGTEVVPDKARLTCAFPEK
MRNRGLDLNSSDLOCDAVLPQSLQTSVPFGTVLALIGAIFLUVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
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Paaflasgsaqpppaercpaacecseaartykcynrnlleypadlppyyrnlflugu
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Mus musculus
Rukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
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Patent: WO 03104277-A 123 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
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Sequence 125 from Patent WO03104277.
AX961914
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/db_xref="GI:40881323"
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/translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSVPSSSTS
PADFLASGSAQPPARRCPAACECSEAARTVKCVRNNLLEVPADLPPVRNLFLTGNO
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VFAGSNASVSAPSPLEELILNHIVPPEDQRQNGSFEGWVAFEGWVAAALRSGIALRGI
TRLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLRSLHLEDNAL
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MRNRGLLDLNSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
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Macaca fascicularis testis cDNA clone: QtsA-11109, similar to human
trophoblast glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              International consortium for macaque cDNA sequencing and analysis. DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
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Sugahara, T., Matsuda, A., Honda, G., Muramatsu, S. and Ishizawa, K.
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oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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/note="unnamed protein product"
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                                  Stat6 activation gene
Patent: WO 03104277-A 125 18-DEC-2003;
Agahi Kagei Kabushiki Kaisha (JP)
Location/Qualifiers
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/db_xref="taxon:10090"

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/db_xref="G1:40881325"
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SNHFLYLPRDVLAQLPSLRYLDLSNNSLVSLFYVSFRNLTHLESLHLEDNALKYLHNG
TLABLQGLPHVRVFLDNNPWVCDCHMADMYTWLKQTGVVQGKDRLTCAFPERGRNRVL
LELNSADLDCDPILPPSLQYSYVFLGIVLALIGAIFLLUYLYLNRKGIRKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
Tokyo, Japan; Division of Genetic Resources, National Institute of Infectious Diseases of Japan, Tokyo, Japan; National Health Research Institute, Taipei, Taimei, Institute of Molecular Biology, Academia Sinica, Taipei, Taimen; Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA; Center for Information Biology, National Institute of Genetics of Japan, Mishima, Japan. Clone distribution: clone distribution information at http://www.nih.go.jp/yoken/genebank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tränslation="mpggcsrqpaagdgrlrlarlalujlgwyssssyssasssss
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Conservative:
Mismatches:
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PRI 15-APR-2005

linear

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5551 bp

HSA012159

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                              King, K.W., Sheppard, P.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 574 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
AJ012159
                                                                    AJ012159.1 GI:3805946
5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Homo sapiens (human)
Homo sapiens
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1093. .5400
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Myers, K.A.
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                                                                                                                                                                                                                                                                                   ROD 15-APR-2005
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Submitted (23-007-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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Mus musculus 5T4 oncofetal trophoblast glycoprotein gene.
AJ012160
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                                                                                                                                           US-10-774-176-10 (1-9) x HSA012159 (1-5551)
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3451. .5779
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Alignment Scores:
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TITLE
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PUBMED
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                                                                                                                                                                                                                                               RESULT 33
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Submitted (13-MMY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Dec 15, 2000 this sequence version replaced gi:11558491.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, RMEL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RR9-42214 is from the library RPCI-3 constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
                                       KVIANSTLAEWGELAHVKVELDNNPAVCDCYVADMYAMLKETEVVPDKARLTGEDNAL
MRNGLLDLDNSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWH
NIRDACRDHWGCYHYRYEINADPRLTNLSSNSDV"
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121909 bp DNA linear PRI 18-MAY-2005
Human DNA sequence from clone RP3-492P14 on chromosome 6q13-15

Contains a single stranded DNA binding protein pseudogene, the TPBG
gene for trophoblast glycoprotein (574-AG) and a CpG island,
                      VFAGSNASVSAPSPLEELIINHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
TRLELASNHPLFLPRDLLAQLPSLRYIDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
MTV1.PAGAPARQPPLADLEALN1.SGNHLKEVCAGAPEH1.PG1.RRLD1.SHNP1.TN1.SAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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/5559. .5764
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Conservative:
Mismatches:
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AL121977
AL1219771 G:11863678
HTG; CpG island; TPBG.
HOMO sapiens (human)
Homo sapiens
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                                                                                                                                       3779. .3865
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3866. .5056
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Direct Submission
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Best Local Similarity:
                                                                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                            polyA_signal
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                                                                                                                                         sig_peptide
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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HSJ492P14
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Danio rerio
                                                                       Percent Similarity:
Best Local Similarity:
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  Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | db | xref = "cOA: Q13641" | db | xref = "cOA: Q13641" | db | xref = "InterPro: IPR000472" | db | xref = "InterPro: IPR000481" | db | xref = "InterPro: IPR0016481" | db | xref = "InterPro: IPR001611" | db | xref = "InterPro: IPR0018591" | db | xref = "UniProt/TrEMBL: Q13641" | translation="MPGGSGRGPAGDGRIRLARLALVILGWVSSSSPTSSASSFSSS | APFLASAVSAQPPLEDCCPALCRSCRAARTYKCVRRITBYTGVPTDLPAYVRNIFTTGNQ | LAVLPAGARARRPPLABLAALMLSGSRLDSVRAGAFEHLPSLRQLDLSHNPLADLSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (10004. .10982)
Jocus taga-RP3-492P14.2-001"
/notea-match: proteins: P81877 Q99LX9 Q9BWW6 Q9CYZ8 Q9D6L4
Q9P038 Q9Y4T7"
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STWIFTLILDBNOTAQLPELIALDISNBLVSLTVSFRULTHESLHEBSDALKVLHNG
TLABLGGLPHIRVPLDINPWVCDCHAADMVTWIKSTEVVQGKORLTGAYPEKRRINRUL
LBINSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRGIKKWMHNIRDAC
regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 300; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="trophoblast glycoprotein"
/note="match: BSTs: AA149121 AA152323 AA555852 AA643734
AL544610 AW471072 AW662538 BR260089 BP306457 BF306926
BP314984 BI196133 BIS62387 BM069633 BM670613
match: CDNA: AJ420536.1 Z29083.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_tag="RP3-492P14.1-001"
/standard_name="OTTHUMP00000016786"
/note="match: proteins: Q13641 Q9QYD9 Q9Z0L0"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="RP3-492P14.1-001"
join(109639. .109916,110631. .116836)
/gene="TPBG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="trophoblast glycoprotein"
'protein id="CA121546.1"
db_xref="G1:56203539"
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                                                                                                                                                                                                                                                                                                                                                                      /note="Clone right end: RP1-93K22"
complement (10004. .10982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Clone_left_end: RP1-90G1"
109639. .116836
/gene="TPBG"
                                                                                                                                                                                                                                                                                                                                                                                                complement (10004. .10982)
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116836
                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                /clone="RP3-492P14"
/clone_lib="RPCI-3"
100
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/map="q13-15"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality: -30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; 8w:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the they.//www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived length of mononucleotide A/T runs and conserved TA repeats. Where the conserved mail the feature found at all regions were conserved the peats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRT 29-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX248521 144888 bp DNA linear VRT 29-APR-2004
Zebrafish DNA sequence from clone CH211-243C14 in linkage group 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 144888)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-APR-2004) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 18A, UK. B-mail enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 29, 2004 this sequence version replaced gi:46406548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-243C14 is from a CHORI-211 BAC library
VECTOR: pTARBAC2.1.
                                  00000
                                                                    Conservative:
Mismatches:
Indels:
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   Length:
Matches:
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Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                           US-10-774-176-10 (1-9) x HSJ492P14 (1-121909)
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                                                                                                                                                                                                                                                                                                                                                                                                                          ROD 21-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 167046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognath; Murinae; Mus.

1 (bases 1 to 167046)
Adams,S., Cotton,M. and Haglund,K.
The Sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                          ACI58516 167046 bp DNA linear ROD 21-JUN-
Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-JUN-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MMD 63108, USA
On May 4, 2005 this sequence version replaced gi:61656412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted:
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                                                                                                                                    144888
                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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Submitted (04-WAY-2005) Genome Seg
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
Wilson,R.K.
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-243C14"
/clone_lib="CHORI-211"
                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                     (1-144888)
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AC158516.2 GI:63025421
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                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                  Alignment Scores:
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AC158516/c
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
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                                                                             DRIGIN
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This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                       If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CSTBL/GJ mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
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SEQUENCE.
                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria Buarchontoglires, Glires, Rodentia, Sciurognathi, Murioldea, Muridae, Murinae, Rattus.

1 (bases 1 to 210237)

Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allan, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Angalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16685._.16712
hote="Sequence derived from PCR product of genomic DNA"
31565...31779
/note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142336. .142347
/note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210237 bp DNA linear
Rattus norvegicus clone CH230-176H20, WORKING DRAFT
AC128294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence repeat."
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assembly was confirmed by restriction digest
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46721. .46808
/note="Unresolved simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC128294.3 GI:25083347
HTG; HTGS PHASE2; HTGS DRAFT;
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP24-511A23"
/clone_lib="RPCI-24"
16685._.16712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    http://genome.wustl.edu
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40.00
                                                                                                                                                                                                                                                                                  MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE INFORMATION:
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Best Local Similarity:
                                                                                                                                                     minimal
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DB:
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LOCUS
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us-10-774-176-10.p2n.rge

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Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bulay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavacos, I., Cadaera, H., Canter, A.,
Cardena, V., Carter, K., Cavacos, I., Cadaera, H.,
Chacko, J., Chavacz, D., Chan, G., Chan, R., Chan, S., Chan, J.,
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Egan, A., Bsockto, M., Eugene, C., Frans, C.A., Falls, T., Fan, G.,
Franandaz, B., Finlay, M., Flagg, N., Forbes, L., Foster, M., Goverz, M.,
Gabregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, T., Garza, M.,
Gabregorgis, R., Hines, S., Hladun, S.L., Hodgson, M., Harmidac, J.,
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannson, S., Bhen, H.,
Rujuy, B., Rallly, M., Ran, Y., Reiter, M., Richard, S., Band, S.,
Banders, M., Savery, G., Scherer, S., Tabey, K.,
Malliams, G., Walley, P., Walles, R., Wall, M., Tabor, P., Taylor, C.,
Taylor, T., Thomas, M., Thomas, S., Tingey, A., Tabor, P., Taylor, Y.,
Maright, D., Walles, R., Wu, J., Yakub, S., Yan, M., Yalas, S., Martiber, B., Marter, B., Sodergren, B., Sodergren, S., Sant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON NOV 19, 2002 this sequence version replaced gi:23265004.

The sequence in this sequence version replaced gi:23265004.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.ed/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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JOURNAL
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AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
JOURNAL
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.----- Genome Center

COMMENT

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* NOTE: Bstimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACLU6962 239076 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
unocaered pieces.
                                                                                                                                                       Assembly program: Phrap, version 0.990329
Consensus quality: 201781 bases at least 040
Consensus quality: 203921 bases at least 030
Consensus quality: 203921 bases at least 030
Consensus quality: 205310 bases at least 030
Stimated insert size: 205310 bases at least 030
Stimated insert in 020 bases; sum-of-contigs estimation
Quality coverage: 7x in 020 bases; sum-of-contigs estimation
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HTG; HTGS_PHASB1; HTGS_DRAFT; HTGS_FULLTOP.
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
Center project name: GZGV
Center project name: GZGV
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Matches:
Conservative:
Mismatches:
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|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-176H20"
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/note="clone_boundary
clone_end:Sp6
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/note="wgs_end_extension
clone_end:Sp6"
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clone_end:T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence: BH360465"
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/note="clone_boundary
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Best Local Similarity:
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AC106962/c
LOCUS
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KEYWORDS
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6.39e+03
40.00
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237415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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AC165904
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Bandaranake, D., Sarber, M., Barnstead, M., Benahmed, F.,
Baldowin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F.,
Bravalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, M., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, M., Carter, K., Cavazos, I., Cesar, H., Center, A.,
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Fraser, C., Glair, R., Gerr, K., Galla, T., Carza, M.,
Gunzarene, P., Haalak, P., Haves, A., Hamilton, C., Hamilton, K.,
Hernandez, R., Hines, S., Hand, S., L., Hodgeon, A., Hernandez, M.,
Gunzarene, P., Havlak, P., Haves, A., Handerson, M., Hodgeon, A.,
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Margam, R., Marlin, K., Martin, R., Martine, B.,
Mander, S., Mcelly, S., Mally, S., Khan, Z., Loux, M.,
Mangun, B., Mapu, P., Martin, K., Martine, B.,
Mander, S., Mcer, C., Mangun, M., Morris, S.,
Marker's, C., Neal, D., Wewton, M., Marton, W., Martin, S.,
Ropper, R., Polyode, D., Primus, B., Pull, L.,
Blatter, S., Paul, H., Perez, A., Roes, M., Rebor, R., Rigge, F.,
Right, D., Shvarten, J., Moore, S., Milliams, G., Walloon, R., Williams, G., Walloon, R., Williams, G., Williams, G
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described
                                                          Euteleostomi;
                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buto
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Assembly program: Phrap; version 0.990329
Consensus quality: 226642 bases at least Q40
Consensus quality: 22269 bases at least Q30
Consensus quality: 234041 bases at least Q30
Consensus quality: 240401 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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4711 234810: gap of unknown length
4811 235924: contig of 1114 bp in length
522 236024: gap of unknown length
6025 237314: contig of 1290 bp in length
7315 237414: gap of unknown length
7315 237414: gap of unknown length
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8 Arredondo, H. Bandaranike, D. Bangura, L. Beltran, B. Beltran, B. Bertan, B. Arredondo, H. Bandaranike, D. Bangura, L. Beltran, B. Beltran, B. Cadore, I. Candada, C. Carcer, C. Cockeal, R. Canaco, I. Chen, A. Cardens, V. Carrer, K. Canaco, I. Chang, M. T. Chu, J. Clarc, K. Cockeal, R. Canaco, I. Chen, A. Chang, M. T. Chu, J. Clarc, K. Deramo, C. Ding, Y. Dinh, H. Davila, M. D. Deramo, C. Ding, Y. Dinh, H. Davila, M. Deramo, C. Ding, Y. Dinh, H. Davila, M. Deramo, C. Ding, Y. Dinh, H. Davila, M. Gencales, C. Peter, P. Canada, C. Denamo, S. Deramo, C. Ding, Y. Dinh, H. Davila, M. Gencales, G. Rid, R. Garcia, R. Garner, T. Ganch, S. Ganch, S. Garcia, R. Garner, T. Ganch, S. Ganch, S. Garcia, R. Garner, T. Ganch, S. Ganch, R. Garcia, R. Garner, T. Ganch, S. Hong, M. Guevara, M. Holder, M. Haaland, W. Haebellen, K. Hall, B. Hamid, H. Hamilton, K. Harbes, B. Harris, R. Hallak, P. Hawell, L. T. Hulyk, S. Hume, J. Tho, K. Jackson, A. Jacch, L. Jang, H. Johnson, B. Johnson, R. Johnson, R. Johnson, R. Johnson, R. Johnson, R. K. Kalafis, K. Kelly, K. Li, Z. Linnell, M. Liu, W. Liu, W. Liu, Y. Liyar, Martinez, B. Maloswari, M. Mahorey, C. Maloy, K. Mansouri, D. Martinez, B. Marcado, C. Metzker, M. Mahorey, L. Lopez, J. Linnell, W. Liu, W. Liu, Y. Julyange, D. Maratinh, J. Davil, M. Santes, M. Mang, C. Metzker, M. Manders, W. Mand, S. Lee, K. Mand, M. Mochara, M. Mang, C. Metzker, M. Mang, C. Metzker, M. Santer, M. Santes, M. Mang, Q. Mang, S. Petel, B. State, M. Wall, M.
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Submitted (19-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine
                                                                                                                                                           Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bos taurus clone CH240-172A22, *** SEQUENCING IN PROGRESS ***, 21
                                                                                                                                                                                   Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap, version 0.990329 Consensus quality: 93363 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
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----- Summary Statistics
Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hgsc-help.tmc.edu
                                                                    AC165904.1 GI:70980581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 66940)
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                            unordered pieces.
                                                                                         HTG, HTGS_PHASE1
                                                                                                                 Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
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JOURNAL
REFERENCE
                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                       AUTHORS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 97762 bases at least Q30
Consensus quality: 100227 bases at least Q30
Estimated insert size: 106512; aum-of-contigs estimation
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 4436 by gap of unknown 1 contig of 4999 by gap of unknown 1 contig of 2322 by gap of unknown 1 contig of 2912 by gap of unknown 1 contig of 2912 by gap of unknown 1 contig of 29137 by gap of unknown 1 contig of 2337 by gap of unknown 1 contig of 2295 by
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11791. .11890
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16223. .16322
/estimated length=unknown
19242. .19341
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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/organism="Bos taurus"

/mol_type="genomic DNA"

/db_xref="taxon:9913"

/clone="CH240-172A22"

3373. .3472
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Direct Submission
Submitted (28-JUL-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 173867 bases at least Q40
Consensus quality: 173877 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 174254; sum-of-contigs
Quality coverage: 7.84x in Q20 bases; sum-of-contigs
Quality coverage: 8.01x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="CH259"
/note="BAC_resource: http://bacpac.chori.org/"
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43336: gap of unknown length
37 99626: contig of 56290 bp in length
87 99626: gap of unknown length
87 174454: contig of 74728 bp in length.
Location/Qualiflers
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                                                                                                                                    Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
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Matches:
Conservative:
Mismatches:
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/organism="Callithrix jacchus"
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/estimated_length=unknown
99727. .174454
/note="assembly_fragment"
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/estimated_length=unknown
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/note="assembly_fragment
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clone_end:T7
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/db_xref="taxon:9483"
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Center clone name: 471J06
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97.5%
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Query Match:
DB:
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AUTHORS
TITLE
JOURNAL
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                                                                                                                COMMENT
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Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Guan, X., Gupta, J., Haghighi, P.,
Logaman, H., Mader, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q.,
Legaspit, R., Madden, M., Maduro, Q.L., Malue, V. B., Margulles, B.H.,
Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paquirigan, C.,
Park, M., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N.,
Schueler, M.G., Shah, K., Sison, C., Stantripop, S.,
Young, A. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACISO616 174454 bp DNA linear HTG 28-JUL-2004 Callithrix jacchus clone CH259-471J6, WORKING DRAFT SEQUENCE, 3 unordered pieces.
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HTG; HTGS PHASE1; HTGS DRAFT.
Callithrix jacchus (white-tufted-ear marmoset)
Callithrix jacchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Callitrichidae; Callitrichidae; Callitrichidae; Callitrixichidae; Callitrixich
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                               35822. .35721
/estimated length-unknown
40358. .40457
/estimated length-unknown
45457. .45556
/estimated length-unknown
47779. .47878
                                                                                                                                                                                                                                                                                                                                                                                                                                              /estimated length=unknown 50274. 50373
/estimated length=unknown 52466. 52565
/estimated length=unknown 55478. 55577
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28707. .28806
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  estimated_length=unknown
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Best Local Similarity:
Query Match:
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL

COMMENT PEATURES

RESULT 41 HSPA32B9/c LOCUS DEFINITION

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Direct Submission

Loud Submission

Loud Submission

Loud Submission

Loud Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

Cn Jul 12, 2002 this sequence version replaced gi:21727582.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.aanger.ac.uk/HGP/ChrX

RP3-333US is from the library RPCI-3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/Dacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL807766 58433 bp DNA linear PRI 18-MAY-2005
Human DNA sequence from clone RP3-383J8 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
Direct Submission
Submitted (24-JUL-1998) Takeshi K Watanabe, Otsuka Pharmaceutical
Co., Lid., Otsuka GEN Research Institute; 463-10, Kagasuno,
Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan
(B-mail:watanabe@otsuka.genome.ad.jp, Tel:81-886-65-2888,
Pax:81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                          1. .440
// Organism="Rattus norvegicus"
// Organism="Rattus norvegicus"
// Mol Lype="genomic DNA"
// D_xref="taxon:10116"
// D_corne="Or13:18/093b02"
// note="0713:18/093b02R=5'-AGCAGTTTCTAGAAGCCCGT-3',
OT23.18/093b02R=5'-TATGACAACCACATACCTGCT-3',
                                                                                                                                                                                                                                                                                                                                                                                                                      4 8 4 0 0 0
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Matches:
Conservative:
Mismatches:
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                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL807766.4 GI:21738718
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1 (bases 1 to 58433)
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38.00
100.0$
88.9$
95.0$
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Best Local Similarity:
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Pred. No.:
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DB:
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AL807766/c
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  TITLE
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Rattus norvegicus, OTSUKA clone, OT23.18/093b02, microsatellite
Bequence, sequence tagged site.
                                                                            421 bp DNA linear STS 21-MAY-1998
H.sapiens flow-sorted chromosome 6 Hindlil fragment, SC6pA32B9,
sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="BBV lymphoblastoid cell line"
/clone_lib="SC6pA"
/dev stage="adult"
/note="The estate purity of the flow-sorted chromosome 6 library is >97%"
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Rattus norvegicus
Rattus norvegicus
Rakaryota, Metacoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buschontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 421)
Mungall, A.U., Huckle, E., Langford, C., Ross, M.T. and Hunt, S.E.
Direct Submission
Submitted (17-APR-1997) The Sanger Centre, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe,T.K., Hishigaki,H., Kanemoto,N., Miyakita-Mizoguchi,A., Oga,K., Okuno,S., Ono,T., Tsuji,A., Hayashi,H., Adachi,M., Yanasaki,Y., Iriye,Y., Takahashi,E., Takagi,T., Nakamura,Y. and
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Matches:
Conservative:
Mismatches:
Indels:
          6457 TTTTTGGGTGTTGTTCTTGCTTTAATT 6483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="SC6pA32B9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    humquery@sanger.ac.uk
Vector: pBSIISK+
                                                                                                                                                                                                                       STS; single read.
Homo sapiens (human)
                                                                                                                                                                                                        294208.1 GI:1945202
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2 (bases 1 to 440)
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Best Local Similarity:
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Query Match: DB:

Pred. No.:

DRIGIN

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL REPERENCE AUTHORS

AUTHORS REFERENCE

DEFINITION

ACCESSION

RESULT 42 AU026869

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ORIGIN

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare procession of the clone being a MAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Ems., EMBL: Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived
Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL954182 151552 bp DNA linear VRT 25-NOV-2003
Zebrafish DNA sequence from clone CH211-205N18 in linkage group 20,
as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-NOV-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 25, 2003 this sequence version replaced gi:38230013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Stinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (Dases 1 to 15155)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP3-38348"
/clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45420 TTCCTAGGAATAGTACTAGCCCTTCTC 45394
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Contact: zfish-help@sanger.ac.uk
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38.00
100.0%
88.9%
95.0%
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AL954182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                        FEATURES
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COMMENT

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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRT 30-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX005450 164218 bp DNA linear VRT 30-NOV-200
Zebrafish DNA sequence from clone CH211-150023, complete sequence.
                                                   Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-205N18 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-NOV-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clon Nov 4, 2003 this sequence version replaced gi:37665469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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this is found the longest good quality representation will be
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Mismatches:
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Center code: SC
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Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-205N18"
/clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
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1. .151552
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38.00
100.0%
88.9%
95.0%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                   source
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BX005450/c
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JOURNAL
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AUTHORS
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SOURCE
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Percent Similarity:
Best Local Similarity:
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No.:
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AUTHORS
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KEYWORDS
SOURCE
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of monouncleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRT 24-AUG-2004
                                                                                                                                                                                                          those
                                                                                                                                                                          Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson Lab, Washu). For further information see http://www.sanger.ac.uk/Projects/D rerio/fishmask.shtml CH211-150023 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@eanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 6, 2004 this sequence version replaced gl:50949643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX323031 164748 bp DNA linear VRT 24-AUG-2
Zebrafish DNA sequence from clone DKEYP-7B3 in linkage group 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
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Indels:
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Matches:
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/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon;7955"

/clone="CH211-150023"

/clone_lib="CHORI-211"
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Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity:
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DB:
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AUTHORS
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KEYWORDS
SOURCE
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one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems., EMBL; Sw., SWISSENCY; Tr., TERMBL; WP:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRUSSZES 166117 bp DNA linear HTG 05-NOV-2004
Danio rerio clone CH211-195E6, *** SEQUENCING IN PROGRESS ***, 25
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                  discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson Lab, Wash). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEYP-7B3 is from a Zebrafish BAC library
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Cyptiniformes, Cyptinidae, Danio.

1 (bases 1 to 166117)
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Mismatches:
Indels:
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Chemistry: Dye-terminator; 100% of reads
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-7B3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR: pIndigoBAC-5.
Location/Qualifiers
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HTG; HTGS PHASE1.
Danio rerIo (zebrafish)
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38.00
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88.9$
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Consensus quality: 158259 bases at least Q40 Consensus quality: 159771 bases at least Q30 Consensus quality: 161055 bases at least Q20 Insert size: 163717; sum-of-contigs Quality coverage: 6.48x in Q20 bases; sum-of-contigs Quality coverage: 6.96x in Q20 bases; sum-of-contigs Quality coverage: 6.96x in Q20 bases; agarose-fp
                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5372 162129: contig of 6758 bp in length

2130 162229: gap of 100 bp

2230 166117: contig of 3888 bp in length.

Location/Qualifiers

1. 166117

/organism="Danio rerio"

/mol_type="genomic DNA"

/db xref="taxon:7955"

/clone="CH211-19586"

/clone="CH211-19586"

1. 2920
                                                                                                                                                                                                                                                                                contig of 6777 bp in length
gap of 100 bp
contig of 9938 bp in length
gap of 100 bp
contig of 21151 bp in length
gap of 100 bp
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gap of 100 bp
contig of 22267 bp in length
gap of 100 bp
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gap of 100 bp
contig of 5789 bp in length
gap of 100 bp
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contig of 5898 bp in length
gap of 100 bp
contig of 2839 bp in length
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contig of 3136 bp in length
gap of 100 bp
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gap of 100 bp
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of 3436 bp in length
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of 2983 bp in length
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of 5453 bp in length
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gap of 100 bp
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gap of 100 bp
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gap of 100 bp
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gap of 100 bp
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gap of 100 bp
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                                                                                                                       (bases 1 to 213305)
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Unpublished
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Rattus.
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
                     Length:
Matches:
Conservative:
Mismatches:
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                       1.36+04
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Alignment Scores:
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AC114043/c
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                     Pred. No.:
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AUTHORS
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Submitted (13-MY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON MAY 13, 2003 this sequence version replaced gi:2364945.

On May 13, 2003 this sequence version replaced gi:2364945.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.trc.edu/projects/raf/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
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Consensus quality: 197649 bases at least Q40
Consensus quality: 199600 bases at least Q30
Consensus quality: 201081 bases at least Q20
Estimated insert size: 210356; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhou, J., Zhou, X., Zhoo, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Baylor College of Medicine

    .213305
    /organism="Rattus norvegicus"

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as soon as it is available and the accession number will
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232746 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-6D9, *** SEQUENCING IN PROGRESS ***,
2 unordered pleces.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Rattus.
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
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Mismatches:
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Matches:
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VERSION

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All Submitted (199-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on May 9, 2003 this sequence version replaced gi:24941526. On May 9, 2003 this sequence version replaced gi:24941526. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.uc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Milosavljevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankeris, S., Nankeris, S., Nankeris, S., Nankelseneh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, J., Perankoch, C., Pathankoch, C., Pullopper, P., Poindexter, A., Popovic, D., Primus, B., Pul. -L., Puszo, M., Quiroz, J., Ren, Y., Reuter, M., Richards, S., Riggs, F., Revis, C., Redily, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Shert, J., Shetty, J., Shvartabeyn, A., Scherer, S., Soct, G., Shatsman, S., Shen, H., Shetty, J., Shvartabeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartabeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Wallson, M., Walker, B., Wang, J., Wallson, M., Walker, B., Wang, J., Wallson, M., Walker, B., Wang, J., Walker, W., Walker, W., Walker, W., Walker, B., Wang, J., Walker, B., Walker, B., Wang, J., Walght, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, U., Yu, F., Zhang, J., Zhou, J., Yakub, S., Yen, J., Walker, B., Walker, B., Wainteck, G. and Gibbs, R.A. Bulth, D. R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine
Center code: BCM
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                     1 230370: contig of 230370 bp in length in 230470: gap of unknown length in 232746: contig of 2276 bp in length. Location/Qualiffers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC097673.5 GI:22855493
HTG, HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Matches:
Conservative:
Mismatches:
Indels:
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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, R.,
Milosavijevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S.,
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Yu, F., Zhang, J., Zhou, J., Yakub, S., Yen, J., Yoon, L.,
Weinstock, G. and Gibbs, R.A.
Milliand, C., Willes, R.,
Direct Submission
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A. Direct Submission

A. Direct Submission
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* CORS: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USB.

Baylor Plaza, Houston, TX 77030, USB.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequence reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Wolsatt: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium.
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Worley, K.C.
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271932
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Score:
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Percent Similarity:
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Best Local Similarity:
Query Match:
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Search completed: April 25, 2006, 20:36:46 Job time : 3098.7 secs

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Run Š

Sequence:

Title: Perfect

Total number

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Abt 07721 Breast ca
Abx76333 Lung canc
Adb80503 Ovarian c
Adn38723 Cancer/an
Aad56198 Human LRR
Abx99349 Human NOV
Aaa27058 Human 1574
Aad56199 Human LRR
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Adv22417 Rat chole
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Abx76332 L
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Acd93536 Human col
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Adul1677 Solid tum
                                                                     April 25, 2006, 10:26:14 ; Search time 295.3 Seconds (without alignments) 203.123 Million cell updates/sec
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Maximum Match 100%
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Adt 66831 HIV-1 env
Ada53303 Human cod
Aah34046 Human col
Ab190312 Human pol
Aak94904 Human ful
                                                                                                                                                                                      Abz39106 N. gonorr
Aac98164 Human col
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ABL15855
ADX62801
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ACL35821
ADC14270
ADC14270
AA159454
ACC83302
ADQ86619
ADQ86619
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ADB63766
ADB63766
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ADT66831
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ABL02796
ADE58711
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AAC98164
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AAK90389
AAK90389
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AAS39945
ADB32906
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AAQ41228
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ABL90312
AAK94904
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ALIGNMENTS

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ADK11793 standard; DNA; 130 BP.
             (first entry)
             06-MAY-2004
        ADK11793
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ds; cytostatic; gene therapy; DXFZp5651133 activity inhibitor; breast cancer; differential expression. Breast cancer differentially expressed gene product #199.

08-JAN-2003; 2003WO-US000657 MO2003057926-A1. sapiens 17-JUL-2003 Ношо

08-JAN-2002; 2002US-0345637P.

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The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKPZp5661133 activity. The methods are useful for treating cancer. e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention.
                                                                                                                                                                                                      Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for inhibition of DKFZp5661133 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; 30 G; 29 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                Claim 30; SEQ ID NO 199; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-9 (1-9) x ADK11793 (1-130)
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(BREN/) BRENTANI R R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson AJG, Neto ED,
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                                                                                                                                              WPI; 2003-577534/54
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; ss.
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                                                                                          Hansen
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30-MAR-2001; 2001WO-US008631

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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (1) at low stringency, preparing aligned-stranded cDNA by reverse transcribing mRNA with (1), amplifying contacting, preparing contacting, preparing contacting, preparing contacting, preparing contacting steps with different primers and sequencing resulting mucleotide sequence of an organism corresponds to an uncleotide sequence of an organism mRNA is obtained from mammalian contact of an open reading frame, for preparing a contig, ancleotide sequence of an organism mRNA is obtained from mammalian corremance of an organism mRNA is obtained from mammalian correct nucleotide sequence of an organism mRNA is obtained from mammalian correct or buman cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of large or small populations. further, it can be used to study living systems to determine if, e.g. there have been genetic shifts which render an individual or populations more or less likely to be afflicted with concernate and so forth. The method can also be used in the study of whether the conditions are likely to be passed to offsepring through over or sperm. The analyses for pathological conditions can be cruiced out in all animals, plants, birds, fish, etc. Using this method is the pathogens which integrate into the genome, such as cruiced on the finegrating viruses such as influence and also be studied in this way. Similarly, the method permits denomes determination of the pathogens which integrate into the determination of the pathogens which integrate into the method of salminates sequencing of non
low stringency for preparing single-stranded cDNA from mRNA of individual.
                                                                                        Example 9; Page 302; 959pp; English
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G; 62 T; 0 U; 0 Other; Sequence 299 BP; 75 A; 84 C; 78

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Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #22978.
          Length:
Matches:
Conservative:
Mismatches:
                                                     Indels:
                                                                                                                                141 Gerchaccecacarraggerrrrecre 167
                                                               Gaps:
                                                                                                         GlyLeuProHisIleArgValPheLeu 9
                                                                                     US-10-774-176-9 (1-9) x ACD93536 (1-299)
                                                                                                                                                                          AAS87174 standard; cDNA; 453 BP.
       2.03
48.00
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                                                                                                                                                                                                                     (first entry)
                                         Best Local Similarity:
                               Percent Similarity:
                                                                                                                                                                                                                                                                                                 Homo sapiens.
Alignment Scores:
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                                                     Query Match:
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WO200175067-A2

11-OCT-2001.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations the properties are possible for genetic disorders or other traits to assess biodiversity and processing the processing of the processing of the processing the processing of the processin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic, gene therapy, expression profile, solid tumour, peripheral blood mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 453 BP; 108 A; 111 C; 113 G; 121 T; 0 U; 0 Other;
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                                                                                                                                                                                                                   Tang YT;
                                                                            31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
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Best Local Similarity:
                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                  P-PSDB; ABG22987
                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity.
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Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.

Breast cancer-associated gene sequence 29.

14-NOV-2002

ABT07721;

ABT07721 standard; DNA; 927 BP.

RESULT 5 ABT07721

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The invention describes a method comprising comparing an expression profile of at least one gene, where the instance expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood mononclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where coth the first and second classes is a subcluster formed by an each of the first and second classes is a subcluster formed by an unsupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, and classed medium including data that represent an expression profile of at second class of patients has a second clinical cutcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at least another storage medium including data that represent an expression profile of the gene. (ii) a peripheral blood sample of a patient who has a solid tumour prognam capable of comparing the expression profile of the gene. (iii) a program capable of comparing the expression profile of executing the expression profile of a second class of patients who have conducted and or protein array componitions of patients who have the gene in peripheral blood expression profile, and (iv) a processor capable of executing the comparising concentrated probes for solid tumour prognosis genes where capted of a second class of patients has a solid tumour, and where the first class of patients has a second class of patients has a second class of patients has a second class of patients as conducting outcome, and the second class of patients has a second class of patients of the invention. Note: The sequence expresents a solid tumour prognosis gene of the invention. Note: The sequence expresents a solid tumour prognosis of the invention, but was obtained nor each o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trepicchio WL, Burczynski ME, Twine NC, Slonim DK; Dorner AJ;
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                                                                                                                                                                                                                                                                                                          29-APR-2003; 2003US-0466067P.
23-JAN-2004; 2004US-0538246P.
                                                                                                                                                                                                     29-APR-2004; 2004WO-US013587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-804779/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMHP ) WYETH.
(STRA/) STRAHS A.
WO2004097052-A2
                                                                                               11-NOV-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strahs A,
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(EOSB-) ROS BIOTECHNOLOGY INC.

Mack DH, Gish KC, Afar D;

WPI; 2002-583738/62. N-PSDB; ABJ05564.

02-PEB-2001; 2001US-0265928P. 09-APR-2001; 2001US-00829472. 09-APR-2001; 2001US-02869BP. 04-MAY-2001; 2001US-0294443P.

24-JAN-2002; 2002WO-US002242.

24-JAN-2001;

WO200259377-A2.

01-AUG-2002.

Unidentified.

Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polymucleotide that selectively hybridizes with breast

Claim 9; Page 372; 414pp; English.

sample with a polynuc cancer nucleic acids.

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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer calls. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07761 cepresent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Length:
Matches:
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Mismatches:
Indels:

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Percent Similarity: Best Local Similarity:

Query Match:

gnment Scores:

Gaps:

126 GGTCTACCCCACATTAGGGTTTTCCTG 152

GlyLeuProHisileArgValPheLeu 9

8

US-10-774-176-9 (1-9) x ADU11677 (1-475)

Gaps:

100.08

505 GGTCTACCCCACATTAGGGTTTTCCTG 531

BP

ADB80503 standard; DNA; 927

GlyLeuProHisIleArgValPheLeu

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US-10-774-176-9 (1-9) x ABX76333 (1-927)
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in creased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, non-small cell corrector to other benign or precancerous lesions, e.g. atlectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, chypersensitivity pneumonitis, intersitial pulmonary fibrosis, asthma and for changes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancervous lesion; bronchitis; chronic obstructive pulmonary disease, hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                                                                                                                                                               Lung cancer-associated polynucleotide #197.
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                                                  ABX76333 standard; DNA; 927 BP.
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; 2001US-0339245P.
; 2001US-0350666P.
; 2001US-0334370P.
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                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                        WO200286443-A2.
                                                                                                                                                                                                                                                                                                                 Unidentified
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09-NOV-2001;
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(EOSB-) ROS BIOTECHNOLOGY INC

18-JUN-2001; 2001US-0299234P. 27-AUG-2001; 2001US-0315287P. 05-SEP-2001; 2001US-031544P. 13-NOV-2001; 2001US-035066EP. 12-APR-2002; 2002US-0372246P.

18-JUN-2002; 2002WO-US019297

cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.

Location/Qualifiers

Homo sapiens

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/\*tag=

WO2002102235-A2

27-DEC-2002

1. .927

Key

Ovarian cancer-associated transcript #34

(first entry)

04-DEC-2003

ADB80503;

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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polymucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
determining tumour prognosis, early detection of pre-cancerous lesions,
and as vaccines. This sequence corresponds to one of the mucleic acids
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                                                                                              WPI; 2003-167431/16.
Mack DH, Gish KC;
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Matches: Conservative: Mismatches:

7.59 48.00 100.0%

Best Local Similarity:

Percent Similarity:

Alignment Scores:

Pred. No.:

Length:

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other diseases such as angiogenic or fibrotic disorders, and to methods
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                                                                                                                                                                                                                              Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
inflammatory disease, autoimmune disease,
                                                                                                                                                                                                                                                           retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                           Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41
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Wilson KE, Zlotnik A;
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                                                              x ADB80503 (1-927)
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DH, Murray R, Watson SR,
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                                                                                                                                               ADN38723 standard; cDNA; 927
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2002US-0347211P.
2002US-0347349P.
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P-PSDB; ADN38724.
         Percent Similarity:
Best Local Similarity:
Query Match:
                                                               US-10-774-176-9 (1-9)
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08-JAN-2002;
10-JAN-2002;
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08-FEB-2002;
13-FEB-2002;
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29-MAR-2002;
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or

Claim 8; SEQ ID NO 41; 1385pp; English

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of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal necvascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                     Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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15-PEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human LRRCAPS related DNA #5.
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polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; cardiant, haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVY; NOV; fertility; metabolic disorder; dlabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                                                                                                                              Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Matches:
Conservative:
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2001US-0274322P.
2001US-0274849P.
2001US-0275238P.
2001US-0275578P.
2001US-027567P.
2001US-0275601P.
2001US-0275601P.
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2001US-0278152P.
2001US-0278894P.
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2001US-0277239P.
2001US-0277321P.
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Best Local Similarity:
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12-MAR-2001;
13-MAR-2001;
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13-MAR-2001;
14-MAR-2001;
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23-MAR-2001;
26-MAR-2001;
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DB:
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voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE;
Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE;
                                                                                                                                                                                                                                                                                                                                           18-OCT-2001; 2001US-0330300P.
31-OCT-2001; 2001US-033501P.
14-NOV-2001; 2001US-0332172P.
14-NOV-2001; 2001US-0332771P.
14-NOV-2001; 2001US-0332184P.
14-NOV-2001; 2001US-0333184P.
         200105-0279344P
200105-0279344P
200105-0279935P
200105-0280802P
200105-0280802P
200105-0280802P
200105-0280900P
200105-0280900P
                                                                                                           2001US-0287424P.
2001US-028806FP.
2001US-0288328P.
2001US-0291190P.
2001US-0291099P.
2001US-029140P.
2001US-0294485P.
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2001US-0309198P.
2001US-0312903P.
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2001US-0337185P.
2002US-0345705P.
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2001US-0318770P.
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2001US-0325681P
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03-DEC-2001; 2001US-0337426P
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P-PSDB; ABP70071.
27-MAR-2001; 2
27-MAR-2001; 2
28-MAR-2001; 2
30-MAR-2001; 2
02-APR-2001; 2
                                                                                                             30-APR-2001; 202-MAY-2001; 203-MAY-2001; 203-MAY-2001; 216-MAY-2001; 216-MAY-2001; 231-MAY-2001; 231-MAY-2001; 231-MAY-2001; 231-MAY-2001; 231-MAY-2001; 219-JUN-2001; 219-JUN-2001; 219-JUN-2001; 2
                                                                                                                                                                                                                                                           10-JUL-2001;
31-JUL-2001;
16-AUG-2001;
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27-SEP-2001;
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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99555 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a andicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, cardiovascular

Claim 16; Page 114-115; 619pp; English.

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disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

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1156
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       Length:
Matches:
Conservative:
Mismatches:
                                        Indels:
       9.82
48.00
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Alignment Scores:
                                     Query Match:
DB:
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US-10-774-176-9 (1-9) x ABV99349 (1-1156)

1 GlyLeuProHisileArgValPheLeu 9 ઠ

AAA27058 standard; DNA; 1263 BP AAA27058 RESULT

AAA27058

(first entry) 22-AUG-2000 Human 5T4 tumour-associated antigen gene.

Human, TAA, tumour-associated antigen, anti-tumour; cytostatic; immunostimulant, vaccine, carcinoma; colorectal cancer; gastric cancer;

Homo sapiens.

WO200029428-A2.

25-MAY-2000

99WO-GB003859 18-NOV-1999; 98GB-00025303. 99GB-00001739. 99GB-00017995. 18-NOV-1998; 27-JAN-1999; 30-JUL-1999 (OXFO-) OXFORD BIOMEDICA UK LTD

Myers KA; Carroll MW,

WPI; 2000-387735/33.

Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors. Example 2; Page 78; 79pp; English.

The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune

60

Length: Matches: Conservative:

11.6 48.00 100.0%

Percent Similarity:

Alignment Scores:

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capriclous related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; p53 pathway; Leucine rich repeat capricious related protein;
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response, preferably CTL or an antibody response in a subject
                                Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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9
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Matches:
Conservative:
Mismatches:
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                    AAD56199 standard; DNA; 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human LRRCAPS related DNA #6.
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                                                                               10.9
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Best Local Similarity:
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                                                               Alignment Scores:
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Conservative: Mismatches: Indels:

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Query Match: DB:

ADJ56299;

RESULT 13

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Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
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                                                                                                                                                        917 GGTCTACCCCACATTAGGGTTTTCCTG 943
                                                                                                                                    1 GlyLeuProHisIleArgValPheLeu
                                                                                              US-10-774-176-9 (1-9) x ADJ56299 (1-2020)
                                                                                                                                                                                                                                                   ACC51052 standard; cDNA; 2053 BP
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666P.
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 Percent Similarity:
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                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a proto-oncogene that is amplified in neuroblastoma cells and is common in small cells activated by the present invention describes these common in small cell lung cancers. The present invention describes these colls molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for acreening assays by identifying molecules or compounds that specifically bind the CDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the print of present from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in MYCN activated cells SegID 105
                                                                                                                                                                                                                                                                                                                                                                                 human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
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Matches:
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                                                                           US-10-774-176-9 (1-9) x AAD56199 (1-1331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STUA) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                          06-MAY-2004
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Pred. No.:
Score:
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cancer.

ADUS 299

ADUS 2

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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 corockethe human bladder cancer-associated proteins given in ABR4814 to ABR48342). Bladder cancer-associated proteins given in ABR4814 to have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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Conservative:
Mismatches:
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                                                                                                                                                                                  Claim 6; Page 296; 307pp; English
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AAD56197
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                                                                                                                                                                                                                                                                                                                                                                                                                        Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; attinflammatory; attiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer-associated polynucleotide #196.
Indels:
                                                                                                                                           931 GGTCTACCCCACATTAGGGTTTTCCTG 957
                    Gaps:
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                                                                                                             GlyLeuProHisIleArgValPheLeu
                                                                 US-10-774-176-9 (1-9) x ACC51052 (1-2053)
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                                                                                                                                                                                                                                               ABX76332 standard; DNA; 2053 BP
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09-NOV-2001, 2001US-0339245P.
13-NOV-2001, 2001US-0339345P.
29-NOV-2001, 2001US-0334370P.
12-APR-2002, 2002US-0372246P.
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P-PSDB; ABU56603.
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Query Match:
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invention

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-bissed activity, where a difference between the test agent-bissed activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; tetinal neovascularistation syndrome; scarring; uterine fibroid; detection; disgnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39

(first entry)

17-JUN-2004

ADN38721;

ADN38721 standard; cDNA; 2053 BP

differential expression; cancer; angiogenic disorder;

Human;

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-blased activity, where a difference between the test agent-blased activity, where a difference between the test agent and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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 Indels:
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                    Gaps:
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                                                                                 1 GlyLeuProHisIleArgValPheLeu 9
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Query Match:
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2001US-0335394P. 2001US-0340376P. 2002US-0347211P. 2002US-0347349P. 2002US-0355250P. 2002US-0355714P.

08-JAN-2002; 10-JAN-2002;

08-FEB-2002; 2 13-FEB-2002; 2 20-FEB-2002; 2

29-MAR-2002; 2002US-0368809P. 04-APR-2002; 2002US-0370110P. 12-APR-2002; 2002US-0372246P. 05-JUN-2002; 2002US-0386614P.

2002US-0396839P 2002US-0397775P 2002US-0397845P 2002US-0409450P

2001US-0350666P. 2001US-0332464P. 2001US-0334393P.

21-NOV-2001; 29-NOV-2001;

13-NOV-2002; 2002WO-US036810

WO2003042661-A2.

22-MAY-2003.

Homo sapiens.

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating antibodies and methods are useful for diagnosing, prognosing and treating cencer and other conditions such as psoriasis, ischaemia, heart disease, Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample. The invention relates to nucleic acids and proteins (ADN38683-ADN40064) Claim 8; SEQ ID NO 39; 1385pp; English P-PSDB; ADN38722 

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Length: Matches: Conservative: Mismatches: Indels:

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Percent Similarity: Best Local Similarity:

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Query Match: DB:

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931 GGTCTACCCCACATTAGGGTTTTCCTG 957

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GlyLeuProHisIleArgValPheLeu 9

US-10-774-176-9 (1-9) x AAD56200 (1-2053)

Gish KC, Glynne R, Hevezi PA; Wilson KB, Zlotník A;

Aziz N, Ginsburg WM, Murray R, Watson SR,

Mack DH, ď

Afar

WPI; 2003-468649/44.

(EOSB-) ROS BIOTECHNOLOGY INC

09-SEP-2002;

Seguence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for reparange are composition for reparanges or treating tumours and cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of human tumour-associated
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith V;
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                                                                               Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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21-AUG-2002; 2002US-0405645P.
23-ESP-2002; 2002US-0413192P.
15-OCT-2002; 2002US-0419008P.
15-NOV-2002; 2002US-0426847P.
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Spencer SD, Wu TD, Zhang Z;
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                                                                                                                                                           Percent Similarity:
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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating speciasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in
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                                                                                                                                                                                                                                                                                            ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
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P-PSDB; ADN03962.
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                                                                                                                                                                      RESULT 20
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overexpression; cancer;

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WO2004030615-A2
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                                                                                                                 Homo sapiens.
                                                                                                                                                                         15-APR-2004.
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ID ADV3
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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the disgnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                         ds; breast cancer, prognosis; gene expression; diagnosis.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   marker used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      931 Gereraceceaearrageerrrreere 957
                                                                                                                             Breast cancer prognosis marker #1305.
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                                     ADR25444 standard; DNA; 2053 BP.
                                                                                                                                                                                                                                                                                                                                   (ROSE-) ROSETTA INPHARMATICS LLC
(NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                         15-JAN-2003; 2003US-00342887.
                                                                                                                                                                                                                                                                            15-JAN-2004; 2004WO-US001100.
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                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-593473/57.
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                                                                                                                                                                                       Homo sapiens
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DB:
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related mucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and nucleic acids,
Tumour dagnosis, call proliferative disorder; breast cancer; colorectal cancer; colorectal cancer; ovarian cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; ovarian cancer; pancreatic cancer; certical acacer; melanoma; leukaemia, hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tumor-associated antigenic target polypeptides and nucleic aci
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for including schizophrenia, bipolar affective disorder (BAD) and autism, as including schizophrenia, bipolar affective disorder (BAD) and autism, as well as Parkinson's and Alzheimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, nootropic, antimanic and antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polymucleotide is a human cDNA sequence of a gene that is differentially expressed in the presence of a therapeutic compound and represents an exemplary efficacy gene for bipolar affective disorder,
                                                                                                                                                                                                                                                                              human; ss; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzhaimer's disease; neuroleptic; nootropic; antimanic; antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
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                                                                                                                                                                                           Human cDNA of an exemplary efficacy gene for BAD SegID174.
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Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PSYC-) PSYCHIATRIC GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2002; 2002US-0349936P. 04-MAR-2002; 2002US-0361834P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-0325150P.
14-NOV-2001; 2001US-0333047P.
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                                                                                             (first entry)
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ADV35098
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2053 9 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 19.2 48.00 100.0% 100.0% Best Local Similarity: Percent Similarity:

gnment Scores:

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1 GlyLeuProHisIleArgValPheLeu 9
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US-10-774-176-9 (1-9) x ADV35098 (1-2053)

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treat disease states involving (II). (II) is activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The colypeptide and polymoraleotide sequences have applications in capponic, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Ascetly-Assessed traperseent novel human diagnostic coding sequences and the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #22979.
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931 GGTCTACCCCACATTAGGGTTTTCCTG 957
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                                                                                                AAS87175 standard; cDNA; 2338 BP
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23-AUG-2000; 2000US-00649167
                                                                                                                                                                           13-FEB-2002 (first entry)
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Pred. No.:
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                                                                                                                                      AAS87175;
                                                           RESULT 24
                                                                                AAS87175
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AAK94253;

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polymucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
                                                                                                                                                                     human, medicine; signal transduction; glycoprotein; transcription; oligo-capping method; 88; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S,
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki
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                                                                                                                                     Full length human cDNA clone SegID 2864.
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                      ADL30831 standard; cDNA; 2359 BP,
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-0018865.
07-JUL-2000; 2000RP-00114089.
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                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                 20-MAY-2004
                                                          ADL30831;
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DB:
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  ADL30831
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BXBXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful length clones were obtained by construction of full length enriched CDNA libraries that were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length CDNA easily without any special methods. The present sequence is a full length Muman cDNA of the invention. Note: The sequence date for this parent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                             Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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                                    Human full-length cDNA, SEQ ID NO: 2864.
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US-10-774-176-9 (1-9) x AAS87175 (1-2338)
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                                                                                                                                                       AAK94253 standard; cDNA; 2359
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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P-PSDB; AAM93333.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Kawai Y; T, Koga H;

2359 0 0 0 0

Human full-length cDNA, SEQ ID NO: 2866.

(first entry)

06-NOV-2001

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RESULT 26

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Score:

Homo sapiens.

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated been determined. Sequences of 5' and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length cDNA are useful libraries that were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                               830 Primers useful for synthesizing full length cDNA clones and their use
in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE; immunogen; STATE activation; allergy; inflammation; autoimmunogen; STATE; activation; allergy; inflammation; cancer; autoimmuno disease; diabetes; hyperlipidaemia; infection; cancer; autoimmuno disease; theumatoid arthritis; osteoarthritis; systemic lupus erythematosus; aepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
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                                                                                                                                                                                                                                                                                                      Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
su A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding protein that promotes STAT6 activation #64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8, SEQ ID NO 2866, 1380pp + Sequence Listing, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                Human, full length cDNA; cDNA synthesis; oligo-capping; ss.
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Mismatches:
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                                                                                                                                                                                             08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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P-PSDB; AAM93334.
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                                                     Homo sapiens.
                                                                                      BP1130094-A2
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein for its splitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression a activity of the compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening composition. Compositions antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allowing a disease associated with STAT6 activation such as allowing a disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthitis, osteoarthitis, systemic lupus extythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activation or inhibition of STAT6. The present sequence represents a compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for the protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                       Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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27-DEC-2002; 2002US-04364G7P.
15-MAY-2003; 2003JP-0017505.
16-MAY-2003; 2003US-0470836P.
                                                                                                                                           05-JUN-2003; 2003WO-JP007123
                                                                                                                                                                                                        2002US-0385912P
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P-PSDB; ADI26163.
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                                                           WO2003104277-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                            ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                   New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
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                                                          human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                            Kawai Y;
T, Koga I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster protein coding sequence, SEQ ID 186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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K, Kojima S, Otsuki
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                           Ota T, Nishikawa T, Isogai T,
Wakamatsu A, Sugiyama T, Nagai
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                                                                                                                                                                                                                        (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                    oligo-capping method; ss; gene.
                                                                                                                                                                                11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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                  (first entry)
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Best Local Similarity:
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                                                                                        Homo sapiens
                                                                                                           BP1396543-A2
                                                                                                                                                                      08-JUL-1999;
                   20-MAY-2004
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ADL30833
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The present invention relates to a method for identifying a compound that inhibits the activity of a protein essential for Drosophila viability. The method comprises: (a) expressing in a recombinant host a DNA sequence encoding a protein essential for Drosophila viability; (b) testing compounds suspected of having the ability to inhibit the activity of the protein expressed in (a); and identifying a compound tested in (b) that inhibits the activity of the protein. The method is useful in identifying a compound that inhibits the activity of a protein essential for Drosophila viability for use as insecticidal, ectoparasiticidal, antiparasitic, antihelminhic or acaracidal agent. The present sequence is the DNA sequence for one such protein essential for Drosophila viability. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a compound that inhibits the activity of a protein for Drosophila viability for use e.g., as insecticidal agent by expressing in a recombinant host a DNA molecule to produce a protein essential for Drosophila viability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from WIPO at ftp.wipo.int/pub/published pct sequences.
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Drosophila melanogaster
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Best Local Similarity:
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WPI; 2001-656860/75
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                                               interactions.
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Pred. No.:
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                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 13249.
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                                                                                                                                                                                                   Claim 1, SEQ ID NO 13252, 21pp + Sequence Listing, English.
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11-JUL-2000; 2000US-00614150.
           23-MAR-2001, 2001WO-US009231.
                                   23-MAR-2000, 2000US-0191637P.
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                                                                                                 Venter JC, Adams M,
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                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABI16176-ABI30511), expressed DNA sequence (ABI16175) and the encoded proteins (ABBS20737-ABB212072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 4357 BP; 1274 A; 932 C; 855 G; 1296 T; 0 U; 0 Other;
                                                                                      Claim 1; SEQ ID NO 13249; 21pp + Sequence Listing; English
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ACN80343 standard; DNA; 787 BP.
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Best Local Similarity:
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invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent mucleic acid markers associated with breast cancer. Note: The Sequence listing does not form part of the specification but may be obtained in electronic format from the USPFO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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/note= "given in the specification but does
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/product= "5T4 antigen"
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The present sequence encodes the canine 574 tumour-associated antigen carcinomas but has a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the human or murine 574 gene sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
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P-PSDB; AAY94351.
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Best Local Similarity:
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                           misc feature
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30-JUL-1999;
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07-OCT-2002

ABK87175;

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Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Feline ST4 antigen protein"
Mismatches:
Indels:
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                                                                               US-10-774-176-9 (1-9) x ABK87175 (1-1260)
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1. .1260
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                                                                                                                   LeuProHisIleArgValPheLeu
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                                                                                                                                                                                                                                            ADB97513 standard; DNA; 1260 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, particularly cancer
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87.5%
85.4%
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                                                                                                                                                                                                                                                                                                                                                                   Feline 5T4 antigen DNA
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P-PSDB; ADB97520.
Best Local Similarity:
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                    Query Match:
DB:
                                                                                                                                                                                                      RESULT 36
                                                                                                                                                                                                                                                                 concocetal lencine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific conseasurement and localisation of 574 in extracts of plasma, urine, tissues, and in call culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of canine and feline
                                                                                                                                                                                                                                                                                                                         Feline; cat; oncofoetal leucine-rich glycoprotein; 57%; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunobherapy; foetal call; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                    cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "5T4 protein"
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                                       2 LeuProHisIleArgValPheLeu 9
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U8-10-774-176-9 (1-9) x AAA27060 (1-901)
                                                                                                                                                              ABK87175 standard; cDNA; 1260 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ayers K, Drury N, Carroll M;
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P-PSDB; AAU98694.
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16-MAY-2002

Pelis sp

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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope of the 5T4 antigen. The invention further provides a polypelitope string of the 5T4 epitope; a nucleic acid comprising the 5T4 epitope string of the 5T4 epitope and the 5T4 epitope and the 5T4 epitope nucleic acid to a cell, a cell pulsed with the 5T4 epitope uncleic acid to a cell, a cell pulsed with the ST4 epitope, a polypelitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease of a pecifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope or its encoding nucleic acid; a method comprising detecting the 5T4 epitope in conjunction with an WHC class specifically recognising the 5T4 epitope in conjunction with an WHC class comprising the 5T4 epitope has cytostatic acid; in the vaccine system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for disquesting the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone cromating a disease. This polymucleotide sequence represents the felline correspondenting a disease. This polymucleotide sequence represents the felline
New major histocompatibility complex class I peptide epitopes from human
5T4 tumor-associated antigen, useful for preventing and/or treating a
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Length: Matches: Conservative:

280 41.00 100.0%

Percent Similarity:

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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
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                                                Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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/product= "Feline 5T4 antigen protein"
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5T4 antigen coding DNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding feline 5T4 protein.
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                                                                                                Alignment Scores:
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a disease medicament, for affecting a disease in vivo, for preparing a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system diseases including Parkinson's disease, periodontal diseases, candiopulmonary diseases, cardiopulmosarular diseases, gastrointestinal diseorders, infections, diabetes, Helicobacter related diseases, and other immune disorders. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibody, ScPv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodoncal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
                                  4000
                                  Conservative:
Mismatches:
Indels:
 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of canine 5T4 protein.
                                                                                                                                                                              847 CIGCCCACGICAGGGICTICCTG 870
                                                                                                                         x ADB97452 (1-1260)
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15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
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                                                                                                                                                                                                                                                                 AAF89736 standard; DNA; 1263
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                                                      Best Local Similarity:
                                                                                                                         US-10-774-176-9 (1-9)
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                                  Percent Similarity:
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                                                                    Query Match:
DB:
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The present invention relates to the isolation of canine and feline oncofectal leucine-rich glycoproteins known as 574, and the polynuclectide sequences encoding them. The 574 proteins are expressed in useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in these animals. The sequences of the invention may also be used in disgnostic kits for rapid, reliable, sensitive, and specific tissues, and in cell culture media. Antibodies specific for the 574 in extracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
encodes a 5T4 protein, which is used to produce ScPv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                           Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                          Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
Conservative:
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P-PSDB; AAU98693.
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Best Local Similarity:
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                                                           Alignment Scores:
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AD034435_4

AD034435_4

Continuation (5 of 7) of AD034435 from base 400001 (Human SLIT-3 genomic sequence.)

WP Fragment Name Begin End 110000

WP AD034435_1 10001 110000

WP AD034435_2 200001 310000

WP AD034435_3 300001 410000

WP AD034435_4 600001 510000

WP AD034435_5 600001 610000

WP AD034435_6 600001 634886
                                                                                                                                                                                                                                                                                                                           om base 300001 (Human SLIT-3 genomic sequence. )
LOCUS ADO34435 Accession Ado34435
            isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es) The present sequence encodes canine 574 protein
protein are useful for isolating foetal cells from maternal blood. The
                                                                               Seguence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Pred.

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nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (i) a transformed cell having a nucleic acid comprising an IMPD nucleic acid dinked to a promoter and a 3' non- translated sequence that caid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for the detection of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the continuous continuous cattle gene expression, or the continuous cattle and cattle gene expression, or the cattle for genetically marrowing acttle. The present sequence is one of the continuous cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine; s8; BST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (expressed sequence tag) nucleic acids. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine EST associated with lactation/muscle/fat deposition #2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 416 BP; 110 A; 60 C; 75 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segdata.uspto.gov/seguence.html?DocID=20020137139
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3442 TTGCCTCACATCCGTATCTTCTC 3465
                                                                                                                                                                                                                   ABX36840 standard; cDNA; 416 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0115707P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bovine LMFD EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002137139-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                      20-FBB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Byatt JC,
                                                                                                                                                                                                                                                                                                      ABX36840;
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(TAON/)
                                                                                                                                    RESULT 42
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Alignment Scores:

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lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are appearing as ABX34836-ABX49347, or complements of them. Also included are 1, (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid cidnotions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and of plyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is practicity of the complementary nucleic acid is practicity of the molecule or pattern of the molecule in a bovine cell or tissue.

The useful for genome mapping, gene identification and analysis, cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and muscle and fat identification and analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                             Bovine BST associated with lactation/muscle/fat deposition #14862.
416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid associated with lactation, and muscl
deposition, useful for genome mapping, gene identific
cattle breeding, or for genetically improving cattle.
Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tao N, Warren WC;
                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 14862; 245pp; English
                                                                                                                                                                                        287 GGCTTACCTCACATTTTTGTGTTTCTC 313
                                                                                             Gaps:
                                                                                                                                                                  1 GlyLeuProHisIleArgValPheLeu
                                                                                                                               US-10-774-176-9 (1-9) x ABX36840 (1-416)
                                                                                                                                                                                                                                                                                 ABX49697 standard; cDNA; 433 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                 40.00
88.9%
88.9%
83.3%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-110599/10.
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                               Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                           21-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Byatt JC,
                                                                                                                                                                                                                                                                                                                        ABX49697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAON/)
(WARR/)
                                                                                                                                                                                                                                            RESULT 43
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the call to express the proteins N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
breeding, preparation of constructs for use in cattle gene expression, of for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon cancer antigen; diagnosis; detection;
                                                                                                                        Sequence 433 BP; 121 A; 75 C; 77 G; 159 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen encoding cDNA SEQ ID NO:3568.
                                                                                                                                                                        433
0 1 0 0
                                                                                    seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                  167 GGCTTACCTCACATTTTTTGTGTTTCTC 193
                                                                                                                                                                                                                                                                                                                              GlyLeuProHisileArgValPheLeu 9
                                                                                                                                                                                                                                                                                            US-10-774-176-9 (1-9) x ABX49697 (1-433)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birse CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH36486 standard; cDNA; 465 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0157137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-2000; 2000WO-US026524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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40.00
88.9$
88.9$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colorectal carcinoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-235357/24.
P-PSDB; AAG77081.
                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999;
03-NOV-1999;
                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH36486;
                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human,
                                                                                                                                                                             ..
9
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ID AAH3
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
 8888888
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The invention relates to an isolated polynuclectide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridiation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones LW;
                                                                                Sequence 465 BP; 96 A; 149 C; 147 G; 68 T; 0 U; 5 Other;
                                                                                                                                  465
11
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                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                354 GGCTACCCCATTTGAGGGTCCTGCTT 328
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                                                                                                                                                                                                                                                                                   GlyLeuProHisIleArgValPheLeu
                                                                                                                                                                                                                                                   US-10-774-176-9 (1-9) x AAH36486 (1-465)
                                                                                                                                                                                                                                                                                                                                                                                   ACH45478 standard; cDNA; 467 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human foetal brain cDNA #6203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-2001; 2001US-00918995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2003 (first entry)
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LABAT I.
STACHE-CRAIN B.
DICKSON M C.
JONES L W.
                                time of publication, me
to 1052, 7921 and 7922
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                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                    Alignment Scores:
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(STAC/)
(DICK/)
(JONE/)
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DB:
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                                                                                                                                                                                                                                                                                                                                                    RESULT 45
ACH45478/
                                                                                                                                                     Score:
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is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/RST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, probe, 88, gene expression, single exon probe, microarray,
alternative splicing event, genomic alteration.
                                                                                                          Sequence 467 BP; 100 A; 139 C; 147 G; 69 T; 0 U; 12 Other;
                                                                                                                                                             467
                                                                                                                                                                                                              400
                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome derived single exon probe #7785.
                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                           426 GGGCTACCCCATTTGAGGGTCCTGCTT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; SEQ ID NO 7785; 80pp; English.
                                                                                                                                                                                                                                                 Gaps:
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                                                                                                                                                                                                                                                                                                                      1 GlyLeuProHisIleArgValPheLeu
                                                                                                                                                                                                                                                                                    US-10-774-176-9 (1-9) x ACH45478 (1-467)
                                                                                                                                                                                                                                                                                                                                                                                                                             ACH74590 standard; DNA; 515 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Rank DR, Hanzel DK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-2002; 2002US-00029386.
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40.00
88.9%
77.8%
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACH74590;
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                                                                                                                                                                             Score:
888888
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contiguous animo, and of the above mentioned amino acid acquences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above.

methods of selling and/or licensing single exon probes or microarrays to methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records cach record including data on the expression of a single exon probe cited above. The probe med apparatus are useful in gene expression analysis. The probes mad apparatus are useful in gene expression or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising calterations in the genomic locus that includes their exon, in assessing alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human called and form part of the printed specification, but was obtained in electronic format directly from USPFOC at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; carcinogen; pharmacodyanamic marker; gene; 88.
cited above, an ORF-encoded peptide comprising at least 8
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 515 BP; 93 A; 164 C; 137 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        segdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
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2000US-0207454P.
2000US-0211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV58745 standard; cDNA; 565
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88.9%
77.8%
83.3%
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pharmacogenomic marker;
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Best Local Similarity:
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25-MAY-2000;
09-JUN-2000;
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Claim 1; Page 10920-10921; 11750pp; English.

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Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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Claim 1, Page 11270-11271, 11750pp, English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker

###X#X000000000000X**&** 

Sequence 565 BP; 164 A; 146 C; 115 G; 137 T; 0 U; 3 Other;

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565
0
0
0
0
      Length:
Matches:
Conservative:
Mismatches:
Indels:
       175
40.00
87.5%
87.5%
83.3%
                              Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                   Query Match:
DB:
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US-10-774-176-9 (1-9) x ABV58745 (1-565)

297 GGTTTGCCTCATTTCAGAGTGTTT 320 œ 1 GlyLeuProHisIleArgValPhe 8 È

ABV56637 standard; cDNA; 615 BP ABV56637; 

Human prostate expression marker cDNA 56628

(first entry)

17-SEP-2002

Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker; pharmacogenomic marker, gene; ss.

sapiens. Homo W0200160860-A2.

23-AUG-2001

20-FEB-2001; 2001WO-US005171

2000US-0189862P. 2000US-0207454P. 2000US-0211314P. 18-JUL-2000; 2000US-0219007P. 13-DEC-2000; 2000US-0255281P. 2000US-0183319P 25-MAY-2000; 09-JUN-2000; 17-PBB-2000; 16-MAR-2000;

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABW00010-ABW62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cell carcinogenic potential of a compound; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242 to AAG81453. The secreted proteins can be used for directing the secretion of proteins of interest from a host cell including bacteria, fungal cells, and cultured higher eukaryotic cells. The present invention also describes fusion proteins, where a secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide for directing secretion of proteins of interest from a host cell including, e.g. bacteria, includes contiguous amino acid residues of polypeptide with specified amino acids.
                                                                                                                                                                                                                                            ; (1) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, secreted protein; secretion; bacterial cell; fungal cell; eukaryotic cell; fusion protein; maltose binding protein; immunoglobulin constant region; polyhistidine tag; ss.
                                                                                                                                                                                                                                                                                 Sequence 615 BP; 164 A; 155 C; 127 G; 166 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human AFP protein encoding cDNA sequence SEQ ID NO:115.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTTGCCTCATTTCAGAGTGTTT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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87.5
87.5
83.3
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P-PSDB; AAG81299.
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Best Local Similarity:
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) comprising the above expression vector comprising the above comprising the above or nucleotide sequences; (b) an amino acid sequence encoded by any of the above comprising: (a) an amino acid sequence encoded by the full-ength coding region of the above mucleotide sequences; or (c) a sequence comprising the above polypeptide; (b) an anilo acid sequences; or (c) a sequence comprising the above polypeptide fused to a heterologous polypeptide; (c) an isolated antibody; (d) an isolated antibody; (d) a unisolated indigospetide that binds to the above polypeptide; (f) a process (c) the above polypeptide; (d) an isolated antigenic target (TAT)
is operably linked via a peptide bond or peptide linker to a second protein selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag and a peptide given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour-associated antigenic target (TAT) cDNA sequence #3919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                        Sequence 933 BP; 163 A; 311 C; 302 G; 156 T; 0 U; 1 Other;
                                                                                                                                             933
7 1
10
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                        529 GGCTACCCCATTTGAGGGTCCTGCTT 503
                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                     1 GlyLeuProHisIleArgValPheLeu 9
                                                                                                                                                                                                                                                                      US-10-774-176-9 (1-9) x AAH52150 (1-933)
                                                                                                                                                                                                                                                                                                                                                                                                                ADQ87043 standard; cDNA; 1333 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-2004 (first entry)
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40.00
88.9%
77.8%
83.3%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-534300/51.
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                                                                                                                          Alignment Scores:
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                                                        in AAG81453
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DB:
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   និដ្ឋប្លិប្តិប្រ
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composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell that above protein; (13) a method of the real above protein; (13) a method of the rapect of the above protein; (14) a method of the rapect of a protein in a sample suspected of containing the presence of a protein in a sample suspected of containing the protein; (16) a method for treating or preventing a cell proliferative calsorier associated with increased expression or activity of the above corrected of containing the protein; (16) a method for treating or preventing a cell proliferative calsorier, and (17) a method for binding an antibody, oligopeptide or protein; and (17) a method of binding an antibody, oligopeptide or or granic molecule to a cell that expresses the protein described above. (17) a method of binding an antibody, oligopeptide of protein; and (17) a method of binding an antibody, oligopeptide of protein; and (17) a method of binding an antibody, oligopeptide of protein; and (17) a method of binding an antibody, oligopeptide of protein; and (17) a method of binding an antibody, oligopeptide or creating or treating cancer. The composition is also used for preparing a mediannel for the above processed with an antibody of an ediagnosing, and an ediagnosing or treating cancer. The composition is also used for preparing an amount of a medicament for the pragent and method or diagnosing of an ediagnosing or preventing or treating cancer. The composition is also used for preparing and an antibody are useful forter diagnosing and an endiagnosing and proliferative disorder or cancer. The present sequence represents a organic molecule that binds to the above polypeptide; (10) a human TAT cDNA sequence from the present invention. binding cell \$

Sequence 1333 BP; 238 A; 397 C; 413 G; 285 T; 0 U; 0 Other;

Matches: Conservative: Mismatches: Indels: Length: 40.00 88.9% 77.8% 83.3% Similarity: Percent Similarity: Alignment Scores: Query Match: Local Best

US-10-774-176-9 (1-9) x ADQ87043 (1-1333)

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Search completed: April 25, 2006, 12:38:19 Job time : 327.3 secs

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Scoring table:

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ACO95699 Rattus no
BV595106 S215F6146
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ACO03062 Mouse Chr
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ACO2999 Homo sapi
ACI23238 Rattus no
ACI33570 Rattus no
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AC006357 Homo sapi
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AC103547 Rattus no
AC006491 Drosophil
AK003690 Drosophil
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BX537258 Mouse DNA
AC149113 Papio anu
AL713960 Mouse DNA
                                  CQ782724 Sequence
AK074786 Homo sapi
BD127283 Primer fo
CQ782726 Sequence
AK961916 Sequence
AK961916 Sequence
AK974790 Homo sapi
AL02137161 Homo sapi
AL121977 Human DNA
AB168308 Macaca fa
ACO55731 Homo sapi
BK855617 Zebrafish
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AC084504 Caenorhab
Continuation (23 o
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BD127282 E
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AC123620 Mus muscu AC128828 Bos tauru AL121871 Human DNA AF079317 Sphingomo AC008659 Homo sapi AC134039 Rattus no AC14495 Rattus no AC44955 Rattus no BX005368 Zebrafish AC090506 Homo sapi AC090506 Homo sapi AC188436 Didelphis	AC119741 Homo sapi AC054648 Homo sapi AC135468 Homo sapi AC135963 Human DNA AC113518 Mus muscu AC163791 Bos tauru AC163791 Bos tauru AC163791 Bos tauru AC119570 Papio anu AC119570 Papio anu AC119570 Papio anu AC119570 Papio anu AC119570 Papio anu AC11968 Homo sapi AC11967 Pan trogil 299108 Bacillus su AC146074 Pan trogil AC15608 Bos tauru AC15608 Bos tauru AC156090 Bos tauru AC156090 Bos tauru AC156090 Bos tauru AC156090 Bos tauru AC156090 Bos tauru AC156090 Bos tauru AC15618 Bos tauru AC15610 Homo sapi AC15610 Homo sapi AC15610 Homo sapi AC15610 Homo sapi AC15610 Homo sapi AC15611 Bos tauru AC15618 Bos tauru AC15618 Pos tauru AC15619 Pos tauru AC15618 Pos tauru AC15618 Pos tauru AC15618 Pos tauru AC15619 Bos tauru AC15619 Bos tauru AC15619 Bos tauru AC15619 Bos tauru AC15619 Bos tauru AC15619 Bos tauru AC161907 Ratus no AC164144 Bos tauru AC16253 Zebrafish AC16253 Zebrafish AC162316 Mus muscu AC16316 Ratus no AC162316 Mus muscu AC162316 Mus muscu AC162316 Mus muscu AC162316 Pos tauru AC162316 Pos tauru AC162316 Pos tauru AC162316 Pos tauru AC162316 Pos tauru AC162395 Mouse DNA AC162396 Homo sapi	Ratt
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2 263827 14 AC094579 AC094579 I 2 264628 14 AC121690 AC121690 I 2 265393 14 CR974457 CR974457 I	2 266802 14 AC118507 AC11820 AC1182	2 281574 14 AC022604 2 283507 14 AC152628 2 283507 14 AC152628 2 287358 14 AC152581 2 287328 14 AC152394 2 289368 14 AC152394 2 2895107 14 AC152440 2 29550 14 AC157896 2 29550 14 AC107896 2 29550 14 AC107896 2 301337 15 AR017082	2 316900 1 TAC1913 AC445065 IN AC45065 IN AC45065 IN AC79158 AC709158 AC709159 AC709158 AC709	ALIGNMENTS  2116 from Patent W02004097052.  1 GI:56210857 ens (human) ens (hum
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COMMENT

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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                       Carroll, M.W. and Myers, K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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PE Corporation (NY) (US)
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Sequence 1 from Patent EP1160323.
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CQ731678
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                       MILES WILLIAM CARROLL, KEVIN ALAN MYERS
C12N15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065,
C07K19/00,
C12N15/00
                                                                             9901739.4 PR
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Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
                                                                                                                                                                           Location/Qualifiers
1. .1263
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Location/Qualifiers
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OXFORD BIOMEDICA LTD
OS Homo sapiens (human)
PN JP 2002530060-A/1
PD 17-SEP-2002
PF 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9917995.4
PI MILES WILLIAM CARROLL, KEVIN ALAN WYERS
PC C12N15/09, A61K39/00, A61K48/00, A61P35/00, C07
PC C12N15/00
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PC C12N15/00
PC C12N15/00
PC C12N15/00
PC Polypeptide
PH Key
PT source Location/Qualifiers
PT /organism='Homo sapiens (human)
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RESULT 4

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אביביבום 2359 bp DNA linear PAT 18-SEP-2002
Primer for synthesizing full-length cDNA and use thereof.
BD127282
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JP 2002017375-A/2713
22-JAN-2002
07-JUL-2000 JP 2000253172
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Primer for synthesizing full-length cDNA and use thereof FH Key
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function="Anchorage of the protein to the cell membrane"
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Homo sapiens (human)
Homo sapiens sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae, Homo.

1 (bases 1 to 2359)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,

Ota,T., Nishikawa,T., Isogai,K., Kojima,S., Otsuki,T. and

Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                             1 GlyLeuProHis1leArgValPheLeu 9
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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BD127282
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/codon_start=1
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LEINSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                               PRI 18-APR-2005
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Direct Submission

Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer Location/Qualifiers

1. 2053

1. 2053

Anol_type="other RNA"

Ab_ref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2053)

Wyers K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.
Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue type="placenta"
clone_lib="lambda gt11 library of J. Milan"
                                                                                                                                                                                                                               H85T4OA 2053 bp RNA linear Homo sapiens 5T4 gene for 5T4 oncofoetal antigen. Z29083
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/product="transmembrane peptide"
/standard name="transmembrane region"
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product="Leucine rich repeat region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="LRR N-terminal flank"
                                                                                                        229083.1 GI:435654
5T4 gene; 5T4 oncofoetal antigen.
Homo sapiens (human)
Homo sapiens
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                                                                              GlyLeuProHisIleArgValPheLeu
                            US-10-774-176-9 (1-9) x CQ731678 (1-2053)
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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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JP 2002017375-A/2714
2-JAN-2002
3-JAN-2000
JP 2000253172
OSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases I to 2161)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="NT2"
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/clone lib="NT2RP2"
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mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
SHINICHI KOJIMA,
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Patent: JP 2002017375-A 2714 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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JP 2002017375-A/2714.
      Unpublished
2 (bases 1 to 2359)
180gai,T. and Otsuki,T.
Direct Submission
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Homo sapiens
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein id="Capes958.1"
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APSGSNASVSAPSPLVELILNHIVPPEDBRQNRSFEGMVVAALLAGRALQGLRRLELA
                                               PAT 17-MAR-2004
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TLAELQGLPHIRVFLDNNPWVCDCHMADMYTHLKETBVVQGKDRLTCAYPEKMRNYL
LELNSADLDCDPILPPSLQTSYVPLGIVLALIGAIFLLVLYLNYANRKGIKK"
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                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                               Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Mismatches:
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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note="unnamed protein product"
                                    2359 bp DN Sequence 2864 from Patent BP1396543. CQ782724
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Matches:
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                                                                                                                                                         Homo sapiens (human)
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Best Local Similarity:
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CQ782724
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PAT 18-SEP-2002

PAT 14-JAN-2004

linear

DNA

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugahara, T., Matsuda, A., Honda, G., Muramatsu, S. and Ishizawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stat6 activation gene
Patent: WO 03104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
                                                                                                                                                                              Sequence 127 from Patent WO03104277. AX961916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .2361
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426. .1688
                      /proteIn_id="CAF06467.1"
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PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2866 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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'note="unnamed protein product"
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CQ782726
                                                                       (426). .(1685)
Location/Qualifiers
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    .2361
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AUTHORS
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VERSION
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CQ782726
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APFLASAVSARAPTLARVRNLTFYPTDLARVRNLFLTGNO
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LAVLPAGAFARRPPLABLAALNLSGSRLDEWRAGAFEHLFSLRQLDLSHNPLADLSPF
AFSGSNASYSARSFYTVELILAHIVPPEDERQNRSFEGAVVAALLAGARALQGJRRLBLA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLBSLHLBDNALKVLHNG
TLEBLGGLPHRYFLDNNPWYCDCHADMYTWLKETEVVQGKORLTCAYPBKRRNYL
LELNSADLDCDPILPPSLQTSYYFLGIVLALIGAIFLYVLYLNRKGIKKWMINIRDAC
RDHMGGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK074790 2361 bp mRNA linear PRI 09-JUL-2005 Homo sapiens cDNA FLJ90309 fis, clone NT2RP2000903, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Yamamoto,J., Wakamatsu,A., Kimura,K., Sakamoto,K., Hatano,N.,
Kawai,Y., Ishii,S., Saito,K., Kojima,S., Sugiyama,T., Ono,T.,
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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Gaps:
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Gaps:

US-10-774-176-9 (1-9) x CQ782726 (1-2361)

ORIGIN

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1. .2379
/gene="TPBG"
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Strausberg, R.
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COMMENT
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                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba, 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5- & 3-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317
IMAGE:4138906), complete cds.
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1 (bases 1 to 2379)
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Colling, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Nagai, K., Sugano, S. and Isogai, T. Signal Sequence and Keyword Trap in silico for Selection of Full-Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped CDNA Libraries
DNA Res. 12, 117-126 (2005)
                                                                                                                                                   Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
                                                                                                                                                                                                                                                                                                                         J. (bases 1 to 2361)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mismatches:
Indels:
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/clone_lib="NT2R92"
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Matches:
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BC037161.2 GI:33872201
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Hopking, R. B., Jordan, H., Money, F., Mang, J., Mang, J.,
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Brank, M. Harcy Perparation Rubin Laboratory
Contect interpretoring the Markeley, R. M., Sendinger, M., Sendinger, S. M., Sendinger, M., Markeley, R. M., Sendinger, M., Markeley, R. M., Sendinger, M., Sendinger, M., Sendinger, M., Sendinger, M
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
Clone 15, 2000 this sequence version replaced gi:11558491.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNFEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
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HSJ492P14

HUMAN BEQUENCE FIRM CLONE RP3-492P14 on chromosome 6q13-15

CONTAINS a single stranded DNA binding protein pseudogene, the TPBG

gene for trophoblast glycoprotein (574-AG) and a CpG island,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Mismatches:
Indels:
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Matches:
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HTG; CpG island; TPBG.
Homo sapiens (human)
codon start=1
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3517. .4690
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Direct Submission
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Best Local Similarity:
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Pred. No.:
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HSJ492P14
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AFSGSNASVSAPSPLVELILINHIVPPEDBRQNRSFEGAVVAALLAGRALGGLRRLELA
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TLAELQGLPHTRYFLDNNPWVCDCTHAADWYTHLKETEVVGGTGRTCAYPERGRRRYL
LEINSADLDCDPILPPSLQTSYVPLGIVLALIGAIFLLUVYTURKGIKKWHNIRDAC
RDHMRGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nswulziby 5551 bp DNA linear PRI 15-APR-2005
Homo sapiens 574 oncofetal trophoblast glycoprotein gene.
AJ012159
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Submitted (13-0CT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King, K.W., Sheppard, P.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 574 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ012159.1 GI:3805946
5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Homo sapiens (human)
Homo sapiens
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Mismatches:
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Corganisms-Home sapiens'

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2704. 2709

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3431. .4693
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Q9P038 Q9Y4T7"
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LAVLPAGAPARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPP
AFSGSNASVSAPSPLVELILMHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
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TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKRTEVVQGKDRLICAYPEKMRNRVL
http://www.sanger.ac.uk/HGP/Chr6
RP3-492P14 is from the library RPCI-3 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VBCTOR: pCYPAC2
                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="trophoblast glycoprotein"
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AL544610 AW471072 AW662338 BE26089 BP316484 BI196133 BI562387 BW069633 BW670613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP1-93K22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="InterPro:IPR003591"
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109639. .116836
                                                                                                          Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Clone_right_end: RP1-93
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                                                                                                                                                                             Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="RP3-492P14"
clone_lib="RPCI-3"
                                                                                                                                                                                                     Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome="6"
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Infectious Diseases, Division of Genetic Recources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan (Email:khashigahih.go.jp, UKL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3.585-1111(ex.2120), Fax:81-3-5285-1181)

The International consortium for macaque cDNA sequencing and analysis consists of: Department of Virology and Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan; Division of Genetic Resources, National Health Research Institute, Taipei, Taiwan; Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan; Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA; Center for Information Biology, National Institute of Genetics of Japan, Mishima, Japan. Clone distribution: clone distribution information can be found at: http://www.nih.go.jp/yoken/genebank/
LBINSADIDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYBINADPRLTNLSSNSDV"
116817. .116822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB168308 2714 bp mRNA linear PRI 18-JUN-2005 Macaca fascicularis testis cDNA clone: QtsA-11109, similar to human trophoblast glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JUNA sequencing and analysis.

DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca fascicularis
Wakaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osada,N., Hirata,M., Tanuma,R., Kusuda,J., Hida,M., Suzuki,Y., Sugano,S., Gojobori,T., Shen,J.C.-K., Wu,C.I. and Hashimoto,K. Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey CDNAs.
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Draili (CACTGTGTG)
Draili (CACCATGTG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
                                                                                                                                    /locus_tag="RP3-492P14.1-001"
                                                                                                                                                                                                                                                /locus_tag="RP3-492P14.1-001"
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Hashimoto, K., Kusuda, J. and Sugano, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111816 GGICTACCCCACATTAGGGTTTTCCTG 111842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-774-176-9 (1-9) x HSJ492P14 (1-121909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuProHisileArgValPheLeu 9
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
Description: 1st strand cDNA was primed with an oligo (dT) primer [ATGTGGCCTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments 41.5kb.The Sfil and size selection was performed to exclude fragments 41.5kb.The Sfil adgested PCR product was cloned into distinct Draili sites of pME188-Fil). XhoI sites just outside the Draili sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Libraries were made from QCCB: cerebellum cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACO55731 152537 bp DNA linear PRI 03-APR-2002
Homo sapiens 3 BAC RP11-588D3 (ROSWell Park Cancer Institute Human
BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                             Custom primers were used for 5' and 3'-end sequencing. The full-insert sequencing was done by primer-walking method using ABI DNA sequencer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Homo.
1 (bases 1 to 152537)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="macaque cDNA library QtsA"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                               OnpA: parietal lobe right Oths: temporal lobe right OflA: frontal lobe left OmoA: medulla oblongata ObrA: bain stem ObrA: occipital lobe right OtaA: testis
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Macaca fascicularis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /proteIn_id="BAB00432.1"
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                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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Homo sapiens
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47.00
100.0%
88.9%
97.9%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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DB:
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VERSION
KEYWORDS
SOURCE
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AC055731
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Anspronge, S. I., Amazatunge, H.C., Agel, K., Banks, I., Banket, C., Briega, M., Brown, B., Brown, M., Brown, P., Bouck, J., Burch, P., Carter, C., Carron, T.F., Carter, M., Cavazos, S. R., Darch, I., Chavez, D., Chen, G., Chen, R., Coyle, M.D., Dathorne, S. R., Davila, M. L., Davis, C., Coyle, M.D., Dathorne, S. R., Davila, M. L., Davis, C., Coyle, M.D., Dathorne, S. R., Davila, M. L., Davis, C., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Bedards, C.C., Bacato, D., Raggis, D., Raggis, D., Edwards, C.C., Edbai, P., Banks, C., Racker, D., Racker, D., Raggis, D., Raggis, D., Radgis, M., Ford, J. Foster, P., Farntz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Harris, C., Harris, K., Harris, C., Harris, R., Hart, M., Havlak, P., Hawes, A., Ha, M., Harris, C., Harris, R., Hodgson, A., Hogues, M., Koll, R., Gorrell, J. H., Guevara, W., Ganks, P., Hawes, A., Handland, S., Karlsson, E., Kalsson, E., Kalsson, E., Kalsson, E., Kalsson, E., Kalsson, E., Kalsson, E., Lichtarge, O., Lide, C., Lidt, J., Liu, J., Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
Submitted (18-Apr.2000) Human Genome Sequencing Center, Department
Submitted (18-Apr.2000) Human Geneme Sequencing Center, Department
Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 152537)
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Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Feb 27, 2001 this sequence version replaced gi:12965217. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 152537)
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

ANNOTATION OF FEATURES:

AUTHORS

Features listing.

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the BST and cDNA sequences. Genes demonstrate at least two exons flanked by consenues splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Exports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT-----

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ntig		152536
ď	in estimate:	223
Average er	(BCM-Phrap estim	õ
e G	lues less	1722
6	nsensus changin	174
Number of	N's in consensus :	0
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29923	3	(6) 6
30031	~	ttactgggtc(t)cttcacaaat
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30083	E	B
30087	gnaaaatttt (a) aaaannancn	ggtaaaattt (t) aaaatgaacc
30092	attttaaaaa (n) nancngnnna	9
30093	ttttaaaaan (n) ancngnnnaa	attttaaaat (g) aaccagctga
30095	Ē	<b>B</b>
30097	3	<u>છ</u>
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30108	3	<u></u>
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30133	gaanannntt (t) tttttaattn	gtaagagcat (a) tttttaattt

	30143	tttttaatt (1	(n) aaannnnag	Ħ
	30147	ttaattnaaa (1	(n) nnnnagnnag	taat
	30149	aattnaaann (1	(n) nnagnnagna	(B)
	30150	attnaaannn (1	(n) nagnnagnaa (n) agnnagnaan	atttaaaata (t) cagogaggaa tttaaaatat (c) agogaggaa
	30154		(n) nagnaantnn	0
	30155	aannnnnagn (1	(n) agnaantnnt (n) aantnntnen	aaatatcagc(g)aggaaattat tatcagggag(g)aaattattog
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	30163 30164	gnnagnaant (1	(n) ntncnannnn (n) tncnannng	gcgaggaaat (t) attccacaga cgaggaatt (a) ttccacaga
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	30172	tnntncnann (r	(n) ngtcccttca	
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	30234	nneeneenn (1	(n) tetttaget (n) tetttageta	
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	52918			£ 3
	59316	tttctctttt (r	(n) totttggtaa	£ (4
	92155	ageteaceat (r		ageteaceat (c) aetggeeatt
	92173			Ŧ
	92180 92226	aaangcaaat (r	(n) aaaaccataa (n) ttaaaaatt	aaatgcaaat (c) aaaaccataa aatgttgttg (a) ttgaaaagtg
	92254	acagatget	aagaggatg	acagatget (g)
Alionment S	Scores:			
No.:		6.8e+03	Length:	152537
Score:	1 2 4 4 4 5 5 5	44.00		
Best Local	nc similarity: Local Similarity:	77.88	Conservative: Mismatches:	-
		91.78 8		000
US-10-774-176	x (6-1) 6-9/	AC055731 (1-19	152537)	
ò	1 GlyLeuPro	GlyLeuProHisIleArgValP	/alPheLeu 9	
Db 57251		GGTATACCCCACCTTAGGGTTTTTCTA	   CTA 57277	
RESULT 20				
LOCUS DEFINITION	BX855617 Zebrafish D	160 DNA sectionce fr	60094 bp DNA from clone DKRYP-	linear VRT 27-APR-2004
1001000	complete sec	ance.		
VERSION	BX855617.8	GI:46559261		
KEYWORDS	HTG. Danio rerio	(zebrafish)		
ORGANISM	Danio rerio	Metazoa: Chord	Craniata.	Vertebrata: Rutelecatomi:
	Actinopterygii; Cypriniformes; C	jii; Neopterygii; T 98; Cyprinidae; Dan	eleostei; io.	
REFERENCE AUTHORS	1 (bases 1 Barker, G.	to 160094)		
TITLE JOURNAL	Direct Subm: Submitted (	Submission ed (27-APR-2004) W	Wellcome Trust Sa	Sanger Institute, Hinxton,

COMMENT

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Birren, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baltwen, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardfyna, S., Grant, G., Hagoe, B., Headrod, A., Horton, L., Howland, J. C., Johnson, R., Mardonald, P., Mardusk, N., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McNemn, P., McGurk, A., McKernan, K., McLaughlin, J., Melfin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 26, 2000 this sequence version replaced gi:6716060. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Mammalia, Butheria, Buarchontoglires, Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: L1788
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g of 10763 bp in length
f 100 bp
g of 12902 bp in length
f 100 bp
g of 16053 bp in length
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of 10002 bp in length
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3100: gap of 100 bp
5910: contig of 2810 bp in length
6010: gap of 100 bp
8871: contig of 2861 bp in length
8971: gap of 100 bp
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of 2048 bp in length
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of 9607 bp in length
                                                 1 (bases 1 to 191959)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 3, clone RP11-247J22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert sizē: 188000; agarose-fp
Insert size: 190759; sum-of-contigs
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                                                                                                     TITLE
JOURNAL
REFERENCE
AUTHORS
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                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                              During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone amen. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm: SEMBL; Sw: SWISSENCY; Tr:, TEREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Length of monoucleonide AT runs and conserved TA repeats. Where this is found the longest good quality representation will be accessed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 3 clone RP11-247J22 map 3, WORKING DRAFT SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Rddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 23, 2004 this sequence version replaced gi:46357718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
DKEYP-123H10 is from a Zebrafish BAC library
VECTOR: pIndigoBAC-5.
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Mismatches:
Indels:
                                                                                                           Center: Wellcome Trust Sanger Institute
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                                                                                                                                                            Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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                                                                                                                                                                                           Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Danio rerio"
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HTG: HTGE PHASE1; HTGS_DRAFT.
HOWD SADIENS (human)
HOWD SADIENS
                                                                                  ---- Genome Center
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DB:
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Bource

FEATURES

. No. :

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION ACCESSION

RESULT 21 AC012217

8

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947 87890: contig of 1694 bp in length 891 87990: gap of 100 bp 991 1207997: contig of 32607 bp in length 1798 1208997: gap of 100 bp 898 156510: contig of 35613 bp in length 1511 1556210: gap of 100 bp 156110: gap of 100 bp 156110: contig of 353349 bp in length 1502020; contig of 35349 bp in length.
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/ Note="assembly_fragment"
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3101. .5910
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|chromosome="3"
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ORIGIN

191959 2 0 0			AC036639 AC03639 AC0
Length: Matches: Conservative: Mismatches: Indels:	(1-191959)	 FTTTTCTA 153358	ACO96699  Rattus norvegicus clone CH230-16735, WORKING DRAFT SEQUENC unordered pieces.  ACO96694  ACO96694  ACO96694  ACO96696 CH330221412  HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.  Rattus norvegicus (Norway rat)  Rattus (Norway ratin (Norway ratin (Norway ratin (Norway ratin)  Rattus (Norway ratin
Scores: 8.64e+03 44.00 milarity: 100.08 Similarity: 77.88 ih: 14	76-9 (1-9) x AC012217 1 GlyLeuProHigileArgV	53332 GGTATACCCCACCTTAGGGTTTTTCTA	ACO96699  Rattus norvegicus clc anordered pieces. ACO96699, 7 GI:305214 ACO96699, 7 GI:305214 Rattus norvegicus (No Ratus). Anyalebechi, V., Aoyag Baldwin, D., Bandarana Baryant, N., Bular, J., Rardena, V., Carter, R. Chacko, J., Chavez, D. Chacko, J., Lava, P., Haaland Bayant, N., Bular, J., Fernandez, B., Honey, P., Haaland Bayant, N., Bulay, C., L., Franandez, B., Howells, S., Goris, C., Kratt, C.L., Franandez, B., Howells, S., Goris, C., Kratt, C.L., Liu, J., Liu, W., Liu, Y. Lorensulbewa, L., Joule, B. Mandun, M., Morris, K., Mandins, S., McLeod, P., Mandhiney, S., McIny, M., Mandestvis, C., Neal, D., Naaokelemeh, O., Okwuc Pacternak, S., Penly, B. Rattus, S., Penly, R. Plopper, F., Poindest, P., Ratily, B., Shvattsbey Sneed, A., Sodergren, B. Steimle, M., Strong, R. Taylor, T., Thomas, N., Valas, R., Vera, V., Wang, Q., Wang, S., War, Williams, G., Wallson, Willson,
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	US-10-774-176-9 Qy 1 GJ	Db 1533	RESULT 22 AC096699 LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ONGANISM AUTHORS AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                 AL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sagetuence version replaced gi:24819505.
The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.chm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working daaft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                 Submitted (23-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Atlas 3.0;
Consensus quality: 211691 bases at least Q40
Consensus quality: 21399 bases at least Q20
Estimated insert size: 21745; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Mederhausern, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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/clone="CH230-167J5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hgsc-hely@bcm.tmc.edu
Contact: project Information
Center project name: GHOC
Center clone name: CH210-16705
Center clone name: CH210-16705
                                                                                                                                                                                                                                                                                                                                       Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                             Unpublished
2 (bases 1 to 246716)
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2005 S215P61468RB5.T0 Clara Pan troglodytes troglodytes STS genomic, sequence tagged site.
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Pan troglodytes troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initial Sequence of the Chimpanzee Genome and Comparison with the
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Mikkelsen,T.S., Hillier,W.L., Eichler,E.E., Zody,M.C. and
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Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
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Matches:
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Mismatches:
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242139. .242238
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/note="wgs_end_extension
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Primer A: No sequence submitted
Primer B: No sequence submitted
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/note="clone_boundary
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44.00
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The sequence of C. elegans cosmid ZC132
                 Unpublished (2001)
3 (bases 1 to 24950)
Waterston, R.
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                                                                 (Gon, Unknown Chimp). Common names: Pan troglodytes verus is the western chimp and Pan troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred scores >= 20, at least 30% of its base calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNQS(30,25) (single strand NQS, the base in question has Phred score >= 30, the surrounding 10 bases in the read have Phred score >= 35), and the read must have at least 200 bp SNQS(30,25) bases. In the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NQS(30,25) standard was applied
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                                                                                                                                                                                                                                                                                                                                                                                                                          exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome
troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps of unknown origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignments (>=95% bases of read A and >=95% bases of read B were
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Genome sequence of the nematode C. elegans: a platform for
investigating biology
Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                              than 100 NQS bases or with SNP rate > 0.01 were discarded.
                                                                                                                                                                                                                                                                                                                                                                        overlapping reads to call NQS bases and SNPs. Alignments two reads) with less
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Caenorhabditis elegans cosmid ZC132, complete sequence.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditia
1 (bases 1 to 24950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pan troglodytes troglodytes"
/mol_type="genomic DNA"
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Location/Qualifiers
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Bradshaw, H. and Devlin, K.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                               Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
Inversity, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
5 (bases 1 to 24950)
Submitted (18-JUL-1997) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-NOV-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-SEP-2004) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-JAN-2005) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-PEB-2005) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
9 (Dases 1 to 24950)
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University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
10 (bases 1 to 24950)
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University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email: submissions@watson.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Genetics, Washington University St. Louis, MO 63110, USA, and Anger Centre, Hinxton Hall Cambridge CB10 IRQ, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
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nore than one m13 subclone.
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For a graphical representation of this clone sequence and its analysis see: http://www.wormbase.org/db/seq/sequence?name=ZC132;class=Sequence

## NEIGHBORING CLONE INFORMATION

The 5' clone is F47D2, 200 bp overlap; the 3' clone is R02D1, 950 bp overlap. Actual start of this clone is at base position 29759 of F47D2; actual end is at 24950 of ZC132.

## NOTES:

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (communication), the chtp://www.ddbj.nig.ac.jp/c-elegans/html/CB INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), silliality to other proteins from Blask x analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kant's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans GenBank submissions are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Mucl. Acids. Res., 25, 955-964).

EAATURES

Bddy, S.R., 1997, Nucl Acids. Res., 25, 955-964).

Location/Qualifiers

1. 24950

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/ mol type="genomic DNA"
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/standard name="2C132.3a"
/note="contains similarity to Staphylococcus epidermidis
Cytochrome d ubiquinol oxidase subunit II-like protein.;
TR:08CPN5; coded for by the following C. elegans cDNAs:
OSTF188A4 1, OSTR188A4 1, Yk783a01.3"
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complement (join.18.7)
complement (join.18.4)
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/standard\_name="ZC132.4"
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/krans

gene

Alignment Scores: 1.67e+03 Length: 24950 Pred. No.: 43.00 Matches: 7 Score: Percent Similarity: 100.0\$ Conservative: 1 Best Local Similarity: 87.5\$ Mismatches: 0 Query Match: 2 Gaps: 0

US-10-774-176-9 (1-9) x AF014939 (1-24950)

Qy 1 GlyLeuProHisIleArgValPhe 8

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 72957)

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

TITLE Homo sapiens, clone RP11-23P8

JOURNAL Unpublished

2 (Dases 1 to 72957)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., AUTHORS

CB 2 (bases 1 to 72957)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Bartien, V., Beda, F., Anderson, S., Baldwin, J., Bartien, V., Batter, G., Caugopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

COMMENT

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f 100 bp

g of 711 bp in length

f 100 bp in length

g of 731 bp in length

g of 731 bp in length

g of 731 bp in length

f 100 bp

g of 734 bp in length

f 100 bp in length

f 100 bp in length

g of 734 bp in length

f 100 bp in length

f 100 bp in length

g of 737 bp in length

f 100 bp in length

g of 738 bp in length

f 100 bp in length

g of 738 bp in length

f 100 bp in length

g of 738 bp in length

f 100 bp in length

g of 739 bp in length

f 100 bp in length

g of 739 bp in length

f 100 bp in length
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g of 722 bp in length
f 100 bp
g of 740 bp in length
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Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Hadford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Marphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Olivar, J., Peterson, K., Plerre, N., Plani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vasillev, H., Vulel, R., Vulel, R
                                                                                                                                                                                                                                                                                                                           Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This record contains 88 individual
* sequencing reads that have not been assembled into
* contiggs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence submissions@genome.wi.mit.edu -------- Project Information Center project name: L4416
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contig of 734 bp in length
gap of 100 bp
contig of 733 bp in length
gap of 100 bp
contig of 734 bp in length
gap of 100 bp
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equences and RT-PCR of 12 day post conception mouse embroyos total
                           A. (bases 1 to 89743)

Ros.B.A. Dr.

Briect Submission

Submitted (06-NOV-1997) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,

67 73019, USA

4 (bases 1 to 89743)

Roe, B.A. Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-FEB-2000) Department Of Chemietry And Biochemietry, The University Of Oklahoma, 620 Parrington Oval Room 208, Norman, 0K 73019, USA
9 (bases 1 to 89743)
Roe, B.A. Dr.
                                                                                                                                                                  Direct Submission
Submitted (16-SEP-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-MAY-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (18-JAN-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-SEP-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
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ON May 3, 1999 this sequence version replaced gi:3845373.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosone="lc"
/clnce="ct-264n1"
/clone_lib="cftbCJ7 mouse BAC library"
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8 (bases 1 to 89743)
Roe, B.A. Dr.
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5 (bases 1 to 89743)
Roe, B.A. Dr.
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6 (bases 1 to 89743)
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7 (bases 1 to 89743)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The genes were identified by comparing with human genomic and cDNA
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 89743)
Galili,N., Baldwin,S., Lund,J., Reeves,R., Gong,W., Chen,F.,
Roe,B.A., Emanuel,B.S., Nayak,S., Mickanin,C., Budarf,M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Region of Mouse Chromosome 16 is Syntenic to the DiGeorge, Velo-Cardio-Facial Syndrome Minimal Critical Region Unpublished
             gap of 100 bp
contig of 730 bp in length
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Chen, F. and Roe, B.A.
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KEYWORDS
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RESULT 28	NOI	ACCESSION AC005816 GI:34787439	KEYWORDS HTG. COURSE Mus musculus (house mouse)		E S		ខ្លួន	TITLE Direct Submission JOURNAL Submitted (14-OCT-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman.		AUTHORS Chen, F., Do, T., Reeves, R.H. and Roe, B.A.	Ħ	OK 73019, USA REPERENCE 4 (bases 1 to 136687)		¥	REFERENCE 5 (bases 1 to 136687) AUTHORS Chen.F. Do.T., Reeves.R.H. and Roe.B.A.			REFERENCE 6 (bases 1 to 136687) AUTHORS Chen, P., Do, T., Reeves, R.H. and Roe, B.A.	TITLE Direct Submission JOURNAL Submitted (6-MAY-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman.	DEFERENCE 7 (hases 1 to 136687)	AUTHORS Chon, P., Do, T., Reeves, R.H. and Roe, B.A. TITLE Direct Submission	Ę	OK 73019, USA 8 (bases 1 to 136687)		JOURNAL Submitted (22-FEB-2000) Department Of Chemistry And Biochemistry, classically Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	OK 73019, USA REFERENCE 9 (bases 1 to 136687)	Chen, F., Do, T., Reeves, R.H. Direct Submission	JOURNAL Submitted (18-JAN-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,	OK 73019, USA REFERENCE 10 (bases 1 to 136687)	AUTHORS Chen, F., Do, T., Reeves, R.H. and Roe, B.A. TITLE Direct Submission	JOURNAL Submitted (17-SEP-2003) Department Of Chemistry And Biochemistry,	i The University Of Oklahoma. 620 Parrington Oval. Room 208. Norman.	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA COMMENT On Sep 17, 2003 this sequence version replaced gi:7019299.
Db 56692 GGGTTACCTCATATTAGATATTTCTTA 56718		e split into 50 fragments ment Name Begin		00001	600001 700001	800001 900001	1000001	1200001	150001	1700001	1900001	2100001 2200001	2300001 2400001	2500001	AR013598 27 2700001 2810000 AR013598_28 2800001 2910000 AR013598 29 2900001 3010000	3000001	3200001 3300001	3400001	3600001 3700001 3800001	3900001	4100001	4400001	98 45 4500001 461 98 46 4600001 471	598_47 4700001 481000 598_48 4800001 491000	598 49 4900001 4941439 on 721 of 50) of AE013598 from base 2000001 (AE013598 Xanthomonas oryzae pv.	ument Scores:	7.84e+03 Length: 43.00 Matches:	ilarity: 88.9% Similarity: 77.8%	<pre>/ Match: 89.6% Indels: 1 Gaps:</pre>	US-10-774-176-9 (1-9) x AE013598 20 (1-110000)	_ _ 1 GlvLeuProHiBIleArgValPhe		

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Atter, N., Antonells, A., Ayele, K., Becketrom-Sternberg, S.W.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, B.,
Larto, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q. L., Maduro, V. B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Raddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K.D., Wiggins, L., Young, A. and Green, B.D.
Inpublished
Unpublished
C. (bases 1 to 153264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153264 bp DNA linear HTG 27-NOV-2002
Bos tarrus clone RP42-427020, WORKING DRAFT SEQUENCE, 3 ordered
AC135216
                                                                                                                                                                                                                                                                                                                                    1. .147412
Corganism="Mus musculus"
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/clone="rp23-374912"
/clone="rp23-374912"
Submitted (08-JAN-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
7 (bases 1 to 147412)
Song, L., Jiang, X. and Roe, B.A.
Song, L., Jiang, X. and Roe, B.A.
Submitted (13-FRB-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.

    (bases 1 to 153264)

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Submitted (09-0CT-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (Dases I to 153-264)
                                                                                                                                                                  Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116229 GGGTTACCTCATATTAGATATTTCTTA 116203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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HTG; HTGS PHASB2; HTGS_DRAFT.
BOS taurus (cow)
BOS taurus
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.06e+04
                                                                                                                                                                                                                                                                          Center code: UOKNOR
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88.94
88.94
89.64
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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
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AC135216/c
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Mus musculus strain C57BL/6J chromosome 16 clone rp23-374p12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-AUG-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 5 (Dases 1 to 147412) Song.L., Jiang.K. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Song, L., Jiang, X. and Roe, B.A.

Direct Submission

Direct Submission

Direct Submission

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

3 (Dases 1 to 147412)

Song, L., Jiang, X. and Roe, B.A.

Direct Submission

Submitted (25-JUL-2002) Department Of Chemistry And Biochemistry, OK 73019, USA

Submitted (25-JUL-2002) Department Of Chemistry And Biochemistry, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-NOV-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
Center: Department Of Chemistry And Biochemistry The University Of Oklahoma Center code:UOKNOR
                                                                                                                                                                                                             /map="16"
/clone="ct7-326b16"
/clone_lib="CitbCJ7 mouse BAC library"
                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Song,L., Jiang,X. and Roe,B.A.
Mus musculus BAC Clone rp23-374p12
Unpublished
                                                                                                          1. .136687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyLeuProHisIleArgValPheLeu 9
                                                                                                                                                                                           db_xref="taxon:10090"
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4 (bases 1 to 147412)
Song, L., Jidang, X. and Roe, B.A.
Direct Submission
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6 (bases 1 to 147412)
8 Song, L., Jiang, X. and Roe, B.A.
Direct Submission
                                                                                     Location/Qualifiers
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AC079831.24 GI:24961478
HTG.
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43.00
88.9%
88.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
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AC079831/c
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Alignment Scores:
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AC022876
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 69854 contig of 69854 bp in length 69854 contig of 89890 bp in length 69855 108944: contig of 89890 bp in length 108945 159044; gap of unknown length 108945 159264; contig of 44220 bp in length 108045 153264; contig of 44220 bp in length.
                    Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 27, 2002 this sequence version replaced gi:23622199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclomes, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblise, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                Center: NIH Intramural Sequencing Center
                                                                                                                                                       Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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1. 69854
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/estimated length=unknown
69955. .108944
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108945. .109044
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                                                                                                                                                                                                                                                Center clone name: 427020
                                                                                                                                                                                                                           Center project name: djz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector side:left" 69855. .69954
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vector_side:right"
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S (Dases I to 189546)

S Birren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouchgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Boyle, M., Fenestor, J., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McMeneters, R., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McMena, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theedore, J., Tirrell, A., Vassiliev, H., Viel, R., Wu, X., Wyman, D., Ye, W.J., Limer, A. and Zody, M.

Limmer, A. and Zody, M.

Li Submitted (16-FEB-2000) Whitehead Institute/MIT Center for Genome Submission

Mar J., 2000 this sequence version replaced gi:6922086.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC022876 158546 bp DNA linear HTG 01-MAR-2000 Homo sapiens chromosome 11 clone RP11-398P9 map 11, WORKING DRAFT SEQUENCE, 44 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13, M7815; 100% of reads Sequencing vector: M13, M77815; 100% of reads Absembly program: Phrap; version 0.960731 Consensus quality: 136264 bases at least Q40 Consensus quality: 146380 bases at least Q30 Consensus quality: 160509 bases at least Q20 Insert size: 170000; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence submissions@genome.wi.mit.edu ------- Project Information Center project name: L6209 Center clone name: 398_P_9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 158546)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-398P9
                               Length:
Matches:
Conservative:
Mismatches:
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Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                       Indels:
                                                                                                                                                                                                      Gaps:
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 158546)
1.11e+04
43.00
88.98
88.98
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                                                                                              Percent Similarity:
Best Local Similarity:
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3: gap of 100 bp
2: contig of 3779 bp in length
3: gap of 100 bp
3: contig of 6538 bp in length
5: contig of 6746 bp in length
6: contig of 6746 bp in length
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                                                  NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                     Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                 1137: contig of 1137 bp in length 1237: gap of 100 bp 2432: gap of 100 bp 3470: contig of 1038 bp in length 3570: gap of 100 bp 516: gap of 100 bp 6469: contig of 1153 bp in length 5316: gap of 100 bp 6469: contig of 1153 bp in length 6589: gap of 100 bp 7759: contig of 1190 bp in length 7859: gap of 100 bp
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GHARSKNWRLSVRCGGWPLRMLMENGFLPDPPRIRYRKKKRILKSQNNSSVDPCMRNL
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BVLERQMCPEBQLKCEFLLLKVYCCSESSFFAKIPYYYYIRBACQGLKBPMLDKIKK
RLNEHGYPQVEGFVQDMRLIFQNHRASYKYKDFGQMGFRLEABFEKNFKEVFAIQETN
                                                                                                                                                                                                                                                                                                                                                   Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is RP11-98F19; the clone sequenced to the right is RP11-395A23. Actual start of this clone is at base position 1 of RP11-69J7; actual end is at base position 174699 of RP11-69J7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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This gene was based on gi(21361373)
Continued from H_NH0098F19.2"
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      NOTICE:
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3 (Dases 1 to 174699)
Waterston, R. H.
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Submitted (29-OCT-2002) Department of Genetics, Washington
University, 4444 Porest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 174699)
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Submitted (15-ARR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MMO 63108, USA
On Nov 28, 2000 this sequence version replaced gi:10337664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 15-APR-2005
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Park Avenue, St. Louis, Missouri 63108, USA
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACUU9949 174699 bp DNA linear PRI 15.
Homo saplens BAC clone RP11-69J7 from 2, complete sequence.
AC009949
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Center code: WUGSC
   158546
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Abbott,A., McLellan,M. and Haub,K.
The sequence of Homo sapiens BAC clone RP11-69J7
Unpublished (2001)
2 (bases 1 to 174699)
Waterston,R.H.
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Contact: submissions@watson.wustl.edu
                                     Matches:
Conservative:
Mismatches:
Indels:
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Submitted (09-MAY-2001)
University, 4444 Forest
5 (bases 1 to 174699)
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Waterston, R.
1.15e+04
43.00
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                                                                   Percent Similarity:
Best Local Similarity:
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Web site: http://www.hgsc.bcm.tmc.edu/
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***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                  KADGQLVSSEKKANMUKDLSKIRGRRRGKPGTHFTQSDRAPQKRVRSRASRKHKDET
POPQAPLLPYUGGYVGOLIHTBKLEQGTLAKCIQTEDGKWFTPWBFBIKGGYABSKWW
RLSVRCGGWPLRRLABEGSLENPPRIYYRNKKRILKSQNNSSVDPCMRNLDECEVCRD
GGELPCCDTCSRVFHEDCHIPPVESEK"
                                                                                                                                                                                                                                                                                                                                   translation="MDTVDIANNSTLGKPKRKRKKKKKGHGWSRMGTRTQKNNQQNDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manualia; Butheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Glurognath; Muroidea; Muridae; Murinae; Rattus.

1 (Dases 1 to 183066)

Muzny, D. Marie., Metaker, M. Lee., Abramazon, S., Adams, C., Alder, J., Allan, C., Allen, C., Allen, C., Allen, C., Allen, C., Allen, C., Andra, C., Andra, C., Balan, H., Baca, E., Baden, H., Badait, J., Baca, E., Baden, H., Badait, J., Barale, C., Bardan, H., Barale, C., Bardan, H., Barale, C., Bardan, H., Burah, C., Burch, P., Burrell, K., Calderon, R., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'notes"Homo sapiens nuclear antigen Sp100 (SP100), mRNA.;
                                                                                   'translation="MAGGGGDLSTRRINECISPVANEMNHLPAHSHDLQ"
                                                                                                                                                                                     /note="Homo mapiens hypothetical protein BC004921 (LOC93349), mRNA.; H NH069307.2 This gene was based on g1(20149710)" codon_start=1
120203. .120283,123538. .123612,124898. .125002,
127066. .127208,128393. .128440,131736. .131777,
135106. .136422,136643. .136786,137777. .138709)
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gene="SP100"
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Continues as H_NH0395A23.1"
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HTG; HTGS PHASB1; HTGS DRAPT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Matches:
Conservative:
Mismatches:
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"gene="SP100"
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/protein_id="AAX8870.1"
/db_xref="GI:62630124"
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db_xref="GI:62630123"
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'gene="SP100"
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AUTHORS
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AL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23815384.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgs.c.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clavetaland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Duih, H., Divya, K., Draph, R., Dun, A., Bagon, C., Falley, M., Flagg, N., Forbes, L., Fosler, M., Fosler, P., Francer, T., Engan-Rochis, R., Garcia, A., Garner, T., Farser, C. M., Gabrer, M., Garcia, A., Garner, T., Garza, M., Guevera, M., Gunaratue, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harvels, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harvels, P., Haaves, A., Henderson, N., Hernandez, J., Howells, S., Hulyk, S., Hune, J., Idlerid, D., Kovar, C., Vargethy, S., Kelly, S., Kelly, S., Kally, S., Ka
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Direct Submission

Walted (129-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

Direct Submission
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Worley, K.C.
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1 (bases 1 to 184044)
Deschamps, S., Oomen, S. and Roe, B.A.
Direct Submission
Submitted (10-JUL-1999) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 184044)
Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, 67 73019, USA (120 18404), Becat, C. and Roe, B.A. Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A. Direct Submission Submitted (11-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Chilahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OK 73019, USA.

(Dases I to 184044)

Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A.

Direct Submission

Submitted (03-MAY-2000) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Direct Submission
Direct Submission
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                 Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Miroldea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-APR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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9 (bases 1 to 184044)
Deschamps.S., Oomen,S., Draber,R., Becat,C. and Roe,B.A.
Direct Submission
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Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                      1 (bases 1 to 184044)
Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A.
Mus musculus Chromosome 16 PAC Clone rp21-598k13
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                                                                                                                     Mus musculus (house mouse)
                            AC008020 -
AC008020.37 GI:24137494
HTG.
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complete sequence,
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                                                                                                                                                                                                                                                                                                                                                         NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS AC008020 184044 bp DNA linear ROD 19-OCT-2002 DEFINITION Mus musculus strain 129S6/SvEvTac chromosome 16 clone rp21-598k13,
                      Center project Information
Center project name: GTDP
Center clone name: GT20-391M15
Center clone name: CH220-391M15
Assembly program: Phrap, version 0.990329
Consensus quality: 157421 bases at least Q40
Consensus quality: 163069 bases at least Q20
Consensus quality: 163069 bases at least Q20
Bstimated insert size: 157850; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 181686: contig of 181686 bp in length 181086: gap of unknown length 7 183066: contig of 1280 bp in length. Location/Qualifiers
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Matches:
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Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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181687. .181786
/estimated_length=unknown
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/note="clone boundary
clone_end:Sp6
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118887. .120169
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complement(180647...1
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="CH230-391M15"
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151817. 153060
/note="wgg contig"
167645. 170206
/note="wgg contig"
178674. 179842
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20220. .121383
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AC008020
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AC102169/c
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Houb sapiene genomic DNA
Published Only in Database (2000)
2 (bases i to 202607)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Bujiect Submission
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP002353 202607 bp DNA linear PRI 17-JUN-2003
Homo sapiens genomic DNA, chromosome 11 clone:CTD-2651C21, complete
                                                                                    OK 73019, USA
13 (bases 1 to 184044)
Deschamps,S., Comen,S., Draber,R., Becat,C. and Roe,B.A.
Direct Submission
Submitted (25-40G-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                   Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A.
Direct Submission
Direct Submission
Submitted (19-OCT-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
ON Oct 19, 2002 this sequence version replaced gi:22475337.
                                                       Submitted (14-JUL-2002) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="rp21-598kl3"
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Library"
   12 (bases 1 to 184044)
Deschamps, S., Oomen, S., Draber, R., Becat, C. and Roe, B.A.
Direct Submission
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The University Of Oklahoma
Center code: UOKNOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/strain="12986/SvEvTac"
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chromosome="16"
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14 (bases 1 to 184044)
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AP002353/c
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Stren, B., Linton, L., Nusbaum, C., Lander, B., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, S., Camarata, J., Campopiano, J., Chang, J., Chazaro, B.,

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Ferreira, P., FitzHugh, M., Galagan, J., Garad-Plerre, N.,

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Jones C., Kamat, A., Karatas, K., Kalls, C., LaRocque, K.,

Lamazares, R., Macdonald, P., Major, J., Marthe, R., Liu, G.,

Maclean, C., Macdonald, P., Major, J., Marthe, S., Meldrim, J.,

Mencus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,

Saman, S., Severti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Direct Submission.

Direct Submission.
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Mus musculus chromosome 10 clone RP23-455E13 map 10, *** SEQUENCING
IN PROGRESS ***, 12 unordered pieces.
AC102169
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gesc.riken.go.jp, WEL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)

On Jun 16, 2003 this sequence version replaced gi:19263027.

Location/Qualifiers

1. 20260

Anol_type="genomic DNA"

//db_xref="taxon:9606"
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN
Mus musculus (house mouse)
Mus musculus
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Mus musculus chromosome 10, clone RP23-455E13
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="11q"
/clone="CTD-2651C21"
                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="11"
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Mus musculus
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Best Local Similarity:
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8
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
AC166253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgaller, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Carum, B., Dakrellano, K., Diaz, J.S., Dodge, S., Dooley, P., Corum, B., Barkean, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, X., Lui, A., Matthews, C., McCarthy, M. Macdonald, P., Major, J., Manthews, C., McCarthy, M. Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M. Naguyen, C., Nicol, R., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasany, U., Raywond, C., Retta, R., Rae, C., Rogov, P., Rochupka, A., Ramasany, U., Raywond, C., Rojanovic, N., Stebs, M., Taster, B., Stange-Thomann, N., Stojanovic, N., Stubs, M., Tastange-Thomann, N., Stojanovic, N., Stubs, M., Tastange-Thomann, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wam, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Submitted (19-FBB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 19, 2004 this sequence version replaced gi:22004590.

All repeats were identified using RepeatMasker: html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6309 138441: config of 3213 bp in length 8442 138541: gap of 100 bp 8542 143561: config of 5020 bp in length 13562 143561: gap of 100 bp 10562 153565: config of 9905 bp in length 1567 153665: gap of 100 bp 1667 183508: config of 29842 bp in length 1669 183508: gap of 100 bp 1669 183508: gap of 100 bp 1669 204343: config of 20735 bp in length 1609 204343: config of 20735 bp in length 1609 204343: config of 20735 bp in length.
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34490: gap of 100 bp
43838: contig of 9348 bp in length
43938: gap of 100 bp
57302: contig of 13364 bp in length
57402: gap of 100 bp
61947: contig of 4545 bp in length
62047: gap of 100 bp
86421: contig of 24374 bp in length
86521: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence submissions@genome.wi.mit.edu ------- Project Information Center project name: L18160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of 100 bp contig of 10386 bp in length gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 9201 bp in length gap of 100 bm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="10"
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57403
61948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
             AUTHORS
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Muzny, D., Admas, C., Agbai II, O., Allen, C., Alebrooke, S., Archer, P., Arredondo, H., Bandaranaike, D., Bangura, L., Beltran, B., Beltran, R., Beraducci, A., Biswalo, K., Blyth, P., Bonham, H., Buhay, C., Burch, P., Cadoree, I., Canada, A., Cardenas, V., Carter, K., Cavazos, I., Chacko, J., Chahrour, M., Chavez, D., Chen, A., Chen, G., Chen, R., Chen, G., Chen, R., Chen, G., Chan, R., Cheng, M., Can, W., Chen, G., Chen, R., Cheng, M., Chan, G., Chen, R., Chan, W., Chan, G., Chan, R., Chan, W., Davila, M., Davila, M., Davila, M., Davila, M., Davila, M., Davila, M., Dunh, H., Davila, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Dunh, H., Davila, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Durbin, K., Dziuda, D., Bgan, A., Escotto, M., Espinosa, V., Bugene, C., Fa, M., Fernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P., Garcia, R., Garner, T., Gaskin, C., Gench, S., Garcia, R., Garner, T., Gaskin, C., Gench, S., Garcia, R., Haris, R., Havlak, P., Hanllon, K., Harbes, B., Harris, R., Havlak, P., Hawes, A., Hawkins, E., Hadllon, M., Hodges, M., Hollins, B., Havlak, S., Hume, J., Imo, K., Jackson, A., Jackson, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC166253 212065 bp DNA linear HTG 31-JUL-2005
Mus musculus clone RP23-231M6, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 212065)
/clone="RP23-455B13"
/clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACI66253.3 GI:71534302
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163476 GGGGTGCCCCACTTGAGAGTATTTTTA 163450
                                                                                                                                                                                 57303. . 57402

/estimated length=100

61948. .62047

/estimated length=100

86422. .86521

/estimated length=100

95723. .95822

/estimated_length=100
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                                                                                               /estimated_length=100
43839. .43938
                                                                                                                                                           length=100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'estimated_length=100
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                                                                  .34490
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43.00
100.0%
77.8%
                                                                                                                                                              /estimated
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BOS taurus clone CH240-121KS, *** SEQUENCING IN PROGRESS ***, 55 unordered pieces.
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HTG; HTGS_DRAFT; HTGS_ENRICHED.
HTG: HTGS_COW)
Bos taurus
Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pecora; Butheria; Lauraeiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 215042)
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               78772: contig of 2082 bp in length 78772: gap of unknown length 106246: contig of 2074 bp in length 106346: gap of unknown length 108423: contig of 2077 bp in length 108523: gap of unknown length 146522: contig of 37829 bp in length 146852: gap of unknown length 149899: contig of 2537 bp in length 149899: contig of 2537 bp in length 205973: contig of 58884 bp in length 206073: gap of unknown length 206073: gap of unknown length 206073: contig of 5992 bp in length.
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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estimated length=unknown
0839. .30938
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/estimated_length=unknown
146247. .106346
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/estimated_length=unknown
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/estimated_length=unknown
78173. .78<u>7</u>72
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146353. .146452
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148990. .149089
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                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="RP23-231M6"
  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108424. .108523
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/estimated_lenc
45898. .45<u>9</u>97
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100.0%
77.8%
89.6%
                                                                                                                                                                                                                                                                                                                                                                           1. .212065
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146353
146453
148990
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205974
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Best Local Similarity:
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DB:
                                                                                                                                                                                                                                                                                                                                                                           source
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
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     Keye, T., Khan, S., King, L., Koyar, C., Kowis, A., Kowis, C., Lara, F., Leal, S., Lee, K., Lee, K., Lee, S., Legall, F. L., Lemon, S., Lewis, L., Li, La, L., Linnell, M., Liu, W. -S., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuhewa, L., Lozado, R., Luk, T., Madu, R., Mahsehwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, B., McClelland, H., McPherson, J., Mercadao, C., Metzker, M., Mattinez, B., McClelland, H., McPherson, J., Mercadao, C., Metzker, M., Muttay, D., Nazarith, L., Ngo, D., Nguyen, M., Norwig-Eastaugh, B., Norty, A., Navis, D., Parker, D., Pasten, S., Patel, B., Petel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Patel, V., Paul, H., Perez, A., Ruiz, S. J., Sana, M., Sanders, W., Santibanez, D., Rachilin, B., Reigh, R., Ren, Y., Reuter, M., Richarde, S., Saleson, I., Saned, A., Sodergren, B., Song, X.-Z., Sorelle, R., Svatek, A., Taylor, B., Taylor, T., Thomas, N., Thorn, R., Thornton, R., Volkov, A., Meldron, L., Walser, B., Wang, S., Warren, J., Well, X., Wang, S., Warren, J., Well, X., Wang, S., Warren, J., Well, X., Wang, S., Warren, J., Well, S., Yan, K., Yan, Y., Yu, F., Zhang, J., Zhang, L., Zhang, L., Zhang, L., Zhang, L., Zhang, L., Junublishen, Unnublished
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------ Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Consensus quality: 224150 bases at least Q40
Consensus quality: 225195 bases at least Q30
Consensus quality: 227145 bases at least Q30
Consensus quality: 227145 bases at least Q30
Estimated insert size: 225835; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kalafus, K., Kelly, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-JUL-2005) Human Genome Sequencing Center, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 31, 2005 this sequence version replaced gi:71480179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUL-2005) Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 212065)
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COMMENT

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Allen, C., Allen, H., Allenbrooks, S., Amin, M., Angulando, D., Angulabechi, V., Moyegi, A., March, M., Raca, B., Baden, H., Bladaranalke, D., Barbrooks, S., Barnetend, M., Benalmed, F., Bladdan, D., Bandaranalke, D., Barbroe, M., Barnetend, M., Benalmed, F., Blawalo, K., Bladri, J., Blanch, P., Burrell, K., Calderon, B., Cardenay, V., Carer, K., Canteron, B., Cardenay, V., Carer, K., Canteron, B., Cardenay, V., Carer, K., Chan, Z., Chu, J., Claveland, C., Corkerl, R., Can, R., Chen, Z., Chu, J., Claveland, C., Corkerl, R., Can, R., Chen, Z., Chu, J., Claveland, C., Corkerl, R., Carcoll, L., Duyal, E., Barden, H., Bayan, Rocha, S., Dunn, A., Duthin, K., Duval, E., Barden, C., Erger, C., Ergen, C., Rang, C.A., Fallst, T., Fan, R., Perser, C.M., Cablsi, A., Carner, T., Garza, M., Gabrageorgis, B., Gaer, K., Gall, R., Garci, M., Gaerra, W., Garza, M., Gabrageorgis, B., Gaer, K., Gall, R., Gardy, M., Gaerra, W., Garza, M., Gabrageorgis, B., Gaer, K., Halde, S., Halme, S., Halde, M., Handliton, C., Hamilton, K., Hanlen, P., Hades, A., Henderson, M., Hernandez, M., Halles, S., Kally, S., Malle, S., Malled, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Loyan, J., Lewis, L., Markeris, S., Mcleod, M., Morris, K., Martin, R., Marlin, S., Malled, S., Rally, S., Revee, R., Revee, R., Pall, R., Ball, M., Revel, C., Rathus, S., Pall, M., Savert, A., Treigas, S., Malled, S., Schelle, M., Savert, A., Treigas, S., Malled, M., Savert, A., Savert, M., Taright, D., Wang, S., Wall, M., Walle, S., Wall, 
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3 (Dases 1 to 215042)

5 (Cow Genome Sequencing Consortium.

Direct Submission

10 Second Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jun 29, 2005 this sequence version replaced gi:66792995.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Na to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                             Consensus quality: 170996 bases at least Q40 Consensus quality: 192270 bases at least Q30 Consensus quality: 201398 bases at least Q30 Setimated insert size: 240476; sum-of-contigs estimation Bstimated insert size: 103626; agarose-fp estimation Quality coverage: 7x in Q20 bases; agarose-fp estimation Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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16: gap of unknown length
9: contig of 5893 bp in length
9: gap of 50 bp
1: contig of 2104
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f unknown length
g of 1635 bp in length
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of 6571 bp in length
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gap of 1309 bp
contig of 1619 bp in length
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Center code: BCM
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Barnstead, M., Benahmed, F.,

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Biswalo, K., Blair, J., Bilankenburg, K., Blyth, P., Brown, M., Bendamed, F., Blankenburg, K., Blyth, P., Brown, M., Bryant, M., Buhy, C., Burch, P., Burcal, K., Calderon, B., Clarder, W., Carter, K., Caveson, I., Ceasar, H., Carder, J., Chu, J., Carder, J., Chen, Z., Chu, J., Claveland, C., Cocker, G., Carcel, M., Cree, A., D'Souza, L., Claveland, C., Cocker, B., Caroll, M., Cree, A., D'Souza, L., Devalad, C., Cocker, B., Devalad, C., Derson, S., Pinl, W., Dith, R., Dity, R., Dever, K., Gill, R., Carcia, A., Carner, T., Garza, M., Gabrer, C., Ramilton, C., Hamilton, K., Handlen, M., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Harver, S., Hadland, W., Hamil, C., Hamilton, C., Hamilton, K., Harver, S., Hadland, W., Liu, Y., Hand, S., Hane, S., Hadly, S., Kally, S., Manton, M., Malloy, K., Marcia, M., Manton, M., Marcia, S., Marcia, M., Marcia, M
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Submitted (17-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dases 1 to 221701)

18 At Genome Sequencing Consortium.

19 Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

10 Nov 20, 2002 this sequence version replaced gi:22553874.

The sequence in this sesmely is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contygs will be indicated in the feature table.
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HTG3. HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunanalia; Rutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi, Murcidea; Muridae; Murinae, Rattus.
1 (bases 1 to 221701)
Murany, Durania, Marie, Moerker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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AC133573 224138 bp DNA linear ROD 20-NOV-2002
Mus musculus strain C57BL/6J clone rp23-139f17, complete sequence.
AC133573
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/clone_lib="RPCI - 23 Pemale (C57BL/6J) Mouse BAC Library"
                   2. (bases 1 to 222589)
Diriv. Hu.K. and Roe, B.A.
Diriv. Hu.K. and Roe, B.A.
Diriv. Hu.K. and Roe, B.A.
Submitted (28-P2B-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 222589)
Li.Y., Hu.K. and Roe, B.A.
Direct Submission
Submitted (10-OCT-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Li,Y., Hu,X. and Roe,B.A.
Li,Y., Hu,X. and Roe,B.A.
Submission
Submitted (15-077-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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1 (bases 1 to 224138)

Deschamps, S. and Roe, B.A.

Mus musculus BAC Clone rp23-139f17
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On Nov 16, 2002 this sequence version replaced gi:23957635.
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The University of Oklahoma
Center code: UOKNOR
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Deschamps, S., Li, Y., Hu, X. and Roe, B.A.
Direct Submission
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="16"
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                Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Context: hgsc-help@bcm.tmc.edu/
Context: hgsc-help@bcm.tmc.edu

Center project Information
Center project name: CH230-230B11
Center clone name: CH230-230B11
Center clone name: CH230-230B11
Center project name: CH230-230B1
                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Mus musculus strain C57BL/6J chromosome 16 clone rp23-357j7,
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Butheria; Buarchontogilres; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (Dases I to 22589)
Deschamps, S., Li,Y., Hu,X. and Roe,B.A.
Mus musculus rp23-357j7
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2 220531: gap of unknown length
2 221701: contig of 1170 bp in length.
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/note="wgs contig"
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220432. .220531
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/db_xref="taxon:10116"
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AC113264.21 GI:25046401
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(bases 1 to 231951)
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Rumanyotta, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Murcidea; Muridae; Mus.

1 (bases 1 to 231951)
Muzny, D., Adams, C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
Beraducci,A., Biswalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
Cadoree,I., Canada,A., Cardanas,V., Carter,K., Cavazos,I.,
Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G.,
Cheng,M.-T., Chu,J., Cferc,K., Cockrell,R., Coyle,M., Cree,A.,
Curry,S., Dai,W., Davila,M.L., Davis,C., Dany-Carroll,L., De
Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,
Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M.,
Pernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fuh,E., Garcia,R., Garcia,R., Garner,T.,
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Mus musculus clone RP24-216B14, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="rp23-139f17"
/clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
Deschamps, S. and Roe, B.A.

Direct Submission

Submitted (14-SEP-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

J (Dases 1 to 224138)
Deschamps, S. and Roe, B.A.

Direct Submission

Submitted (16-NOV-2002) Department Of Chemistry And Biochemistry,
OK 73019, USA

Direct Submission

Submitted (16-NOV-2002) Department Of Chemistry And Biochemistry,
OK 72010, USB, Norman,
                                                                                                                                                                                                                             OK 73019, USA
4 (bases 1 to 224138)
4 (bases 3 and Roe, B.A.
Direct Submitsion
Submitted (20-NOV-2002) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                OK 73019, USA
ON 720, 2002 this sequence version replaced gi:25046357.
On Nov 20, 2002 this sequence version replaced gi:25046357.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
Mus musculus (house mouse)
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/mol type="genomic DNA"
/strain="C578L/6J"
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Gaskin, C., Gench, S., Ghose, S., Gill, R., Gonzalez, D.,
Gonzalez-Garay, M., Guevara, W., Holder, M., Haaland, W., Havbey, B.,
Hall, B., Hanid, H., Hanilton, K., Harbey, B., Harrias, R.,
Hawkins, E., Hayes, S., Hemphill, L., Hernandez, J.,
Hines, S., Hitchens, M., Hodgson, A., Hogues, M., Hollins, B.,
Howell, L., T., Hully, S., Hume, J., Imo, K., Jackson, A., Jackson, L.,
Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kalafus, K., Kelly, S.,
Keys, T., Khan, Z., King, L., Kovar, C., Kowis, A., Kowis, C., Lara, F.,
London, P., Lopez, J., Lorenshewa, L., Losado, R., Lewis, L., Li, B.,
Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y. S., Liu, Y., Liyanage, D.,
London, P., Lopez, J., Lorenshewa, L., Losado, R., Lewis, L., Li, B.,
Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y. S., Liu, Y., Liyanage, D.,
Mahoshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, R.,
Malosuljevic, A., Minja, R., Morgan, M., Morris, S., Munidasa, M.,
Milosavljevic, A., Minja, R., Morgan, M., Morris, S., Munidasa, M.,
Nutray, D., Nazarith, L., Ngo, D., Nguyen, N., Norwig-Rastaugh, E.,
Nott, A., Nwaokelmenh, O., Obregon, M., Ochi-Okorie, C., Odeh, E.,
Okwuonu, G., Okwuonu, K., Parker, D., Peatrosino, J., Pham, T.,
Primus, R., Pul, L., Puzzo, M., Ruiz, S. J., Sana, M., Sanders, W.,
Santobara, J., Santos, R., Savery, G., Scherer, S., Shen, H., Shen, Y.,
Sisson, I., Saned, A., Sodergen, E., Song, K.-Z., Sorelle, R.,
Svatek, A., Taylor, E., Taylor, T., Thomas, N., Thorn, R., Thornton, R.,
Trejos, Z., Usmanl, K., Vargo, C., Verduzco, D., Villasana, D., Varbo, J.,
Wei, X., Wheeler, D., Williams, G., Wang, O., Ward, S., Shen, J.,
Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.,
R., Shang, L., Shang, S., Yan, K., Yuan, Y., Yu, F., Zhang, J., Zhang, L.,
Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.,
R., Chang, R., Shang, R., Shang, C., Wang, C., Ward, S., Yan, K., Yush, Y., Yu, Yu, Y., Yu, Yu, Y., Yu, Y., 
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 222533 bases at least Q40
Consensus quality: 233090 bases at least Q30
Consensus quality: 233474 bases at least Q20
Estimated insert size: 248318; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Lorenshwa, L., Loulseged, H., Lozado, R.J., Lu, K., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mawheshwari, M., Mahindartne, M., Martin, R., Martinez, B., McLeod, M.P., Mortel, R., Mortel, S., Montemayor, J., Moore, S., Morgan, M., Mortel, R., Mortel, S., Munidas, M., Murphy, M., Nair, L., Nankeria, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Paul, H., Paul, H., Paul, H., Perz, M., Perz, L., Pfannkoch, C., Plopper, P., Pouldexter, A., Popovic, D., Primus, B., Pu, L.-L., Plopper, P., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Plopper, P., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shags, P., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, R., Reigh, R., Sanders, W., Savery, G., Scherer, S., Scotl, G., Shatsman, S., Shen, H., Sheet, J., Sodergran, B., Song, X.-Z., Sorelle, R., Shatsman, S., Shen, H., Sheit, J., Shvartsbeyn, A., Sisson, I., Shatsman, S., Smaj, D., Challe, R., Warge, M., Wang, S., Warren, J., Walcen, R., Walcon, L., Walker, R., Walliams, G., Wallson, M., Walder, M., Walder, M., Walder, R., Waldron, L., Walker, R., Walliams, G., Wallson, M., Walder, M., Walse, R., Smith, D., Williams, G., Walliams, R., Warren, J., Yakub, S., Yen, You, V., Weinstock, G. and Gibbs, R.A., Smith, D. R., Holt, R., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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   1278 158306: contig of 54029 bp in length 1307 158406: gap of unknown length 160899: contig of 2493 bp in length 160899: gap of unknown length 1600 188597: contig of 27598 bp in length 1598 188697: gap of unknown length 1888 231951: contig of 43254 bp in length 16022100/Qualifiers
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Mismatches:
Indels:
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/estimated length=unknown
160900. .150999
/estimated length=unknown
188598. .188697
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Matches:
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104178. .104277
/estimated_length=unknown
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                                                                                                                                                                                  /organism="Mus musculus"
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/db_xref="taxon:10090"
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HTG; HTGS_PHASBI; HTGS_DRAFT; I
Rattus norvegicus (Norway rat)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                   Submitted (27-JJL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 212670) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houseron, TX 77030, USB.

Baylor Plaza, Houseron, TX 77030, USB.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project Information
Center project name: GQQQ
Center clone name: GH230-102H13
Center clone name: CH230-102H13
Assembly program: Phrap; version 0.990329
Consensus quality: 217907 bases at least Q40
Consensus quality: 217939 bases at least Q20
Estimated insert size: 241705; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
(bases 1 to 232670)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: BCM
                                                                                      Direct Submission
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REFERENCE
AUTHORS
TITLE
JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allan, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D.,
Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranalke, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blatr, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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Cleveland, C., Cockrell, R., Cox, Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Daramo, C., Ding, Y., Dinh, H., Divya, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACU99417 252441 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-2M18, WORKING DRAFT SEQUENCE.
AC099417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
as soon as it is available and the accession number will be preserved.
                                                       1 230429: contig of 230429 bp in length 0 230529: gap of unknown length 0 232670: contig of 2141 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC099417.6 GI:30467912
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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Conservative:
Mismatches:
Indels:
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    .1154
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                                                                                                                                                                                                                                                                                                                             4426...5307./note="clone_boundary
clone_end:Sp6
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43.00
100.0%
77.8%
89.6%
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Best Local Similarity:
                                                                                                          230530
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DB:
                                                                                                                                                        Bource
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ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap
                                                                                                                               PEATURES
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Submitted (109-MRV-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON May 9, 2003 this sequence version replaced gi:24819659.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.ngs.bm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, T., Hawes, S., Haddm, S.L., Hodgesn, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, J., Jacob, L., Jánag, H., Johnson, B., Johnson, K., Johnson, K., Colivec, A., Karpathy, S., Kaly, S., Kaly, E., King, L., Kovar, C., Liu, J., Liu, M., Liu, Y., London, P., Longare, B., Johnson, R., Mangum, A., Maheshwari, M., Mahindarine, M., Mahindarine, M., Martinez, E., Mores, J., Lorensuhewa, L., Louiseged, H., Lozado, R.J., Lu, X., Ma, J., Mangum, A., Mahoshwari, M., Mahindarine, M., Martinez, E., Martinez, E., Mangua, P., Mores, S., Mangua, P., Moreis, S., Martinez, B., Moreod, M.P., Moreis, S., Morias, S., Munidasa, M., Murphy, M., Nari, L., Nankervis, C., Neal, D., Newton, G., Olarmpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Carnoun, G., Olarmpunsagoon, A., Pal, S., Reigh, R., Pluzo, M., Vullacker, M., Perez, A., Perez, M., Pal, S., Shen, H., Shen, H., Shetty, J., Shwartsheyn, A., Sacherer, S., Soct, G., Shatsman, S., Shen, H., Shetty, J., Shwartsheyn, A., Steinlin, B., Revers, K., Sequer, M., Regier, M., Renter, M., Shetsman, S., Shen, H., Shetty, J., Shwartsheyn, A., Susson, I., Siter, C.D., Smajs, D., Shetty, J., Shwartsheyn, A., Susson, I., Shtrama, S., Wang, S., Waright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, V., Willams, G., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weinser, R., Shith, M., Mang, M., Williams, G., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, V., Willedrhausern, A., Walss, R., Shith, M., Soler, S., Shith, M., M., Soler, S., Shith, M., Shith, M.
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Direct Submission
Submission
Submission
Moltcular and Human Genome Sequencing Center, Department
of Moltcular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
A (bases I to 252441)
Rat Genome Sequencing Consortium.
Direct Submission
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Center code: BCM
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Unpublished
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Wed May

000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 1.86e+04 43.00 100.0% 66.7% 89.6% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: Score:

US-10-774-176-9 (1-9) x AC099417 (1-252441)

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AC097908/c

Rattus norvegicus clone CH230-150L5, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 10 unordered pieces. DEFINITION

AC097908.7 GI:30520969 HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED. Rattus norvegicus (Norway rat) Rattus norvegicus ACCESSION VERSION KEYWORDS SOURCE

ORGANISM REPERENCE

Enkaryota, Marazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Guirognathi, Muroidea, Muridae, Murinae, Rattus.

1 (bases 1 to 258569)

Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., AUTHORS

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Cesaer, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Y.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Dapaper, H., Dugan Rocha, S., Dunn, A., Durbin, R., Duval, B., Baves, K.,
Eapan, A., Escotto, M., Gante, R., Garcia, A., Garrer, M., Garza, M.,
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Gunaratne, P., Haland, W., Hall, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Handersen, M., Horgues, M.,
Garpathy, S., Kally, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, J.,
Jackson, L., Jacob, L., Jang, H., Oohnson, B., Johnson, R., Jolivet, A.,
Marpathy, S., Kally, S., Kally, S., Khan, Z., King, L., Kovat, C.,
Kowle, C., Katt, C.L., London, P., Longor, P., Loger, J.,
Liu, W., Liu, Y., London, P., Longor, P., Loger, J.,
Mandshwari, M., Mali, Y., London, P., Longor, P., Martin, R.,
Mandliney, S., Welced, M. P., Martin, R., Martinez, S.,
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoh, S., Rait, S.,
Raige, C., Redey, T., Royler, S., Stock, G., Shait, S.,
Sanders, W., Savery, G., Scherer, S., Scock, G., Shait, S.,
Mang, S., Wartebeyn, A., Sisson, I., Stock, M., Tabor, S.,
Mang, W., Walas, R., Yule, Sandy, J., Zhou, J., Zhou, Y., Yalas, M., Walse, R., Salten, S., Stock, G

}

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 2 (bases 1 to 258569) Worley, K.C. Direct Submission Unpublished REFERENCE AUTHORS TITLE JOURNAL TITLE

3 (bases 1 to 258569) Rat Genome Sequencing Consortium. Direct Submission AUTHORS TITLE REFERENCE JOURNAL

COMMENT

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on May 10, 2003 this sequence version replaced gi:24819718.

On May 10, 2003 this asembly us a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.

Center: Baylor College of Medicine

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Scillognaturi, wuroldee; Murinae; Katus.
Stillognaturi, Wuroldee; Murinae; Katus.
Stillognaturi, Wuroldee; Milee., Abramzon, S., Adams, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyaqi, A., Ayodeji, M., Baca, E., Badan, H.,
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavaz, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
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Fraser, C.M., Gabisi, A., Ganta, R., Chen, Y., Hornandez, S., Filley, M., Flagg, N., Forbes, L., Foster, M., Guerra, W.,
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Narpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACLIZIOS 263882 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-65D16, WORKING DRAFT SEQUENCE, 4
unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus (Nordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Murinae; Rattus.
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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                     NOTE: Betimeted insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21832: contig of 21832 bp in length 21932: gap of unknown length 26406: contig of 4474 bp in length 26506: gap of unknown length 244662: contig of 218156 bp in length 245801: contig of 1039 bp in length 245801: gap of unknown length 245801: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 249318: gap of unknown length 1319 251049: contig of 1731 bp in length 150 251468: contig of 1319 bp in length 150 252468: gap of unknown length 151 254250: contig of 182 bp in length 151 254250: gap of unknown length 151 254550: contig of 182 bp in length 151 258569: contig of 4319 bp in length 1601251 258569: contig of 6319569: contig of 6319569: contig of 6319569 258569: contig of 6319569 258569: contig of 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 218156 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245901: gap of unknown length
247216: contig of 1315 bp in length
247316: gap of unknown length
249218: contig of 1902 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organiam="Rattus norvegicus"
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COMMENT

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Query Match:
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AR520225
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AR504928
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2 (bases 1 to 263882)

38 Worley. K.C.

Direct Submission

AL Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 263882)

3 At Genome Sequencing Consortium.

Direct Submission

4 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Shajor Plaza, Houston, TX 77030, USA

5 Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

6 Molecular and Human Genetics, Baylor College of Medicine, One Baylor Department of Molecular and Human Genetics, Baylor Talas and Whole Sequence version replaced gi:24942501.

7 The sequence in this sequence version replaced gi:24942501.

7 The sequence in this sequence version replaced sacribed and whole genome shotepum sequencing reach seaffold;

8 Assembly (a 'contig-seaffold'). Within each contig described in the feature contigs are ordered and oriented, and sequence contigs are ordered and oriented, and sequence contigs within a contig-seaffold that consist entirely of whole genome shotepun sequence reads. Both end sequences and whole genome shotepun sequence readfold that consist entirely of whole shotepun sequence readfold that consist entirely of whole reals.
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Ffannkoch, C.,
Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puazo, M., Quiroz, J., Rachiln, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rais, C., Rodery, T., Rojas, A., Rose, M., Rose, M., Riggs, F.,
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Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
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Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
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Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Direct Submission
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PAT 22-SEP-2004
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Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L., Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
Drosophila sequences
Patent: 105 6703491-A 25185 09-MAR-2004;
Exelixis, Inc.; South San Francisco, CA
Location/Qualifiers
1 258509: contig of 258509 bp in length 5510 258609: gap of unknown length 59776 contig of 1165 bp in length 59775 259874: gap of unknown length 8875 251421: contig of 1547 bp in length 1422 261521: gap of unknown length 1522 261521: gap of unknown length 150cation/Qualifiers
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Matches:
Conservative:
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Matches:
Conservative:
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Sequence 25185 from patent US 6703491.
AR520225
AR520225.1 GI:52455700
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/organism="unknown"
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Pred. No.:
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polya tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuracly this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription shout this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to candoffuitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MKPTAGĢTGFLALLILFCLLSCVSAYNYLVVLHTAARSHYHVGSA
LAKGLAAAGHQVTIISPFELKKPINNIKDVPAKSILTSMQGRIANLIJGSKRFPIKQI
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MARAEQNGYGVTVHYEELSSAKLLAAIQKIINNPEATQRVRDMSDRYRDQQQTPLERA
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                                                   INV 28-MAR-2003
                                                                                                                                                                                                                                                                 1 (bases 1 to 1980)
Stapteton, M., Brookstein, P., Hong, L., Agbayani, A., Carlson, J., Chapteo, M., Grookstein, P., Hong, L., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Man, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
                                                                                                                                                                                            Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-MAR-2003) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
                                                   3T006007 1980 bp mRNA linear
)rosophila melanogaster RE18708 full insert CDNA.
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142. 1728
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                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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        linear PAT 22-SEP-2004
                                                                                                                                                                             1 (bases 1 to 1017)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L., Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
Patent: US 6703491-A 9888 09-WAR-2004,
Exelixis, Inc.; South San Francisco, CA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.
Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 28130 27-SEP-2001;
PE Corporation (NY) (US)
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Sequence 9888 from patent US 6703491.
AR504928
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|mol_type="unassigned DNA"
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The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKPZp5661133 activity. The methods are useful for treating cancer, e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention.
                                              Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for inhibition of DKFZp5661133 activity.
                                                                           Claim 30; SEQ ID NO 47; 257pp; English.
                                                                                                                                                                                                            US-10-774-176-8 (1-9) x ADK11641 (1-246)
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A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
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                                                                                                                                                                    therapy; expression profile; solid mononuclear cell; PBMC; prognosis;
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                     41
                                                                                                                                              Solid tumour prognosis gene seqid 2116.
AlailePheLeuLeuValLeuTyrLeu
                      GCTATTTTCCTCCTGGTTTTTGTATTTG
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                                                                       ADU11677 standard; DNA; 475 BP
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23-JAN-2004; 2004US-0538246P.
                                                                                                                      27-JAN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Trepicchio WL,
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Immerman F, Dorner AJ;
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(STRA/) STRAHS A.
                                                                                                                                                                      cytostatic; gene
peripheral blood
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                                                                                                                                                                                                          Unidentified.
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ds, cytostatic, gene therapy, DKFZp5661133 activity inhibitor; breast cancer, differential expression.

08-JAN-2002; 2002US-0345637P. 08-JAN-2003; 2003WO-US000657

WO2003057926-A1. Homo sapiens.

17-JUL-2003

Breast cancer differentially expressed gene product #47.

(first entry)

06-MAY-2004

ADK11641 standard; DNA; 246 BP.

RESULT 1 ADK11641

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The invention describes a method comprising comparing an expression profile of at least one gene in a paripheral blood sample of a patient to at least one selection of at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood monomuclear cells (PBMCs) of a first class of patients have the solid tumour, and each of the first and second classes is a subcluser formed by an centre of patients and second classes is a subcluser formed by an each of the first and second classes is a subcluser formed by an analysis of the first class of patients has a second classe of patients has a second claim out come. Also described are: a system comprising (i) a memory or a patient who have the second class of patients has a first clinical outcome, and the majority of the second class of patients has a first clinical outcome, and cutcome. Also described are: a system comprising (i) a memory or a cutcomed patient in a paripheral blood sample of a patient who has a solid tumour, (ii) at least one gene in a paripheral blood sample of a patient who has a solid tumour comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the comparing the expression profile, and (iv) a processor capable of executing the comparing the expression profile, and (iv) a processor capable of executing the comparing the expression profile, and (iv) a processor capable of executing the comparing the expression profile, and (iv) a processor capable of executing the comparing the expression profile, and (iv) a processor capable of executing the comparison profile, and (iv) a processor capable of executing the expression levels of the gene in paripheral blood comprising uncomes of the patients who have the solid tumour prognosis genes is differentially expressed in program, where both the first and second classes of patients has a first class of patients as econd class of patients has a second class of patients and the second class of patie
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475 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: US-10-774-176-8 (1-9) x ADU11677 (1-475) 174 41.00 100.0% 100.0% Score: Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

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AAA27060 standard; DNA; 901 BP AAA27060; RESULT 3 

Canine 5T4 tumour-associated antigen gene. (first entry) 22-AUG-2000

Canine; TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;

Location/Qualifiers misc\_feature Canis sp.

1. 858 /\*tag= a /product= "5T4 antigen" 61. 74 /\*tag= b

Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors. /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /\*tag= e /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /\*tag= h
/note= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids"
572. .583 /\*tag= k /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" but does not seem to t 2 but does not seem to /\*tag= c /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" not seem to encode any //ore= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /\*tag= g /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" 644. .653 /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" 714. .723 /nore= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /\*tag= d /note= "given in the specification but does: be part of the coding sequence and does not corresponding amino acids" (OXFO-) OXFORD BIOMEDICA UK LTD. 98GB-00025303. 99GB-00001739. 99GB-00017995. 99WO-GB003859. 122. .436 /\*tag= f /\*tag= /\*tag= Carroll MW, Myers KA; WPI; 2000-387735/33. P-PSDB; AAY94351. WO200029428-A2 misc\_feature 18-NOV-1999; 18-NOV-1998; 27-JAN-1999; 30-JUL-1999; 25-MAY-2000 

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The present sequence encodes the canine 5T4 tumour-associated antigen carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been human or murine 5T4 gene sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
                                                                                                                                                                                                             Sequence 901 BP; 178 A; 246 C; 212 G; 153 T; 0 U; 112 Other;
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Matches:
Conservative:
Mismatches:
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            Disclosure, Page 78-79; 79pp; English
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02-FEB-2001; 2001US-0265928P.
09-APR-2001; 2001US-00829472.
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04-MAY-2001; 2001US-0288590P
29-MAY-2001; 2001US-0294443P
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Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polymucleotide that selectively hybridizes with breast

Claim 9; Page 372; 414pp; English

cancer nucleic acids.

WPI; 2002-583738/62. N-PSDB; ABJ05564.

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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a blological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer calls. Genes identified by the method of the invention can be used in diagnostic purposes and also as taxgets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
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Best Local Similarity:
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in cased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated cell to treat lung cancer in a patient and for treating a memmal having lung cancer by administering lung cancer, such as small cell lung cancer, non-small cell to treating lung cancer, such as small cell lung cancer, non-small cell contracting lung cancer, cher benign or precancerous lesions, e.g. atelectasis, emphysema, bronchtis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, intersitial pulmonary fibrosis as atemperation for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
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                                                  Claim 22; Page 336; 453pp; English
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2001US-0315287P.
2001US-0317544P.
2001US-0350666P.
2002US-0372246P.
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                   expression in lung cancer.
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05-SEP-2001;
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12-APR-2002;
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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                              The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polymeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
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(EOSB-) BOS BIOTECHNOLOGY INC.
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21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
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                                     Mack DH, Gish KC;
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Plowman GD, Funke RP, Lioubin MN,

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate p53 pathway-modulating agent for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                         Human; p53 pathway; Leucine rich repeat capricious related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         775 GCTATTTTCCTCCTGGTTTTGTATTTG 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 74-75; 99pp; English.
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                                                LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                 22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                   21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Belvin M, Schleithoff L, Pi
Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV99349 standard; DNA; 1156
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100.0%
100.0%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                  WO2003035831-A2
                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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ABV99349
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glynne R, Hevezi PA;
B, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Afar D, Aziz N, Ginsburg WM,
Mack DH, Murray R, Watson SR,
                       14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-034731IP.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355714P.
20-FEB-2002; 2002US-0359077P.
                                                                                                                                                                                                                                                                                                                                                                                                     (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                          12-APR-2002; 2002US-0372246P-
05-UUN-2002; 2002US-0386614P-
16-UUL-2002; 2002US-0396839P-
22-UUL-2002; 2002US-0397775P-
                                                                                                                                                                           29-MAR-2002; 2002US-0368809P.
                                                                                                                                                                                                                                                                                                                              2002US-0397845P
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DB:
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Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; noctropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; BP. Human NOV8a coding sequence. (first entry) 27-JAN-2003 

ВР

AAD56198 standard; DNA; 973

RESULT 8

.. 0

Human LRRCAPS related DNA #5.

(first entry)

07-AUG-2003 AAD56198;

AADS6198
ID AADS
XX
AC AADS
XX
OT 07-A

973 00 00 00

Length: Matches: Conservative: Mismatches:

Indels:

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CAM;

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABB70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disquesting diseases such as metabolic disorders, diabetes, obsestly, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, immune disorders, haematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disturbances associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in
                                                                      Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli RA, Vernet CAM, Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss RZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                     New NOVX polypeptides and polynucleotides, useful for preventing, diagnoshing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                             Claim 16; Page 114-115; 619pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic or diagnostic methods
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   03-JAN-2002; 2002US-0345705P.
08-MAR-2002; 2002US-00093463.
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100.0%
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                                             (CURA-) CURAGEN CORP.
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Best Local Similarity:
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bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
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2001US-0275235P.
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2001US-0275579P.
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2001US-0276000P.
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2001US-0276994P.
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2001US-0288342P.
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2001US-0291190P.
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2001US-0294889P.
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2001US-0299027P,
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13-MAR-2001; 2
13-MAR-2001; 2
14-MAR-2001; 2
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08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
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19-MAR-2001;
20-MAR-2001;
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20-MAR-2001;
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26-MAR-2001;
27-MAR-2001;
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30-MAR-2001;
02-APR-2001;
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                                                          Homo sapiens.
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12-MAR-2001;
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04-APR-2001;
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31-MAY-2001;
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04-DEC-2001;
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Matches: Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                                                                                        Novel canine or feline 514 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Major Histocompatibility Complex class I peptide epitope; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                /product= "5T4 protein"
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                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 68; 68pp; English.
                                                                                                                                                                                                                                               (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB97513 standard; DNA; 1260 BP
                                                                                                                                                                                                                                                                               Carroll M;
                                                                                                                                                                                                               13-NOV-2000, 2000WO-GB004317.
                                                                                                                                                                               13-NOV-2001, 2001WO-GB005004.
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P-PSDB; AAU98694.
                                                                                                                                                                                                                                                                             Myers K, Drury N,
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Best Local Similarity:
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The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 574 antigen. The invention further class I peptide epitope of the 574 antigen. The invention further class I provides a polypeptope string of the 574 epitope; a vector system capable of delivering the 574 epitope; a uncleic acid to a cell, a cell pulsed with the 574 epitope ancleic cacid to a cell, a cell pulsed with the 574 epitope. Proventing a disease comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising detecting the presence of the 574 epitope or its encoding nucleic acid; a method comprising detecting the presence of the 574 epitope or its encoding nucleic acid; and the vector specifically rocognising the 574 epitope in conjunction with an MHC class comprising the 574 epitope has cytostatic activity. The vaccine of method is useful for disposance. The detection method is useful for disposance of the 574 epitope or its encoding nucleic acid and the vector comprising the progression of a cancerous disease, and for detecting the present of a useful for disposance of the 574 epitope or its nucleic acid and the or clone computating a disease. This polynucleotide sequence represents the feline correcting a disease. This polynucleotide sequence represents the feline correction of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New major histocompatibility complex class I peptide epitopes from human 574 tumor-associated antigen, useful for preventing and/or treating a
574 antigen, 574 epitope, polyepitope string, vaccine, T cell, cytostatic, cancer, feline, gene, ds.
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/product= "Feline ST4 antigen protein"
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                                                                                                                                         Location/Qualifiers
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Best Local Similarity:
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                                                                                                       Unidentified
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ADB97452
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cancer;

ADB97452;

Unidentified

Key

21-AUG-2003

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The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour idagnosis, targeting and immunotherapy. Mice in which tumours had been induced were incoulated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
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                                                           Human, TAA, tumour-associated antigen, anti-tumour; cytostatic; immunostimulant, vaccine; carcinoma; colorectal cancer; gastric
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Conservative:
Mismatches:
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                  Human 5T4 tumour-associated antigen gene.
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99GB-00001739.
99GB-00017995.
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Best Local Similarity:
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                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a Major Histocompatibility Complex (WHC) class II peptide epitope of the ST4 antigen. The vaccine or T-call line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for disagnosing or monitoring the progression of a canceroum disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                                                                                                               gene; ds; feline; Major Histocompatibility Complex class II; WHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1260
/*tag= a
/product= "Peline 5T4 antigen protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll M, Harrop R, Kingsman S;
                                                                                                      DNA encoding feline 574 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD BIOMEDICA UK LTD
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                                                             04-DEC-2003 (first entry)
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Best Local Similarity:
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22-AUG-2000 (first entry)

AAA27058;

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Query Match: DB:

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Key

25-MAY-2001

Myers KA,

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell compositions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in disagnostic kits for rapid, reliable, sensitive, and specific compositions and specific compositions are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The colls may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).

The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                    Location/Qualifiers
1. .1263
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers K, Drury N, Carroll M;
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P-PSDB; AAU98693.
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                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes the use of a single chain antibody (SCFV), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The SCFV antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a medicament of a disease. The SCFV antibody is also useful for treating treatment of a disease. The SCFV antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune disease, cancers, central nervous system disorders including Parkinson's disease, pariodontal diseases, cardiopulmonary diseases, cardiovascular diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce SCFV of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canine, dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 26, 118pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                    /*tag= a
/product= "5T4"
                                                                                                                                                                                                                                                                                                                     18-NOV-1999; 99WO-GB003859.
15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                                                                                                                                                                                                                           13-NOV-2000; 2000WO-GB004317.
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Query Match:
DB:
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                                                                                                                                                                                     WO200136486-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kingsman A,
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1263 9 0 0 0

ABK87174;

RESULT 15 ABK87174

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WO2003035831-A2
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                                                                                                                                                                                                                                                                                                                      The present sequence encodes the mouse 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                       Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                           |mmunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; p53 pathway; Leucine rich repeat capricious related protein;
                                Mouse; TAA; tumour-associated antigen; anti-tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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           Mouse 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                                                                                                                      Example 2; Page 78; 79pp; English.
                                                                                                                                                                                                       (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AADS6199 standard; DNA; 1331 BP
                                                                                                                                                            98GB-00025303.
99GB-00001739.
99GB-00017995.
                                                                                                                                         99WO-GB003859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human LRRCAPS related DNA #6.
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41.00
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                                                                                                                                                                                                                                                  WPI; 2000-387735/33.
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                                                                                             WO200029428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                          Mus musculus.
                                                                                                                                         18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                             .8-NOV-1998;
                                                                                                                                                                        27-JAN-1999;
30-JUL-1999;
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                                                                                                                   25-MAY-2000
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DB:
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                    comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA differentially expressed in MYCN activated cells SeqID 105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; 88; MYCN activated cell.
                                                                                                                                                                                                                                                     ፤
                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate p53 pathway-modulating agent for treating
                                                                                                                                                                                                                                                  Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                     Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 75-76; 99pp; English.
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                                                                                                22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                 21-OCT-2002; 2002WO-US033540
                                                                                                                                                                                                                                                  Belvin M, Schleithoff L, P. Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2002; 2002US-00084817
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41.00
100.0%
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                                                                                                                                                                                                   (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                              WPI; 2003-421410/39.
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01-MAY-2003
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ID ADJ5
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03-AUG-2001; 2001US-0310099P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protonogene that is amplified in neuroblastoms cells and is common in small call lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, well as for screening assays by identifying molecules or compounds that expectifically thind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the US Patent Office at
                                                                                                                            New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bladder cancer associated cDNA sequence SEQ ID NO:192.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                 Shohet JM;
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                                                                                                                                                                                          Claim 1, SEQ ID NO 105, 27pp; English.
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23-FEB-2001, 2001US-0270784P
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41.00
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100.0%
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                                                                                 Stuart 8G, Nuchtern JG,
                      STUART S G.
NUCHTERN J G.
                                             PLON S E.
SHOHET J M.
                                                                                                       WPI; 2003-635698/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                      (STUA/) (NUCH/) 1 (PLON/) 1 (SHOH/) 2
                                                                                                                                                                     cancer.
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DB:
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated proteins given in ABR48146 to have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer-associated polynucleotide, gene, ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                               Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynuclectide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    various screening and diagnostic methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AlailePheLeuLeuValLeuTyrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 296; 307pp; English.
                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-035066F.
12-APR-2002; 2002US-0372246P.
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                                                                                                                                                                                                                                                           WPI; 2003-201532/19.
P-PSDB; ABR48236.
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                                                                                                                                                                                                Mack DH, Aziz N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200286443-A2
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent acitvity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; p53 pathway; Leucine rich repeat capricious related protein;
                                                                                                                                                                                                                                                                            Plowman GD, Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 73-74; 99pp; English.
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                                                                                                                                22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                        21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                          Belvin M, Schleithoff L, P
Francis-Lang H, Friedman L;
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15-FEB-2002; 2002US-0357600P.
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                                                                                                                                                                                                                             (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-421410/39.
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Best Local Similarity:
WO2003035831-A2.
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                                             01-MAY-2003
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in cased or decreased expression in lung cancer samples. Lung cancer cased or decreased or decreased or properties are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful contracting a modulatory compound identified. The methods are useful complysems, bronchitis, chronic obstructive pulmonary disease, fibrosis, camphysems, bronchitis, chronic obstructive pulmonary fibrosis, asthma and compounds that modulate lung cancer, such as antibodies. Sequences or dense path as a targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                                                                                                                                          Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 335; 453pp; English.
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                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
                                      10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-03393470P.
29-NOV-2001; 2001US-0373246P.
                                                                                                                                                                                                                                                                                                                                                                                                               expression in lung cancer.
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                                                                                                                                                                                                                                                                   WPI; 2003-093161/08.
P-PSDB; ABU56603.
                                                                                                                                                                                                                          Aziz N, Murray R;
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RESULT 24
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                                                                                                                                                                                  The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway-modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                         Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; differential expression; cancer; anglogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis, drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                  Li D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39
                                           Belvin M, Schleithoff L, Plowman GD, Funke RP, Lioubin MN, Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                              Disclosure, Page 76-77; 99pp; English.
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2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
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 01-MAR-2002; 2002US-0361196P
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                         (EXEL-) EXELIXIS INC.
                                                                                      WPI; 2003-421410/39.
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29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
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DB:
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
conter diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
content by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising
concleic acid of the invention; antibodies which specifically bind a
colypeptide of the invention; use of such antibodies for druge targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
cancer and other conditions such as psoriassis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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3, Zlotnik A;
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Wilson KE,
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Murray R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                              (BOSB-) ROS BIOTECHNOLOGY INC
                                                2002US-0355250P.
                                                                                                 2002US-0359077P.
                                                                                                                                                                               2002US-0372246P
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2002US-0397775P.
2002US-0397845P.
2002US-0347211P
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Query Match:
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                                                                      13-FEB-2002;
20-FEB-2002;
29-MAR-2002;
04-APR-2002;
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Mack DH, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL06473;
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The invention relates to novel polymucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                         Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of
                                                                                                                                                                                                                                           New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                        Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breast cancer prognosis marker #1305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x ADN03961 (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROSB-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                        Clark H, Jackman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                  25-SEP-2003; 2003WO-US030907.
                                                                    25-SEP-2002; 2002US-0414006P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR25444 standard; DNA; 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004; 2004WO-US001100
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                                                                                                                                                                                            WPI; 2004-305105/28
                                                                                                     (GETH ) GENENTECH
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Best Local Similarity:
                                                                                                                                                                                                             P-PSDB; ADN03962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
08-APR-2004
                                                                                                                                         Bodary S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR25444;
                                                                                                                                                                                                                                                                                   mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polymucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for diagnosing or treating tumours and cancer. The present sequence represents a human TAT CDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                   Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or
                                                                                                                                                                                                                                                                                                                                   Hillan KJ, Polakis P, Polson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 53; 319pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN03961 standard; cDNA; 2053
                                                                                                                                                                                         21-AUG-2002; 2002US-0405645P.
23-SEP-2002; 2002US-0413192P.
15-OCT-2002; 2002US-041908P.
15-NOV-2002; 2002US-0456847P.
02-JUL-2003; 2003US-0484959P.
                                                                                                                                                                                                                                                                                                                                 Desauvage FJ, Frantz G, Hil
Spencer SD, Wu TD, Zhang Z;
cancer; cytostatic; gene; ss
                                                                                                                                        19-AUG-2003; 2003WO-US025892
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                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-257144/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, use
treating cancer.
                                                                   WO2004016225-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004028479-A2
                                  Homo sapiens.
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                                                                                                                                                                          .9-AUG-2002;
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                                                                                                   26-FBB-2004
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ADN03961;

Query Match: DB:

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Score:

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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoms; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
to control levels.
                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
   genes in a cell sample taken from patient,
                                     Disclosure, SEQ ID NO 1305, 226pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1186 GCTATTTTCCTCCTGGTTTTGTATTTG 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AlailePheLeuLeuValLeuTyrLeu 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-2003; 2003WO-US028547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-347921/32.
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
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the interaction features to minimal removal answers and many thus services of the district elated mucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus service as effective targets for the disquests and treatment of cancer in mammals. The invention also relates to mucleic acid and polypeptide polypeptide are sequences at least 80% identical to the TAT nucleic acids and polypeptide and polypeptide and antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; dusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or disquess of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists. Minding molecules and compositions are useful for disquesing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancer, cancers of the central nervans system melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acids may further be represents a TAT nucleic acids in expense.
invention relates to human tumour-associated antigenic target (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; ss; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimenic; antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laeng P;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA of an exemplary efficacy gene for BAD SeqID174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PSYC-) PSYCHIATRIC GENOMICS INC.
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25-SEP-2001; 2001US-0325150P.
14-NOV-2001; 2001US-0325150P.
18-JAN-2002; 2002US-034934P.
04-MAR-2002; 2002US-0361834P.
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Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-118903/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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P-PSDB; ABG22988

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This invention relates to a novel screening method identified as a multice parameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharamecutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders (BAD) and autism, as well as Parkinson's and Alzheimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, nootropic, antimanic and antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and differentially expressed in the presence of a gene that is different than every and and and antidepressed in the presence of a character of the compounds may be rapidly screened with a minimal amount of labour and different than every second and and different and antidepressed in the presence of a character of the compounds may be rapidly screened with a minimal amount of labour and different than the presence of a character of the compounds may be rapidly screened of the presence of a character of the compounds may be rapidly screened of a minimal amount of labour and different than the presence of a character of the compounds may be rapidly and the presence of a character of the compounds may be rapidly and the presence of a character of the compounds may be rapidly and the compounds may be rapidly and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplification of the invention.
                           Identifying a compound that can treat disease or disorders, such as,
                                              neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contacted with the test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder; 88.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                        ID NO 174; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AlailePheLeuLeuValLeuTyrLeu 9
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Best Local Similarity:
Query Match:
                                                                                                                                                        Example 6; SEQ
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Tang YT

Drmanac RT, Liu C, WPI; 2001-639362/73

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US008631 31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167

WO200175067-A2. Homo Baptens.

11-OCT-2001.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caraction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polymorleotide sequences have applications in disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences Abs64197-Abs94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in
                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                              Claim 1; SEQ ID NO 22979; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    electronic format directly from WIPO at
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2000JP-00118774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
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11-JAN-2000;
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셤
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated bean determined. Sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length colones were obtained by construction of full length enrished cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                         830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human, medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                              Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
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100.0%
100.0%
100.0%
                                                                                                                           genetic manipulation.
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P-PSDB; ADL30832.
                                                     2001-524255/58
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Best Local Similarity:
Query Match:
DB:
                                                                        P-PSDB; AAM93333
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA from coth the 5' and 3' entl length human cDNA from coth the 5' and 3' full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and their use
              oligonucleotide primers (830 cDNAs) useful for synthesizing full
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                               Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Matches:
Conservative:
Mismatches:
                                                                   Example 1; SEQ ID NO 2864; 1340pp; English
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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P-PSDB; AAM93334.
                                  length human cDNAs.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful composition. Composition, autoimmuse diseases, diabetes, that treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmuse diseases, diabetes, thyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention for training disease. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischeemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 compounds for treating and preventing diseases, subarachnoid haemorrhage, compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.

506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;

Sequence 2361

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Be; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetee; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
          length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
clarifying the function of the protein encoded by the cDNA. The full
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding protein that promotes STAT6 activation #64.
                                                                                                                   U; 0 Other;
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Conservative:
Mismatches:
                                                                                                                   Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0
                                                                                                                                                           Length:
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DB:
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New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
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T, Koga
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi K, Ish
K, Kojima S,
                               Conservative:
                                          Mismatches:
          Length:
Matches:
                                                     Indels:
                                                                                                                              1527 GCTATTTCCTCCTGGTTTTGTATTTG 1553
                                                                                                                                                                                                                                        Full length human cDNA clone SeqID 2866.
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                                                                                                         AlailePheLeuLeuValLeuTyrLeu
                                                                                     US-10-774-176-8 (1-9) x ADI26162 (1-2361)
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                                                                                                                                                                         ADL30833 standard; cDNA; 2361 BP
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
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                                          Similarity:
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                               Percent Similarity:
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Alignment Scores:
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is

Claim 4; SEQ ID NO 127; 1368pp; English.

diabetes and cancer

New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.

Ishizawa K;

Muramatsu S,

Ö

Honda

Matsuda A,

Sugahara T,

WPI; 2004-122214/12

P-PSDB; ADI26163.

(ASAH ) ASAHI KASEI KK.

16-MAY-2003;

2002US-0385912P. 2003JP-00137505

06-JUN-2002; 26-DBC-2002; 27-DEC-2002; 15-MAY-2003;

2002US-0436467P 2003US-0470836P

05-JUN-2002; 2002JP-00164257

Claim 4; SEQ ID NO 125; 1368pp; English

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셤
                              This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematoeus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding protein that promotes STAT6 activation #63.
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                                                                                                                                                   Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
            Example 1; SEQ ID NO 2866; 1340pp; English.
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                                                                                                                                                                                                                                                                                                                    1527 GCTATTTCCTCCTGGTTTTGTATTTG 1553
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                                                                                                                                                                                                                                                                                                                                                                ADI26160 standard; cDNA; 2557 BP
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2002UP-00377326.
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2003JP-00137505.
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                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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15-MAY-2003;
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26-DEC-2002;
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                                                                                                                                                                          dnment Scores:
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DB:
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as a largic diseases, inflammation, autoimmune diseases and cancers. Compositions are useful for prevention diseases and cancers. Compositions are useful contractive diseases and cancers. Compositions are useful for treating diseases compositions disease and cancers. Compositions are useful contractive diseases and cancers. Compositions are useful contractive diseases and cancers. Compositions are useful contractive diseases and cancers. Compositions are useful contractive disease. Also useful in theumatoid arthritis, osteoathritis, systemic lupus erychematosus, sepsis, asthma, allergic rhinitis, and AlDS. The protein has efficient promoting STAT6 compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds contraction of STAT6. The protein begins a general activation or inhibition of STAT6. The protein begins a detivation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activation or inhibition of STAT6. The present sequence represshuman cDNA encoding a protein which promotes STAT6 activation.
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26-DEC-2002; 2002US-00377326.
27-DEC-2002; 2002US-043647P.
15-MAY-2003; 2003US-00137505.
16-WAY-2003; 2003US-0470836P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral hepatitis and AIDS. The protein has efficient promoting STATE activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive
                                                                                                                                                                                                                 The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as
                                                                                                                                                                                                                                                                                                                                                                                          allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, actima, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                       New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human cDNA encoding a protein which promotes STAT6 activation
                              Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2557 BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;
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                                                                                                                                                                                       Claim 4; SEQ ID NO 123; 1368pp; English.
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                              Honda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibition of STAT6
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ID AAX20580 standard; DNA; 19142
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                             Sugahara T, Matsuda A,
(ASAH ) ASAHI KASEI KK.
                                                            WPI; 2004-122214/12.
P-PSDB; ADI26159.
                                                                                                                                                        diabetes and cancer
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Best Local Similarity:
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Pred. No.:
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Query Match:
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98WO-US013041.

23-JUN-1998;

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New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
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                                                                                                                                                                                                                                   AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis infection; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                Sequence 19142 BP; 4629 A; 5539 C; 4716 G; 4238 T; 0 U; 20 Other;
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlailePheLeuLeuValLeuTyrLeu 9
                                                                                                                                                                                                                                                                                                                              biosynthetic products such as enzymes
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97US-0050667P.
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                                (HUMA-) HUMAN GENOME SCI INC
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Query Match:
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                                                                    Praser CM;
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18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
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                                                                                                                                      Query Match:
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                  The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for represents an E. faecalis polynucleotide of the invention. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating call signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 13127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; 8EQ ID NO 13127; 21pp + Sequence Listing; English.
                                                                                                                                                          Sequence 204 BP; 68 A; 24 C; 38 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                            68 1000
4
                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Disclosure, SEQ ID NO 2468; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers EW;
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                                                                                                                                                                                                                                                                                                 1 AlailePheLeuLeuValLeuTyrLeu
                                                                                                                                                                                                                                                                           US-10-774-176-8 (1-9) x ADH84583 (1-204)
                                                                                                                                                                                                                                                                                                                                                                   ABL06215 standard; cDNA; 1058 BP
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37.00
100.0%
88.9%
90.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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P-PSDB; ABB62112.
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                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                          ABL06215;
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DB:
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                   Sequence 1058 BP; 298 A; 288 C; 259 G; 213 T; 0 U; 0 Other;
                                                                                                                                    1058
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                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
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99US-0130891P.
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99US-0132407P.
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99US-0134941P.
99US-0135124P.
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90.2%
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                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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01-APR-1999;
06-APR-1999;
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135353 135629 1362621 136762 137222 137528 137528 138094	013847P 0139452P 0139452P 0139452P 0139456P 0139456P 0139456P 0139450P 0139450P 0139450P 0139450P 0139450P 0139450P 0139450P 0139450P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P 0139453P	14422547 14400557 1440057 1440057 1440057 1440057 1443317 1443337 1443337 1443337 1443337 1443337 1443337	144814 145814 1458086 11458088 1145818 145818 145818 145818 145818
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	CON-1999; CON-19		
22-4-22-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2	0.04001010101010101010101010101010101010		1111 22222221 222222221 22222222222222
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PR 02-AUG-1999; PR 02-AUG-1999; PR 02-AUG-1999; PR 04-AUG-1999; PR 05-AUG-1999; PR 05-AUG-1999; PR 06-AUG-1999; PR 06-AUG-1999; PR 10-AUG-1999; PR 11-AUG-1999; PR 12-AUG-1999; PR 12-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999	2.000   100

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99US-0136392P.
99US-0137222P.
99US-0137528P.
99US-0137528P.
99US-0138094P.
99US-0138094P.
99US-0138640P.
99US-0138140P.
                                                                                99US-0139452P.
99US-0139453P.
99US-0139492P.
99US-0139454P.
99US-0139455P.
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99US-013946DP.
99US-0139462P.
99US-0139462P.
99US-0139750P.
99US-0139750P.
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9905-0144325P.
9905-0144331P.
9905-0144332P.
9905-0144333P.
9905-0144333P.
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99US-0143989P.
99US-0140353P.
99US-0140695P.
99US-0140691P.
99US-0140891P.
99US-0141287P.
99US-0141287P.
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99US-0143624P.
99US-0144005P.
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99US-0144884P.
99US-0144814P.
99US-0145086P.
99US-0145088P.
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99US-0145089P.
99US-0145192P.
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99US-0146388P.
99US-0146389P.
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99US-0142803P.
99US-0142920P.
99US-0142977P.
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99US-0145218P.
99US-0145224P.
99US-0145276P.
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99US-0145918P.
99US-0145919P.
99US-0145951P.
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99US-0136021P
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99US-01394:
99US-01394:
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10-70N-1999;
14-70N-1999;
16-70N-1999;
16-70N-1999;
18-70N-1999;
18-70N-1999;
18-70N-1999;
18-70N-1999;
       27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
                                                                                                                                                                   8-JUN-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                            1421
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                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 13915.
                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       371 GCGATTTTCTTGCTAATCGTCTACTTA 397
                                                                                                               1 AlailePheLeuLeuValLeuTyrLeu 9
                                                                                                US-10-774-176-8 (1-9) x AAC46422 (1-1421)
                                                                                                                                                            BP
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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9908-0125788P.
9908-0125788P.
9908-0126763P.
9908-01267463P.
9908-01267463P.
9908-0120714P.
9908-0130891P.
9908-0130891P.
9908-0131448P.
9908-0132484P.
9908-0132484P.
9908-0132484P.
9908-0132487P.
9908-0132487P.
9908-0132487P.
9908-0134218P.
9908-0134218P.
9908-0134218P.
9908-0134218P.
9908-0134218P.
9908-0134218P.
9908-0134218P.
                                                                                                                                                            AAC36467 standard; DNA; 1422
                                          2.82e+03
37.00
100.0$
77.8$
90.2$
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                                                                                                                                                                                        17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DS:
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                        AAC36467;
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RR 03-AUG-1999) 99US-014703RP.
RR 04-AUG-1999) 99US-0147124P.
RR 05-AUG-1999) 99US-0147124P.
RR 05-AUG-1999) 99US-0147124P.
RR 05-AUG-1999) 99US-0147124P.
RR 11-AUG-1999) 99US-0147124P.
RR 11-AUG-1999) 99US-0147131P.
RR 11-AUG-1999) 99US-014815EP.
RR 11-AUG-1999) 99US-0148131P.
RR 12-AUG-1999) 99US-0148131P.
RR 22-AUG-1999) 99US-0149131P.
RR 23-AUG-1999) 99US-0149131P.
RR 23-AUG-1999) 99US-0113131P.
RR 11-SER-1999) 99US-0113131P.
RR 12-CET-1999) 99US-0113131P.
RR 13-CET-1999) 99US-0113131P.
RR 13-CET-1999) 99US-0113131P.
RR 13-CET-1999) 99US-0113131P.
RR 13-CET-1999) 99US-0113131P.
RR 14-CET-1999) 99US-0113131P.
RR 11-CET-1999) 99US-0113131P.
RR 22-CET-1999) 99US-0113131P.
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polymucleotide having any of 5544 mucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (CSEQ ID NO: 555-1088). The CDNAs and proteins are from corn. soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a recombinant DNA construct comprising the transforming colypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant tolerance to herbicides, for increasing the rate of improving plant tolerance, for improving plant tolerance, for improving plant tolerance to herbicides, for increasing the rate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant; ss; gene; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates a recombinant DNA construct comprising a
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                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                  JS-10-774-176-8 (1-9) x AAC36467 (1-1422)
                                                                                                                                                                                                                                                                                                                                                ADT15316 standard; cDNA; 1689 BP.
99US-0161993P
99US-0162142P
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                                                                   2.82e+03
37.00
100.0%
77.8%
90.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant cDNA, Seq ID 642.
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                                                                                                        Percent Similarity:
Best Local Similarity:
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28-OCT-1999;
29-OCT-1999;
                                                      Alignment Scores:
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                                                                                                                                               Query Match:
                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                             RESULT 42
                                                                                           Score:
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Claim 1; SEQ ID NO 13124; 21pp + Sequence Listing; English.

Sequence 3298 BP; 893 A; 751 C; 688 G; 966 T; 0 U; 0 Other;

3298 0 0 0 0

Length: Matches: Conservative: Mismatches:

6.76e+03 37.00 100.0% 100.0% 90.2%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Indels: Gaps:

1799 ATTTTCCTCCTTGTCCTGTATCTT 1822

ABL33308 standard; DNA; 6224 BP.

**ABL3330**8 RESULT

ABL33308;

IlePheLeuLeuValLeuTyrLeu

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US-10-774-176-8 (1-9) x ABL06214 (1-3298)

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chomologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improvement by modification of photosynthesis, for modification of photosynthesis, for modification of carbohydrate, nitrogen or phosphorus use and/or uptake anditivity ased protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and carbohydrate, in the field of blant growth and carbohydrate, and for yield improvement by providing improved and compositions of the present invention are useful in the field of blochemistry and the present invention are useful in the field of blochemistry and carbohydrate, in particular for producing transgenic plants with improved conditions and improving plant colerance to cold or heat, improved nitrogen flow, increasing plant tolerance to cold or heat, improved nitrogen flow, increasing plant tolerance to cold or heat, improved nitrogen colerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and arrays of molecules, plant breeding markers, computer-based storage and arrays of molecules, plant from sequence data for this patent did not form part of the printed specification, but was obtained in celectronic format directly from USPNO at a celectronic format directly a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1689 BP; 430 A; 371 C; 326 G; 486 T; 0 U; 76 Other;
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Best Local Similarity:
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                       Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; noctropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiarthritic; antidiabetic; antisporiatic; antiarthrimatic; antiarthrimanic; anticlammatory; cancer; eye disease; arteriosclerosis; anamia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1281; 32pp + Sequence Listing; German.
                                                                           Human immune system associated gene SEQ ID NO: 1281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin
                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000DE-01032529. 01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP007537.
                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ϋ
                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                               03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        olek A,
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Myers EW;

Li PWD,

Venter JC, Adams M, WPI; 2001-656860/75. P-P8DB; ABB62111.

(PEKE ) PE CORP NY

23-MAR-2001; 2001WO-US009231 23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150

WO200171042-A2

27-SEP-2001.

T; 0 U; 4 Other;

Sequence 6224 BP; 1471 A; 222 C; 1628 G; 2899

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This invention relates to chemically pre-treated DNA of genes associated with apoptosis. The nucleic acids are used to allocate patients for specific therapy for HIV infection, Bloom syndrome, cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours and cancers. This nucleotide sequence represents a chemically treated apoptosis gene. Even SEQ ID numbers are the complementary DNA strands to the odd SEQ ID numbers. The sequence data for this patent is not represented in the printed specification but is based on information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       syndrome; cardiopathy; neurodegenerative disorder; renal ischaemia; amyotrophic lateral sclerosis;
             including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
used in the diagnosis and treatment of immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer.
                                                                                                            Sequence 6224 BP; 1471 A; 222 C; 1628 G; 2899 T; 0 U; 4 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemically treated apoptosis gene #28.
                                                                                                                                                                                                                                                                          US-10-774-176-8 (1-9) x ABL33308 (1-6224)
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07-APR-2000; 2000DB-01019173.
30-JUN-2000; 2000DB-01032529.
01-SEP-2000; 2000DB-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001WO-EP003969.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis; HIV; Bloom
Herpes simplex virus;
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                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                         gnment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; ds.
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AAX12939 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Entercoccus faecalis genome with commercial importance. The products can be used to detect the presence of Entercoccus faecalis in samples. They can also be used for diagnosing Entercocccal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Entercoccus faecalis, in vitro. In particular the polypeptides encoded by the Entercocccus faecalis nucleotide sequences can be used in vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Enterococcus faecalis polymucleotides and polypeptides used to develop products for the detection of Enterococcus and for uvaccines for prevention or attenuation of Enterococcus infection.
                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32768 BP; 10797 A; 5960 C; 7083 G; 8921 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                           faecalis genome contig SEQ ID NO:399.
                                         Conservative:
Mismatches:
Indels:
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Matches:
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Matches:
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                                                                                                                                                                        4116 ATATTTTATTAGTTTTATATTA 4139
                                                                                                                     US-10-774-176-8 (1-9) x ABL54355 (1-6224)
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                                                                                                                                                                                                                                              AAX13336 standard; DNA; 32768 BP
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97US-0046655P.
97US-0066009P.
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                                                            Similarity:
                                            Percent Similarity:
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16-MAY-1997;
14-NOV-1997;
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Alignment Scores:
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                                                                         Query Match:
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Conservative:

Percent Similarity:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer readable medium having recorded on it a Enterococcus faecalis nucleotide sequence useful for detecting diseases related to Enterococcus infections in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer readable medium; Enterococcus faecalis; microbe; growth; pathogenicity; vaccine; resistance; Enterococcal infection; commercial; therapeutic; industrial; fermenting; mayar source; metabolite; vaccine; biochip technology; antibacterial; modulator of nucleic acid expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32768 BP; 10797 A; 5960 C; 7083 G; 8921 T; 0 U; 7 Other;
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    Mismatches:
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Gaps:
                                                                                               US-10-774-176-8 (1-9) x AAX13336 (1-32768)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00070927
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88.9%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KUNS/) KUNSCH C A.
(DILL/) DILLON P J.
(BARA/) BARASH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-750065/81.
  Best Local Similarity:
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                           Query Match:
DB:
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                                                                                                                                                                                                                                                               ABS 99131.
ABS 59131.
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Length: Matches: Conservative: Mismatches: Indels:

7.35e+04 37.00 100.0% 88.9% 90.2%

> Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

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The present invention relates to methods for distinguishing between individuals homozygous for and therefore afflicted with Van Buchem's disease, individuals heterozygous for and therefore carriers of Van Buchem's disease and individuals who are not afflicted with Van Buchem's disease comprise identifying a large genomic deletion in chromosome 17 at 17421. The method is useful for identifying individuals who are afflicted with or carriers of diseases associated with one or more genomic deletion, particularly Van Buchem's disease, which is a rare autosomal creessive disocder that results in a bone dysplasia referred to a cranictubular hypercois. The present sequence is a 92Kb gene fragment in human chromosome 17 at 17421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis; autosomal recessive disorder; chromosome 17; chromosome 17q21; bone dysplasia; 92Kb gene fragment; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
5799. .57515
/*taga - .77516
/*tote= "This region is deleted in individuals afflicted
or carriers of Van Buchem's disease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methods for identifying subjects who are afflicted with or carriers of diseases associated with genomic deletion(s), e.g. Van Buchem's disease, by determining the presence of a deletion in the 92 kb region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 92139 BP; 23017 A; 22243 C; 23264 G; 23612 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92139
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Conservative:
Mismatches:
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US-10-774-176-8 (1-9) x ABS99131 (1-32768)
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                                                                                                                                                                                                                                       AAD31364 standard; DNA; 92139 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLTECH R & D INC. (STRA/) STRAEHLING HAMPTON K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000US-0221855P. 06-JUL-2001; 2001US-0303386P.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening of bloactive agent capable of bloadidates; (ii) for screening of bloadive agent capable of modulating the activity of CAP; (iii) for screening of a bloadive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (vii) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a blochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                         Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                    Sequence 127369 BP; 37839 A; 19829 C; 21590 G; 38607 T; 0 U; 9504 Other;
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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Indels:
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                                                                   Claim 1; SEQ ID NO 238; Opp; English
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 from base 1600001 (Haemophilus influenzae complete LOCUS AAT42063 Accession Aat42063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
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Matches:
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ACN44006 standard; DNA; 127369 BP.
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PAT 17-JUL-2003
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Methods for prognosis and treatment of solid tumors
Patent: WO 2014097052-A 2116 11-NOV-2004;
Wyeth (US); Burczynski, Michael B. (US)
Location/Qualifiers
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Carroll, M.W. and Myers, K.A.
Polypeptide
Patent: JP 2002530060-A 3 17-SEP-2002;
OXFORD BIOMEDICA LTD

    .475
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BD249733.1 GI:33059503
JP 2002530060-A/3.
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AY987187 Morphuus
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AY987193 Oroaetus
AY987293 Oroaetus
AY987201 Hieraaetu
AX987201 Haliaetus
AX987202 Shigella
AX987202 Haliaetus
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AX987204 Hieraaetu
AX987104 Harpyhali
AY987105 Leptodon
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Mammalia, Eutheria, Euarchontoglires; Primates, Catarrhini;
Hominidae, Homo.
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AY987167 Chondrohi
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 32642 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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Homo sapiens
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PAT 14-DEC-2001

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
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Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
screening for modulators of breast cancer
batent: WO 02059377-A 57 01-AUG-2002;
EOS Biotechnology, Inc. (US)
Location/Qualifiers
1. .927
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                       Carroll,M.W. and Myers,K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 3 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
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Sequence 57 from Patent WO02059377.
AX829164

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Sequence 3 from Patent EP1160323.
AX316088
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AX316088
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Canis sp.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Canis sp. (dog)
JP 2002530060-A/3
17-SEP-2002
18-NOV-1999 JP 2000582415
18-NOV-1999 GB 9901739.4 PR
JUL-1999 GB 9217395.4
MILES WILLIAM CARROLL, KEVIN ALAN MYERS
CI2N15/09, A61K39/00, A61K48/00, A61P35/00, CO7K7/06, CO7K14/065, C12N15/00,
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Polypeptide
Patent: WO 029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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AX025013
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PAT 17-JUL-2003
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis
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DP 2402530060-A/1.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homanalia; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1263)
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AX821548
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lauraslatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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Patent: WO 03068816-A 1 21-AUG-2003;

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Patent: WO 0238612-A 3 16-MAY-2002, Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 1 from Patent WO03068816.
AX821533 1 GI:39724929
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AX467373 from Patent W00238612.
AX467373 GI:21900603
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PAT 08-JUN-2001
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W., Bllard, F.M. and Myers, K.A.
Antibodies
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/note="5T4"
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other sequences; artificial sequences.
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Sequence 14 from Patent WO0136486.
AX149553 AX149553.1 GI:14347991
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Sequence 1 from Patent EP1160323.
AX316086.1 GI:17899278
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                                       1 AlailePheLeuLeuValLeuTyrLeu
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Best Local Similarity:
Query Match:
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AX149553
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AX316086
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Carroll, M.W. and Myers, K.A.

Polypeptide
Datenti JP 2002530060-A 1 17-SEP-2002;
OXFORD BIOMEDICA LID
OS Home sapiens (human)
DY 2002530060-A/1
DP 17-SEP-2002
PP 18-NOV-1998 JP 2000582415
PP 18-NOV-1999 JP 2000582415
PP 18-NOV-1999 GB 991799-4
30-JUL-1999 GB 9825303.2,27-JAN-1999 GB 9901739.4 PR 30-JUL-1999 GB 991799-4
PC CIZNIS,00, PC COTKI9/00, AGIK48/00,AGIP35/00,COTK7/06,COTK14/065,PC COTKI9/00,PC COTKIP/00,PC COTKI9/00,PC COTKIP/00,PC CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1263 | Continue | 1. .1263 | Continue | 1. .1263 | Continue | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 1. .1263 | 
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1. 1263
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/db_xref="taxon:9606"

    .1263
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AX025011
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Homo sapiens
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carroll, M.W. and Myers, K.A.
Polypeptide
Patent: WO 0029428-A 2 25-MAY-2000;
BIOMEDICA LID (GB)
ILOCATION/Qualifiers
1. .1281
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/mol_type="unassigned DNA"
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             Location/Qualifiers
1. .1281
/organism='Mus musculus (mouse)'.
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Matches:
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    1281
    /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

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Sequence 2 from Patent W00029428
AX025012
AX025012.1 GI:10184933
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                                                       Location/Qualifiers
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Mus musculus
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Mus musculus
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AX316087
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                             linear
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                             Myers, K., Drury, N. and Carroll, M. Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002,
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    1. .1263
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                                                                                                                                          AX467371 1263 bp
Sequence 1 from Patent WO0238612.
AX467371
  Gaps:
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                                                          1 AlailePheLeuLeuValLeuTyrLeu 9
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                              US-10-774-176-8 (1-9) x AX316086 (1-1263)
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Mus musculus (house mouse)
Mus musculus
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Carroll, M.W. and Myers, K.A.
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BD249732
BD249732.1 GI:33059502
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Best Local Similarity:
Query Match:
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Cancer

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/traislation="Meggcsropaagigrlrlarlalvilgwyssspyssasspssasspassasppraavsaqpplpdgcpalcecsraartvkcvnrnifevptdlpayvrnlfilgno
lavlpagafarrpplaelaalmisgsrldbyragafehlpsirqldlshnpladispf
afsgsnasysapsplublilnhivpbedbronrsfegwyvaallagralggirrlea
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LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLUVLYLNRKGIKKWMHNIRDAC
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                       Hominidae; Homo.

1 (bases 1 to 2053)

Myers, Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.

1 (solation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains leucine-rich repeats

J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                                                                                                                                                                                                           Submitted (16-DEC-1993) Myers K. A., Paterson Institute for (Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="placenta"
/clone lib="lambda gt11 library of J. Milan"
62. 372
/product="LRR N-terminal flank"
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/db_xref="InterPro:IPR001611"
/db_xref="InterPro:IPR001611"
/db_xref="UniProt/TrEMBL:Q13641"
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/product="LRR C-terminal flank"
           229083.1 GI:435654
5T4 gene; 5T4 oncofoetal antigen.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
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2 (bases 1 to 2053)
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Direct Submission
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misc_RNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                   Carroll,M.W. and Myers,K.A.

5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 2 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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PB Corporation (NY) (US)
Location/Qualifiers
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Matches:
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Matches:
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Query Match:
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HELIX RESEACH INSTITUTE
BELIX RESEACH INSTITUTE
OF HOME Sapiens (human)
PN JP 2002017375-A/2713
PD 22-JAN-2002
PP 72-JAN-2002
PP 77-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC C12P21/02,C12Q1/68//C12P21/08,G06P17/30,C12N15/00,C12NS/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                    3D127282 2359 bp DNA linear PAT 1 Primer for synthesizing full-length cDNA and use thereof.
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Sequence 2864 from Patent BP1396543.
CQ782724
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Location/Qualifiers
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JP 2002017375-A/2713.
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Homo sapiens
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Paarlasgsadppparcdadrecsrartykkynrillevpadlppyyrrnieltoro
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MRNRGLLDLTSSDLDCDATLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
                                                                                                                Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-MAY-1998) School of Biomedical Sciences, University
Of St. Andrews, Bute Medical Buildings, St. Andrews, Pife KY16 9TS,
UK
                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)

Rattus norvegicus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Ruarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

I (bases I to 233)

Ninkina, N. N. and Buchman, V.L.

Structure and expression of the rat 5T4 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
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                                  1483 GCTATTTTCCTCCTCGTTTTGTATTTG 1509
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US-10-774-176-8 (1-9) x HS5T4OA (1-2053)
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/gene="5T4"
364. .1644
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2315. .2320
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2 (bases 1 to 2333)
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Direct Submission
Submitted (125-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Bconomy, Trade and Industry of Japan; cDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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TLABLQGLPHIRVFLDNNPWVCDCHMADMVTWLKGTEVVQGKDRLTCAYPEKMRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLUXYLNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK074786 2359 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90305 fis, clone NT2RP2000694, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
Primers for synthesizing full length cDNA clones and their use
Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Homo sapiens (human)
Homo sapiens
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bul/1283 2361 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD127283
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases I to 2361)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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/note="cloning vector: pME18SFL3
mRNA_from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2714 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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organism="Homo sapiens"
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JP 2002017375-A/2714
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JP 2002017375-A/2714.
Homo Bapiens (human)
Homo Bapiens
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3 (bases 1 to 2361)
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                REFERENCE
AUTHORS
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                                                                                                   FEATURES
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APFLASAVSARPPLEDOCPALCECSRAATVKCVRRNITETDLARVRNIFELTGNO
LAYLPAGARPREPPLEDOCPALCECSRAATVKCVRRNITETGNO
LAYLPAGARPARRPPLANINGSSRIDEVRAGAFEHLFSLRQLDISHNPLADLSPP
AFGGSRASYGARSPYVALILAHI VPPEDERQRRSFEGHVVALLLAGRALQGIRKLELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNITHLESLHLEDNALKVLHNG
TLABLQGIPHRVPLDNNHWCDCHMDNWTWLKETEVVQGNORLTCAYPEKRNRYL
LELNSADLDCDPILPSSLQTPSYVEGIVLALIGAIFLKOMMINIRDAC
RDHMEGYHYRYEINADPRLTMLSSNSDV"
                                                                                                                                                                                       PAT 17-MAR-2004
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                               Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Primers for synthesizing full length cDNA clones and their use
Patent: EP 1396543-A 2866 10-MAR-2004;
Research Association for Biotechnology (JP)
                                                                                                                                                                                       linear
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Matches:
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note="unnamed protein product"
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                                                                                                                                                                                                         Sequence 2866 from Patent EP1396543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA"
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426. .1688
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Indele:
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                 Gaps:
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                                                                                     1 AlailePheLeuLeuValLeuTyrLeu
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                                                 US-10-774-176-8 (1-9) x BD127283 (1-2361)
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                         CQ782726
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Query Match:
DB:
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AX961916
                                                                                                                                                                     CQ782726
LOCUS
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AFSGSNASVSAPSPLVELILMHIVPPEDERQNRSFEGMVVAALLAGRALLQGIRRLELA
RHEFXLPRDVLAQLPSLERHIDLSNNSLVSITYVSFRNLTHIBSLHLEDNALKVLHNG
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LELNSADLDCDPILPPSLQTSYVPLGIVLALIGAIFLLGAIPKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV*
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highly similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Yamamoto,J., Wakamatsu,A., Kimura,K., Sakamoto,K., Hatano,N.,
Kawai,Y., Ishili,S., Saito,K., Kojima,S., Sugiyama,T., Ono,T.,
Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A.,
Okumura,K., Nagai,K., Sugano,S. and Isogai,T.
Signal Sequence and Keyword Trap in silico for Selection of
Full-Length Human cDNAs Encoding Secretion or Membrane Proteins
from Oligo-Capped CINA Libraries
DNA Res. 12, 117-126 (2005)
Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Staté activation gene
Staté activation gene
Patent: WO 03104277-A 127 18-DBC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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2361 bp mRNA linear PRI 09-J
Homo sapiens cDNA FLJ90309 fis, clone NT2RP2000903, highly s
to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
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oligo capping; fis (full insert sequence)
domo sapiens (human)
Homo sapiens
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Mismatches:
                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                            /mol_type="unassigned DNA"
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426..1688
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                                                                                                                                                                1. .2361
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                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAF06467.1"
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                                                                                                                              Location/Qualifiers
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WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center. Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Tpbg protein"
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TFAGSNVSVSTPSPLLBLILNHIVPPEDQRQNGSFEGWVAFEGWVAAALRSGLAIRGL
HHLELASNHFYYLPRDLLDQLPSLXHLDLRNNSLVSLTYASFRNLTHESLHLEDNAL
KHLNSTLAEMGGLAHVRYLDNNPWTDCYMADMVSWLKSTEVVPDKARLTCAFPEK
MRNRGLLDLTSSDLDCDATLPQSLQTSYVFLGIVLALIGAIFLIVYILNRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
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                                                                                                                                                                           Direct Submission
Submitted (02-DRC-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/Johne Ilb="NH MGC 234"
/Jab host="DH10g"
/note="Vector: pExpress1"
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Matches:
Conservative:
Mismatches:
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             numan and mouse cDNA sequences
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Director MGC Project.
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Strausberg 1 to 2011)
Klausner, R.D., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Roung, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Direct Submission
Subm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cloning vector: pME185FL3
mRNA from NT2 neuronal precursor cells after 2-weeks
retinoic acid (RA) induction"
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1527 GCTATTTTCCTCCTGGTTTTTGTATTTG 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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/clone="NT2RP2000903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AlailePheLeuLeuValLeuTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-774-176-8 (1-9) x AX074790 (1-2361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC087011.1 GI:56268819
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                                     TITLE
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

BC037161

ACCESSION

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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.D., Colling, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.B., Rubin, G.M., Hong, L.,
Stapleton, M., Soares M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunazatne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodersen, R.J., Lux, Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APFLASAVSAQPPLPDCCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFBHLPSLRQLDLSHNPLADLSPF
AFSGSNASVSAPSPLVELILMHIVPPEDERQNRSFBGMVVAALLAGRALGGLRRLELA
STRIPLYLPRDVLAQLPSLRHLDLSNNSLLYSFSVSFRNLTHLESLLHEDNALKVLHVG
TLAEL/GGLPHTAVFLINNPWVCDCHAADMVSLTVGKFRSTRVQGKORLTCAYPERKRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC058198 Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 IMAGS:533871), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,

Sciucognathi, Murcidea, Muridae, Musinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ST4 oncofetal trophoblast glycoprotein"
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/db_xref="GeneID:1162"
                                                                                                                          tissue type="Muscle, rhabdomyosarcoma"/clone Tib="NIH MGC 17"
/lab host="DH10B-R"
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427. .1689
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|db_xref="taxon:9606"
|clone="mGC:15317 IMAGE:4138906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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Matches:
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organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AlailePheLeuLeuValLeuTyrLeu 9
                                                                                                                                                                                                                                   'note="Vector: pOTB7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TPBG"
/codon_start=1
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BC058198.1 GI:34849573
                                                                                                                                                                                                                                                                  1. .2379
/gene="TPBG"
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

Is Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Rausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Rlausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Alsechul, S.F., Zeelbrg, B., Buerow, K.H., Schaefer, C.F., Bhat, N.K., Hokkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Dlatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stagleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEvan, P.J., Malek, J.A., Gunarathe, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butkerfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Generation and initial analysis of more than 15,000 full-length browns and marra, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Akhter,N., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiallo,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.

Location/Qualifiers
                                                                                                     2379 bp mRNA linear PRI 29-JUN-2004 Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317 BLMAGE:4138906), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (103-88P-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MgC help desk
Email: cgapbs-remeil.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
   1483 GCTATTTTCCTCCTCGTTTTGTATTTG 1509
                                                                                                                                                                                                                                                                         BC037161.2 GI:33872201
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

PEATURES

JOURNAL

TITLE

JOURNAL

REMARK COMMENT

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PAAFLASGSAQPPPARKCPAACECSRAARTVKCVNRNLLEVPADLPPYVRNLFLTGNQ
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TRIBLASNHFIFLFERDLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLBSLHHEDNAL
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MRNRGLIDINSSDLOCDAVLPQSLQTSYVETSIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
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                                                        COG4886, Leucine-rich repeat (LRR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene
Stat6 activation gene
Patent: WO 03104277A 123 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                                                                                                            1299. .1415
/gene="Tpbg"
/note="LRRCT; Region: Leucine rich repeat C-terminal
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Matches:
Conservative:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="unassigned DNA"
/db_xref="taxon:10090"
556. .1836
                                                                                protein [Function unknown]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1521 GCTATTTTCCTCCTCGTTTTGTATTTG 1547
                                                                                                                                                                                                                              /db xref="CDD:smart00082"
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|protein id="CAF06465.1"
|db_xref="G1:40881323"
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                                                        Region:
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                                                        /note="COG4886;
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100.0%
100.0%
100.0%
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Best Local Similarity:
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Best Local Similarity:
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       misc_feature
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-raemail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Maryland;
Web site: http://www.nisc.nih.gov/
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
TBurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGG:68145 IMAGB:5353871"
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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PAAFLASGSAQPPPAERCPAACECSEAARTVKCVNRNLLEVPADLPPYVRNLFLTGNQ
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TCELBASNHPLELPRDLARAQLDSLRYTDLRNBSLVSLYTASRRALTHESIHLESDNAL
KVLHNSTLARAQGLAHVALAQLDNPPWYCDCTWADMYMIKETEVVPDKARLTGAPPER
MRNRGLLDLNSSDLACDAVLPQSLQTSYVPLGIVLALIGAIFLLVLYLNRKGIKKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dlckson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854.
Location/Qualifiers
                                                                                                                                                                                                  2 (bases 1 to 2423)
Strausberg,R.
Direct Submission
Submitted (15-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD. 20892-2590,
                                                                                                                            human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIRDACRDHMEGYHYRYBINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |organism="Mus musculus"
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|strain="FVB/N"
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402...1682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Tpbg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="Tpbg"
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FEATURES

CDS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 32

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AX961914

Bource

FEATURES

CDS

AUTHORS TITLE

JOURNAL

REFERENCE

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Hashimoto, K., Kusuda, J. and Sugano, S.
Hashimoto, K., Kusuda, J. and Sugano, S.
Hashimoto, K., Kusuda, J. and Sugano, S.
Direct Submission

Bubmitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of
Submitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan
1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan
The International consortium for macaque cDNA sequencing and
analysis consists of: Department of Virology and Human Genome
Center, Institute of Medical Science, The University of Tokyo,
Tokyo, Japan, Division of Genetic Resources, National Institute of
Infectious Diseases of Japan, Tokyo, Japan, National Health
Research Institute, Taipei, Taiwan, Department of Roology,
Academia Sinica, Taipei, Taiwan, Department of Roology & Evolution,
University of Chicago, Chicago, Liu, USA; Center for Information
Biology, National Institute of Genetics of Japan, Mishima, Japan.
Clone distribution: clone distribution information can be found at:
http://www.nih.go.jp/yoken/genebank/
Lab host:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percor: pMRIBS-FL3 (Acc.No. AB009864)
R. Sitel: DraIII (CACTGTGTG)
R. Sitel: DraIII (CACTGTGTG)
R. Sitel: DraIII (CACCATGTG)
R. Sitel: DraIII alter of product was synthesized to caccate the DraIII sites of pMRIBS-FI3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Libraries were made from CACCATG CACCAG CACCATG CACCATG
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THETYLPROVLAQLPSLIKTLLGSNBLVSLTVSPRNLTHLESLHLESDALKVIHNG
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IELNSADLCOPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWHKNIRDAC
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LAVLPAGAFARRPPLAELAALNLSGSRLDEVRGGAFEHLPSLRQLDLSHNPLAYLSPF
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/note="unnamed protein product; Homo sapiens trophoblast
glycoprotein (TPBG), mRNA, RefSeq: NM_066670.3"
                                Osada,N., Hirata,M., Tanuma,R., Kusuda,J., Hida,M., Suzuki,Y., Sugano,S., Gojobori,T., Shen,J.C.-K., Wu,C.I. and Hashimoto,K. Substitution rate and structural divergence of 5'UTR evolution:
                                                                                                                                                       Comparative analysis between human and cynomolgus monkey cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Macaca fascicularis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDHMEGYHYRYEINADPRLTNLSSNSDV*
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                                                                                                                                                                                                Unpublished
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TITLE
JOURNAL
REFERENCE
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                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPAGSNASVSAPSPLEELILMHIVPPEDQRQNGSFEGWVAFEGWVAALRSGLALRGL
TRLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLBDNAL
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MRNRGLDLNSSDLOCDAVLPGSLOTSYVFGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLITHLSSNSDV"
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BNA sequences of macaque genes expressed in brain or testis and its evolutionary implications
Unpublished
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mtvlpagafargppladlealnlsgnhilkeycagafehlpglrrldlshippltnlsaf
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Stat6 activeLion gene
Patent: WO 03104277A 125 18-DEC-2003;
Asahi Kasel Kabushiki Kaisha (JP)
                                                                                                                                                                                                                                         linear
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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note="unnamed protein product"
                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                         AX961914 2557 bp DN
Sequence 125 from Patent W003104277.
AX961914
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    1 AlailePheLeuLeuValLeuTyrLeu 9
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DEFINITION

AB168308

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ACCESSION VERSION KEYWORDS SOURCE

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LAVLPAGAFARRPPLAELAALMLSGSRLDBVRAGAFEHLPSLRQLDLSHNPLADLSPF
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LELNSADLOCDPILPPSLQYSYVPLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
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AJ012160.
AJ012160.1 GI:3805948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                              /product="574 oncofetal trophoblast glycoprotein" 5331. .5336
5331. .5336
5380. .5385
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Direct Submission
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Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
AJ012159
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Submitted (13-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
                                                                                                                                                                                                                                                                                                                                              AJ012159.1 GI:3805946
5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Homo sapiens (human)
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Mismatches:
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Matches:
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HSA012159
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AP008208	Alignment Sco Pred. No.: Score: Percent Simil Best Local Si Query Match: DB:	Qy Db 82	RESULT 37 AP004082/C LOCUS DEFINITION ACCESSION VERSION	SOURCE	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL COMMENT

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18095. .19752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="minitssysriamdknykvalrgrranysllivvlpliilloidp
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    Genes were predicted from the integrated results of the following:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="hypothetical protein"
protein id="BAD22998.1"
db_xref="G1:48716389"
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//game="0.01149 C12.5"
complement (5014. .5134)
//game="0.01149 C12.5"
/note="3' terminal repeat"
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/clone="0J1149_C12"
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us-10-774-176-8.p2n.rge

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Q9P038 Q9Y4T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APFLASAVSAQPPLPPQCPALCECSBARTYKCVNRNIJTEVPTDLPAYVRNLFLTGNQ
LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPF
AFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNITHLESLHLEDNALKVLHNG
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                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 300); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                   http://www.sanger.ac.uk/HGP/Chr6
RP3-492P14 is from the library RPCI-3 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="trophoblast glycoprotein"
//product="trophoblast glycoprotein"
//note="match: E8Ts: AA149121 AA152323 AA565852 AA643734
AL544610 AW471072 AW662538 BE260099 BF2306457 BF306926
BF314984 B1956133 B1562387 BW069633 BW670613
match: cDNAs: AJ420536.1 Z29083.1"
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/note="maEch: proteins: Q13641 Q9QXD9 Q9Z0L0"
/codon_start=1
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join(109639. .109916,110631. .116836)
/gene="TPBG"
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/protein_id="CAI21546.1"
/db_xref="GI:56203539"
Further information can be found at
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complement(10004. ..10982)
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109639. .116836
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/db_xref="InterPro:IPR01611"
/db_xref="InterPro:IPR003591"
/db_xref="UniProt/TrEMBL:Q13641"
                                                                                                                                                           Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .10982)
                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="q13-15"
/clone="RP3-492P14"
/clone_lib="RPCI-3"
100
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                                                                                                                                                                                                                                                                             Contact: vega@sanger.ac.uk
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                                                                                                                                     VECTOR: pCYPAC2
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
BMB: SWB: SWISSPROT; Tr:, TREMBL; Wp:, WORWDEP; Information on the WORMPEP database can be found at
                                                                                                   GPKPLNAILKRKREADSGNATDFGSKREEHSGGDEEGSQNDFRNIEDDIVGMATEGNG
BRAFQPEDDVYGDSLESPADDIAABAADDASRELEBGQDVETAEBYDYEMDDVNAAEB
NDYQSYEDBDDLEDDDDFARKVGWNIT"
complement (32006. 33785)
/gene="OJ1149 C12.9"
/gene="OJ1149 C12.9"
/gene="OJ1149 C12.9"
/note="SUDDOTEGD by full-length cDNA(8): AK098955"
/complement (join(32120. 32537,33266. 33783))
                      QRILIKQRRLINNPRSGQVSDRHNVYPEDERHDRHRQRGERQASNDGVSSSRLRGRIRLP
AETTFDRLGLQPEKERDRGPRARLSPPSQTDLRGKLHDRLKAKPNEDVSGNVQSSLSK
ANEDABSLNPAGPKSLAELKAKKVAGSLMKSSRSLTGPVRMTSEIVTIKDSSDPVLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="Migraiggvagalplvlertrycypppwamtplhhycspprpp
opspslshspcaaadddppptvdydpbeekkeedregspwegavvyrrdasvhhleyat
tleriglgdlssthsraraatwgililsstnitgtkoddtpvlvsldvarrgrirld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIVRTVITLGCYGCAEPAPQGI FANPSLLLTEDRVEEPDVVDLGTI PEERQTKAPSLT
GSQEDGDDEDIDWDDRLHPPAGEKEIDISKHIRDI HILBITLDALCSPTCKGLCLGCG
ENLNTSSCSCNAEKQQAKNVQRRGPLKDLLKPLQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSJ492P14 18-MAY-2005 Husan DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RP3-492P14 on chromosome 6413-15 Contains a single stranded DNA binding protein pseudogene, the TPBG gene for trophoblast glycoprotein (574-AG) and a CpG island,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
/translation="MLRQTHDSYGFERSHRGSAEKLLSESRFSQREPMPLTADSSDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (36443. .40501)
/gene="OJ1149 C12.10"
complement (join(36443. .36783,36987. .37068,37163. .37200,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                    /gene="OJ1149 C12.9"
/note="contains full-length cDNA(s): AKO61847,AK098955
similar to Oryza sativa chromosome 4, OSJNBb0085F13.19"
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="unknown protein"
/protein_id="BAD23002.1"
/db_xref="GI:48716393"
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HTG; CpG island; TPBG.
Homo sapiens (human)
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1 (bases 1 to 121909)
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Best Local Similarity:
Query Match:
DB:
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VERSION
KEYWORDS
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JOURNAL
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                                                        FEATURES
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Direct Submission

Direct Submission

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 128, UK. B-mail enquiries: vega@anger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em: FMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPRP; Information

on the WORMPEP database can be found at

http://www.aanger.ac.uk/Projects/C elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping

Group. Further information can be found at

http://www.aanger.ac.uk/HGP/Chr6

RPII-31N4 is from the library RPCI-11.2 constructed by the group

of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALS89666 129010 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RP11-32.N4 on chromosome 6 Contains the 3' end of the gene for sorting nexin 14 (SNX14), the 3' end of the NTSE gene for 5'-nucleotidase, ecto (CD73) and a novel gene, complete sequence.
TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKMRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
mammalla; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 129010)
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Matches:
Conservative:
Mismatches:
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116836
                                                                                                                                                                                                        /locus_tag="RP3-492P14.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112071 GCTATTTTCCTCCTGGTTTTGTATTTG 112097
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VECTOR: pBACe3.6
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Gaps:
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HTG; NTSB; nucleotidase; SNX14.
HOmo sapiens (human)
Homo sapiens
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                                                                                                                                                                                  /gene="TPBG"
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                                                                                   polyA_signal
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join(AL135903.12:164584. .164922,11372. .11594,15549. .15737, 29547. .29744,31647. .31801,33806. .33911,34820. .34969, 36289. .36489,38153. .38316)
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32289. .36489,38153. .40090)
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29547. .29744,31647. .31801,33806. .33911,34820. .34969,
36289. .36489,38153. .40090)
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STREF PLERNMCTITMENLANLPFGGFDED VOLKGSFLIKAR FEHSVHSYGGSTGBFL
QVGGTHVVVDLSRKEGDRVVKLDVLCTKCRVDS YDELKADBVYKVI LLPWFLANGGDGF
OMI KDELLRHDSGDQD INVVSTYI SKMKVI YPAVEGRI KFSTGSHCHGSF8LI FLSLM
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   confirmed by restriction digest,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="march: proteins: SNTD BOOMI SNTD BOVIN SNTD DISOM SNTD HARIN SNTD HUMAN SNTD LÜTLO SNTD MÖUSE SNTD RÄT AAKR9580 APV AEDAE CAD28125 CAD28126 034313 Q05700 Q95P65 Q96B60 Q9U9I6 Q9V824 Q9V233" /codon_start=1
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BB547456 BB891902 BC294369 BI756281 BM006258 BM762339
BM847311 BM926263 BM937597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="RP11-321N4.1-002"
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AW271686 BE677446 BF476532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            match: cDNAs: BTSNUC DOSNUCLT HS5NUASB MMBSNA RNSRPHP S64302"
one subclone, and the assembly was confirmed by restrexcept on the rare occasion of the clone being a YAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="RP11-321N4.1-002"
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AC158516 167046 bp DNA linear ROD 21-JUN-2005
Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
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Direct Submission
Submitted (21-JUN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On May 4, 2005 this sequence version replaced gi:61656412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases I to 167046)
Wilson, R.K.
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Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
join (complement (AL136082.22:8981. .9287), complement (118570. .118680), complement (116610. .116686), complement (116149. .116527), complement (102288. .1102372), complement (102288. .102372), complement (91618. .91862), complement (9213. .92688), complement (91818. .91862), complement (91629. .91709), complement (91424. .91538), complement (87917. .88072), complement (87494. .87618), complement (87914. .91538), complement (177911. .78112), complement (77914. .75744. .75744), complement (77918. .7674), complement (76380. .76549), complement (76380. .62360),
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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1 (bases 1 to 167046)
Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
2 (bases 1 to 167046)
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Matches:
Conservative:
Mismatches:
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Contact: submissions@watson.wustl.edu
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Center project name: M_BB0511A23
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AC158516 AC117768
AC158516.2 GI:63025421
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Best Local Similarity:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                           /locus tag="RPI1-321N4.1-003"
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WENLAWLPFCGTPLOVQLKGSTLKKAPEHSVHRYGGSTGEFLQVGDLKECCPICINQ
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db_xref="G05.05302"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |locus tag="RP11-321N4.1-003"
|standard_name="OTTHUMP00000016810"
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|standard_name="OTTHUMP0000016811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="GOA:Q5JRQ1"
'db_xref="UniProt/TrEMBL:Q5JRQ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="RP11-321N4.1-002"
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/locus_tag="RP11-321N4.1-001"
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15881. .15886
/gene="NT5E"
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assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
>=30); an attempt was made to resolve all sequencing problems, such
                                                   as compressions and repeats; all regions were covered by at least one plasmid subcitone, fosmid chome or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         minimal
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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu MAPPING INFORMATION:

The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org SOURCE INFORMATION:

/chomosome="RE24-511A23"
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/clone="RR24-511A23"
/clone="Lib="RPCI-24"
/loote="Sequence derived from PCR product of genomic DNA"
31565: 313779
/note="Unresolved simple sequence repeat." 142336. 142347 /note="Sequence derived from one plasmid subclone." /note="Unresolved simple sequence repeat." This sequence is the entire insert of the clone. organism="Mus musculus" |mol type="genomic DNA" |db\_xref="taxon:10090" Location/Qualifiers 1. .167046 misc\_feature unsure source ungure ungure PEATURES

0000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 2.57e+04 41.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: .. 9 Score:

ORIGIN

TITLE

US-10-774-176-8 (1-9) x AC158516 (1-167046)

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ACIS5741 208985 bp DNA linear HTG 01-JUL-2005 Bos taurus clone CH240-40N24, WORKING DRAFT SEQUENCE, 13 unordered Bos taurus pieces. AC155741/c LOCUS VERSION KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia; AC155741.2 GI:68265036
AC155741.2 GI:68265036
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.
BOS taurus (cow)

COMMENT

HTG 01-JUL-2005

Tecudar Dovinace; Dovinace Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 28, 2005 this sequence version replaced gi:57900766.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig-scaffold individual sequence contigs are ordered and orlented, and separated by sized gaps filled with Ns to the estimated size. The sequence Submitted (19-JAN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Cow Genome Sequencing Consortium. (bases 1 to 208985) (bases 1 to 208985) Submission Unpublished Worley, K.C. REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL REPERENCE AUTHORS JOURNAL REFERENCE

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No.:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                      * NOTE: Bstimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                      Assembly program: Atlas 3.0;
Consensus quality: 203744 bases at least Q40
Consensus quality: 205219 bases at least Q30
Consensus quality: 206413 bases at least Q30
Estimated insert size: 209875; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                     Center: Baylor College of Medicine
                                                                                                                                                                                             Center clone name: CH240-40N24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
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206827
206927
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PEATURES

gap gap

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Anyalebera 1 to Jacks 1. Alabrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, H., Bardaranaike, D., Barder, M., Bardar, E., Baderi, H., Baldwin, D., Bandaranaike, D., Barder, M., Bardared, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bundar, C., Cavazos, I., Cassar, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, M., Davas, C., Davis, C., Pan, G., Fernandez, S., Pane, C., Panse, C., Fernandez, S., Pane, C., Panse, C., Fernandez, C., Ragen, C., Coyle, M., Cree, A., Garcia, A., Hanilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Haries, S., Hladu, S. L., Hodgeon, A., Hornandez, J., Haries, S., Hladu, S. L., Hodgeon, A., Hornandez, J., Jackson, L., Jacko, H., Levan, J., Levis, L., Liu, Y., London, P., Longacre, S., Lopez, J., Luu, J., Luu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Luu, J., Luu, M., Maholu, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACL128294 210237 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE.
AC128294
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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Query Match:
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SOURCE
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FEATURES
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Submitted (19-Nov-2002) Human Genome Sequencing Center, Department
Submitted (19-Nov-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23265004.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
                               Pasternak, S., Paull, Percez, A., Pfannkoch, C., Plopper, P., Poindexter, A., Popovic, D., Primus, B., Pul. -L., Plopper, P., Poindexter, A., Popovic, D., Primus, B., Pul. -L., Plopper, P., Rachlin, B., Revers, K., Redier, M.A., Reigh, R., Railly, B., Ratilly, Renter, M., Richards, S., Rigs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Socht, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Waldron, I., Waldron, I., Walder, B., Wang, J., Waldron, I., Walder, B., Wang, J., Waldron, D., Walder, R., Wal
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NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. App between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 210237)
3 (bases 1 to 210237)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: CH230-176H20
Center clone name: CH230-176H20
Assembly program: Phrap; version 0.990329
Consensus quality: 201781 bases at least Q40
Consensus quality: 203921 bases at least Q30
Consensus quality: 205310 bases at least Q30
Estimated insert size: 205531; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 20237: contig of 210237 bp in length.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forley, K.C.
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE AUTHORS TITLE JOURNAL

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is loades 10. Albacoks, S., Amin, A., Angulano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
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BOB taurus clone CH240-40B14, *** SEQUENCING IN PROGRESS ***, 20
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIS6733.2 GI:68265384
HTG; HTGS_PHASE1; HTGS_BRAPT; HTGS_ENRICHED.
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                                                                                                                                                                                                                                                                                                                                                                       end_sequence:BH360464"
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1 (bases 1 to 218269)
                                                                                                                                               clone="CH230-176H20"
Location/Qualifiers
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Bos taurus
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Best Local Similarity:
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of 6450 bp in length unknown length of 30184 bp in length

of 6763 bp in length

17189 bp in length

2056 bp in length 50 bp of 7548 bp in length 8204 bp in length

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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                               47698: contig of 47698 bp in length
47748: gap of 50 bp
53619: contig of 5871 bp in length
53669: gap of 50 bp
58241: contig of 4572 bp in length
65054: contig of 6763 bp in length
65104: gap of 50 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6: contig of 3925 bp in length
6: gap of unknown length
9: contig of 1033 bp in length
9: gap of unknown length
9: contig of 2070 bp in length
9: gap of unknown length
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gap of 50 bp
contig of 15342 bp in length
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/estimated length=50
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gap of unk
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/organism="Bos taurus"
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/estimated_length=50
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The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submission
Direct Submission
Direct Submission
Of 303-FBB-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 218269)
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Consensus quality: 213025 bases at least Q30
Consensus quality: 214500 bases at least Q20
Sstimated insert size: 217823; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
Web alte: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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COMMENT

50 bp of 29867 bp in length

50 bp

14091 bp in length

50 bp of 140

1119 bp in length

unknown length of 1522 bp in length

/estimated length=50

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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
unocéared pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                      218269
9
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                        /estimated_length=unknown
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                                                                                                                                                                                                         'estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                        5727 decarrirecrierierecreratecrie 5701
                                                                                                                                                                                                                                                                                                                  Gaps:
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                                                                                                                                                                                                                                                                                                                                          US-10-774-176-8 (1-9) x AC156733 (1-218269)
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                                                                                    /estimated_length=50
                       .161304
                                               191172. .191221
                                                                                                                                             11590. .211689
                                                                                                                                                                                            15382. .215481
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                                                                                                                                                                                                                                                      3.21e+04
41.00
100.0%
100.0%
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Query Match:
                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                         No.
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Direct Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:22857070.

The sequence in this sequence version replaced gi:22857070.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.edu/projects/rat/). Rach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martin, R., Mangum, B., Mapua, P., McMeill, T. Z., Meenen, B., Milosavijevic, M., Miner, G., Minja, E., Meenen, B., Milosavijevic, Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parke, K., Parez, L., Petankoch, C., Pasternak, S., Paul, H., Perez, L., Petankoch, C., Plopper, P., Pouldexter, A., Popovic, D., Primus, B., Pu, L. -L., Plopper, P., Poindexter, A., Popovic, D., Primus, B., Pu, L. -L., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shep, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, R., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Riggs, F., Shartenen, S., Scherer, S., Socht, G., Shatteman, S., Shen, H., Shetty, J., Shvartebeyn, A., Scherer, S., Sochle, G., Shatteman, S., Shen, H., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C. Taylor, T., Thomas, N., Thomas, D., Walder, M., Walker, B., Wang, J., Warren, C., Walles, R., Warren, J., Warren, R., Weits, R., Walco, L., Yoon, L., Yoon, V., Wright, D., Wright, R., Wu, J., Zakou, S., Dunn, D., Von Niedezhausern, R., Weise, R., Smith, D.R., Smith, R., Neller, R., Weinstock, G. and Gibbs, R.A.
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: ngsc-help@bcm.tmc.edu
Conter project Information
Center project name: GQPI
Center clone name: CH230-87110
Center clone name: CH230-87110
Center clone name: CH230-87110
Consensus quality: 232269 bases at least Q40
Consensus quality: 232269 bases at least Q30
Consensus quality: 234041 bases at least Q20
Consensus quality: 234041 bases at least Q20
Consensus quality: 234041 bases at least Q20
Consensus quality: 24041 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission

Burnetted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Bases I to 239076)

Rat Genome Sequencing Consortium.
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Center code: BCM
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Treponema pallidum subsp. pallidum str. Nichols section 86 of 87 of the complete genome.
AE001270 AE000520
AE001270.1 GI:3323350
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                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser,C.M., Noriss,S.J., Weinstock,G.M., White,O., Sutton,G.G., Dodson,R., Roriss,S.J., Weinstock,G.M., White,O., Sutton,G.G., Sodson,R., Gwinn,M., Hickey,E.K., Clayton,R., Ketchum,K.A., Sodsorgren,B., Hardham,J.M., McLeod,M.P., Salzberg,S., Peterson,J., Khalak,H., Richardson,D., Howell,J.K., Chidambaram,M., Pujii,C., Garland,S., Hatch,B., Horst,K., Roberts,K., Watthey,L., Weidman,J., Smith,H.O. and Venter,J.C.
Direct Submission
Submitted (06-WAR-1998) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
1
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0
0
                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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complement (79. .1446)
complement (79. .1446)
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                                                                                                           40.00
100.0$
88.9$
97.6$
                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                 Scores:
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LOCUS
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REFERENCE
AUTHORS
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                                                                                                                    Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UHAS18259 387 bp DNA linear ENV 05-DEC-2003
Unidentified bacterium partial 16S rRNA gene, clone Mul2P2-78.
AJ518259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (18-NOV-2002) Bleul C., Institute for Medical
Microbiology, Dresden University of Technology, Fiedlerstrasse 42,
Dresden, 01307, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wobus, A., Bleul, C., Maassen, S., Scheerer, C., Schuppler, M., Jacobs, E. and Roske, I.
Marcobial diversity and functional characterization of sediments from reservoirs of different trophic state
FEMS Microbial. Ecol. 46 (3), 331-347 (2003)
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                            1 234710: contig of 234710 bp in length
1711 234810: gap of unknown length
1811 235924: contig of 1114 bp in length
1825 236024: gap of unknown length
1825 237314: contig of 1290 bp in length
1835 237414: gap of unknown length
1835 239076: contig of 1662 bp in length.
1939076
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /environmental_sample
/country="Germany:Saxony"
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/gene="16S rRNA"
<1. .>387
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Best Local Similarity:
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IESERQYRFEQILAVTFTNKAAREMETRACALESAAGGATICTFHALGYWILRRYAVRL
GINPHESIYDDHUNRALLEKILPHCHERAGHLAGGAGGATICTFHALGYWILRRYAVRL
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FVSYVRHEHTGELEWYRQNDEREGTGCAWNAGILGERRYDDALGERRYLMYVACT
RAMDSLYLTAACAYFRRWGRHTAMRPSRFLTELDSALLEITDPRHFR"
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PTGAGCVTAARPAPSSGRQGGGGALYLQFSVRRGSFVSPRAFRAAAQRTCPFSWHRIM
SARNV"
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PID:43242 percent identity: 39.18; identified by sequence
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LILGATVVIATAGAIRPGSYSKRAAPVERPRAVDGTYTVALAIGHAEDVQYRHALGYVQC
KDNFYGQHSPHTMPHAELTQKWHANIACNTLASEKESAALFVLGSVRRVRTGAVLLV
IGNOTRRAGGLEDIQVHDTENAIRVAVBAVKLLITQDSPR*
SRVAYTHLSTLTGAAPYASITPTAYAEAWHDYCVLCSRGGSEPFMRLLATANLHNPFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MESYLSALNEAQRQAVCHYGSPLLILAGAGSGKTRVITTKIAHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein; identified by Glimmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="hypothetical protein; identified by Glimmer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC65978.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6064. .8076)
/gene="TP1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (8159. .8845)
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complement (8864. .9361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (6064. .8076)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (8159. .8845)
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                                                                                                                                                                                                                                                            similarity; putative"
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/transl_table=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="TP1030"
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                                                                                                                                 5272. .6048
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COMPlement (2520. . 2948)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="TP1025"
note="similar to GB:AE000783 percent identity: 54.35;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to SP:P07842 percent identity: 54.47; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="ribosomal protein L13 (rplM)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         producE="ribosomal protein S9 (rpsI)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="TP1024"
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transI tabl
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CDS

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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Bloom, T., Boguslavkiy, L., Arachchi, H.M., Barna, N., Bastien, V.,

Bloom, T., Boguslavkiy, L., Cook, A., Cooke, P., Corum, B.,

Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,

Dakrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,

Brickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,

Galagan, J., Gardyna, S., Graham, L., Grand-Plerre, N., Hafez, N.,

Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,

Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,

MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,

Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Micol, R., Norbu, C.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pterre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.,

Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Zimmer, A., and Zody, M.,

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                         Sirren, B., Innton, L., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brown, A., Camazata, J., Campoplano, A., Chang, J., Chagaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacCanth, M., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKwan, P., McKernan, K., Meldrim, J., Matchews, C., McCarthy, M., McRwan, P., McKernan, K., Meldrim, J., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollaray, V., Raymond, C., Reta, R., Ribesck, M., Riley, R., Rise, C., Schupback, R., Stange-Thomann, N., Schupback, R., Stange-Thomann, N., Strauss, N., Strauss, N., Spencer, B., Stange-Thomann, N., Strouss, N., Strauss, N., Strauss, N., Travis, N.,
                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 16448)
Birren, B., Nusbaum, C. and Lander, B.

Mus musculus chromosome 15, clone RP24-137J5
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                                                                                                    Mus musculus (house mouse)
                                           AC121542.8 GI:54606954
                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 164489)
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
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AUTHORS
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JOURNAL
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Mus musculus chromosome 15, clone RP24-137J5, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS AY596297 Accession AY596297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4000
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AC163932 212987 bp DNA linear HTG 01-JUL-2005
Bos taurus clone CH240-107F10, WORKING DRAFT SEQUENCE, 9 unordered
pieces.
AC163932
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complement(1558..15672)
/rpt_family="55"..16040)
complement(15917..16040)
/rpt_family="RLTR9C"
16043..16401
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17740_.17789
/rpt_family="Ar_rich"
complement(17790..17903)
/rpt_family="RMERIB"
17921_.17981
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                                                                                                                                                                                                                /rpt_family="(CAAAA)n"
complement(10591..10752)
/rpt_family="L1_MM"
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rpt family="Lx6"
2945. .13038
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complement (13055. .13284)
rpt family="Lx6"
3333. .14048
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rpt family="MIR"
.4835. .15021
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rpt family="RSINB1"
5456. .15491
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                              /rpt_family="LiP5"
9257. .9301
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   complement (8429. .8775)
/rpt family="LiP5"
complement (8810. .9256)
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2010. .12217
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                                                                           /rpt_family="(CA)n"
9301. .9347
                                                                                                                                                                                  rpt family="ORRID"
0298. .10371
                                                                                                                /rpt family="(TA)n"
complement (9302. .99
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6689. .16868
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6614. .16670
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Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., MacCarthy, M., Maldrim, J., Meneus, L., Mihova, T., Marga, V., Murphy, T., Naylor, J., Manwer, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Romann, J., Schauer, S., Schupback, R., Seaman, S., Schuer, F., Samann, S., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Mu, X., Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'clone="RP24-137J5"
'clone_lib="RPCI-24 Male Mouse BAC"
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complement (752...1481)
/rpt family="(TTTC) n"
complement (752...1481)
/rpt family="L1_MM"
1481...1569
1554...259
/rpt family="L1"
2554...259
/rpt family="NTD"
2659...2820
/rpt family="MTD"
2825...2899
/rpt family="MTD"
3866...3745
/rpt family="MTD"
3866...3745
/rpt family="MTB"
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3807. .3888

3867. .3888

7rpt family="(T)n"

4393. .4499

7rpt family="RSINE1"

4512. .4586

7rpt family="CA)n"

complement (5848. .5956)

6357. .458
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/rpt family="Lx8"
complement (7993. .8292)
/rpt_family="LIMA9"
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/db_xref="taxon:10090"
/chromosome="15"
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Center clone name: 137_J_5
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78. .751
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family="PB1D7"
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Submitted (15-UUN-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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On Jun 29, 2005 this sequence version replaced gi:67763874.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
AC163932.2 GI:68300994
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Bos taurus (cow)
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Cow Genome Sequencing Consortium.
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2 (bases 1 to 212987)
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                                                                                                      Bos taurus
                                                                                                   ORGANISM
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(http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as mins of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Alias 3.0;
Consensus quality: 209389 bases at least Q40
Consensus quality: 210366 bases at least Q30
Consensus quality: 211128 bases at least Q20
Estimated insert size: 212035; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
and whole genome shotgun sequencing reads assembled using Atlas
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85396: gap of 50 bp
102085: contig of 16689 bp in length
102135: gap of 50 bp
211461: contig of 109326 bp in length
211561: gap of unknown length
212987: contig of 1426 bp in length
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gap of 294 bp
contig of 17901 bp in length
gap of 50 bp
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of 10867 bp in length
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                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine
Center code: BCM
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Center project name: PHP
Center clone name: CH240-107F10
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/db_xref="taxon:9913"
/clone="CH240-107F10"
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56235. 56528
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102086. .102135
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NOTE: This record contains 74 individual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC101062 63024 bp DNA linear HTG 23-NOV-2001
Mus musculus clone RP23-87F10, LOW-PASS SEQUENCE SAMPLING.
AC101062
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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------ Project Information
Center project name: L14879
Center clone name: 87_P_10
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                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/estimated_length=50
211462. .211561
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HTG; HTGS PHASEO.
Mus musculus (house mouse)
Mus musculus
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AUTHORS
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                          contig of 756 bp in length gap of 100 bp contig of 772 bp in length gap of 100 bp gap of 100 bp contig of 769 bp in length gap of 100 bp gap of 100 bp contig of 739 bp in length gap of 100 bp gap of
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## ALIGNMENTS

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Mouse spliced transcript detection oligonucleotide SEQ ID NO:29022.
                  ABN56274 standard; DNA; 65 BP.
                                                                                                          (first entry)
                                                                                                          15-JUL-2002
                                                                 ABN56274;
ABN56274
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Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library, ss.

20-JUL-2001, 2001WO-IB001903. 28-JUL-2000; 2000US-0221607P. WO200210449-A2. Mus musculus 07-FEB-2002. 

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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcribtome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several cligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The cligonucleotide libraries are useful for detecting mRNAs from a cultiple contactively or projected sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptom, and in detecting RNA transcripts and splice variants of human or animal contactions. The libraries may also be used as specialised minical contaction of the libraries to detect transcripte of a sub-transcriptom under a particular biological or pathological state, and so allowing the detection of tissue contaction or pathological state, and so allowing the detection of tissue contacts or pathological state, and so allowing the detection of tissue considered a specific genes such as those genes only expressed in specific genes; and to detect RNA transcriptom of a transcriptom of a transcriptom of a partient specific genes; and to detect the sequences from disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from crass, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format contactly from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                  New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                         Faigler S;
                                                                                                         Mintz L,
                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 29022; 47pp; English
                                                                                                            Mintz B,
02-MAY-2001; 2001US-0287724P
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                                                                                                            Shoshan A, Wasserman
                                                      (COMP-) COMPUGEN INC.
                                                                                                                                                            WPI; 2002-257383/30.
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Sequence 65 BP; 9 A; 21 C; 12 G; 23 T; 0 U; 0 Other;

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      Length:
Matches:
Conservative:
Mismatches:
                                      Indels:
     0.783
43.00
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                   Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
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US-10-774-176-7 (1-9) x ABN56274 (1-65)

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Human colon cancer cell expressed cDNA #6082. BP. ACD97670 standard; cDNA; 108 23-SEP-2003 (first entry) ACD97670; RESULT 

Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; gene; ss.

Homo sapiens.

RESULT 3

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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonuclectide primer (1) at low stringency, preparing with a single oligonuclectide primer; (1) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (1), amplifying contacting the product, and repeating the contacting, preparing contected and string steps with different primers and sequencing resulting muclectide sequence from a genome of an organism corresponds to an uncleotide sequence from a genome of an organism corresponds to an uncleotide sequence from a genome of an organism, mNAA is obtained from mammalian of nucleotide sequence of an organism mNAA is obtained from mammalian of nucleotide sequence of an organism mNAA is obtained from mammalian or hundle of an organism mNAA is obtained from mammalian or hundle or nucleotide sequence of an organism mNAA is obtained from mammalian or hundle or nucleotide sequence of an organism mNAA is obtained from mammalian or hundle or nucleotide sequence of an organism mNAA is obtained from mammalian or hundle of an organism. MNAA is obtained from mammalian conductions of subjects and can be used to carry our genetic analyses of large or small populations. further, it can be used to study living systems to determine if e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with an individual or population more or less likely to be afflicted with the study of whether the conditions are likely to be passed to offending through over or sperm. The analyses for pathological conditions can be strucked to determine if resistance genes are present, defects in plant connective out in all animals, plants, birds, fish, etc. Using this method is also applied to eukaryotic pathogens, such as retroviruses and other integrating viruses such as introvaries and other integrating viruses such as retroviruses and other integrating viruses such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 866; 959pp; English.
                                                                                                                                                                                          99US-00406117.
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                                                                                                                                                                                                                                                                                                                                                                                     SIMP/) SIMPSON A J G.
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(BREN/) BRENTANI R R.
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US2002155438-A1
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                                                                                               24-OCT-2002
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G; 35 T; 0 U; 0 Other Sequence 108 BP; 18 A; 33 C; 22

108 000 000 000 Length: Matches: Conservative: Mismatches: Indel8: 1.39 43.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-10-774-176-7 (1-9) x ACD97670 (1-108)

60 recenseaacererransferences 86 σ SerLeuGlnThrSerTyrValPheLeu

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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess DNA encoding novel human diagnostic protein #22978 AAS87174 standard; cDNA; 453 BP. 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT; (first entry) Drmanac RT, Liu C, WPI; 2001-639362/73 (HYSE-) HYSEQ INC P-PSDB; ABG22987 WO200175067-A2 blodiversity. Homo sapiens 13-FEB-2002 11-OCT-2001. AAS87174; 

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed carivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The copypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the constant of the product of the prod Claim 1; SEQ ID NO 22978; 103pp; English.

and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 453 BP; 108 A; 111 C; 113 G; 121 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: 43.00 100.0% 100.0% 100.0% 6.99 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Score:

US-10-774-176-7 (1-9) x AAS87174 (1-453)

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The invention describes a method comprising comparing an expression profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood monouclear cells (BMMCs) of a first class of patients as compared to PBMCs of a second class of patients, where continued the first and second classes is a subcluster formed by an ansuparvised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome. Also described are a system comprising (1) a memory or a curcome. Also described are a system comprising (1) a memory or a storage medium including data that represent an expression profile of at least one gene in a peripheral blood sample of a patient who has a solid tumour, (ii) at least one mother storage medium including data that represent a least one peripheral blood sample of a patient who has a solid tumour, (iii) at least one peripheral blood sample of a patient who has a solid tumour capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the program; where expression levels of the genes, where comparinang concentrated probes for solid tumour prognosis genes is differentially expressed in peripheral blood sample of a second class of patients who have the solid tumour prognosis genes is differentially expressed in peripheral where a solid tumour prognosis genes is differentially expressed in contentrated probes for solid tumour prognosis genes is differentially expressed in peripheral where the first class of patients has a second class of patients has a second class of patients as old tumour, and where the first class of patients has a second class of patients and intention, system, and array are useful for prognosing gene of the invention. No
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                                                                                                                                                                                                                                                                                                           cytostatic, gene therapy, expression profile, solid tumour, peripheral blood mononuclear cell, PBMC; prognosis, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trepicchio WL, Burczynski ME, Dorner AJ;
                                           238 rcccrccaaaccrcrrargrcrrccrc 264
1 SerLeuGlnThrSerTyrValPheLeu 9
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23-JAN-2004; 2004US-0538246P.
                                                                                                                                  ADU11677 standard; DNA; 475
                                                                                                                                                                                                                         (first entry)
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(STRA/) STRAHS A.
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Immerman F,
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/note= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids"
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encode any
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                                                                                                                                                                                                                                                                                                                                                                                               Canine, TAA, tumour-associated antigen, anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note="given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids"
of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= f
/note= "given in the specification but does
be part of the coding sequence and does not
corresponding amino acids"
                                        Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other;
                                                                               Conservative:
Mismatches:
Indels:
Gaps:
                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                    Canine 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                      1 SerleughnThrSerTyrValPheLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product= "5T4 antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                             US-10-774-176-7 (1-9) x ADU11677 (1-475)
                                                                                                                                                                                                                                                                                      AAA27060 standard; DNA; 901 BP
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43.00
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BP.

ABT07721 standard; DNA; 927

RESULT 6 4BT07723

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The present sequence encodes the canine 574 tumour-associated antigen (TAA). The TAA 574 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were incoulated with a virus expression vector containing the human or murine 574 gene sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elicit an immune response, preferably CTL or an antibody response in a
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                                                         be part of the coding sequence and does not encode any corresponding amino acids"
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/ore= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids"
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be part of the coding sequence and does not
corresponding amino acids"
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be part of the coding sequence and does not
corresponding amino acids"
corresponding amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-00025303.
99GB-00001739.
99GB-00017995.
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                                                                                             644. .653
                                                                                                                                                                                                                                                   784. 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY94351
                                                                                                                                                                                                                                                                                                                                                 WO200029428-A2
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27-JAN-1999;
30-JUL-1999;
              misc_feature
                                                                                          misc_feature
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Sequence 901 BP; 178 A; 246 C; 212 G; 153 T; 0 U; 112 Other; 00000 Length: Matches: Conservative: Mismatches: Indels: 15.2 43.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: Score:

US-10-774-176-7 (1-9) x AAA27060 (1-901)

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608 TCCCTGCAGACTTCTTATGTCTTCCTA 634
 σ
SerLeuGlnThrSerTyrValPheLeu
н
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Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast
                                                                       Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
                                                      Breast cancer-associated gene sequence 29
                                                                                                                                                                            24-JAN-2001; 2001US-0265928P.
02-FEB-2001; 2001US-0265928P.
09-APR-2001; 2001US-00829472.
09-APR-2001; 2001US-0282698P.
04-MAY-2001; 2001US-0288590P.
29-MAY-2001; 2001US-0288590P.
                                                                                                                                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                           24-JAN-2002; 2002WO-US002242
                                                                                                                                                                                                                                                                  Afar D;
                                                                                                                                                                                                                                                                                                                                            cancer nucleic acids
                                                                                                                                                                                                                                                                                  2002-583738/62.
                                                                                                                                                                                                                                                                 Mack DH, Gish KC,
                                                                                                                                                                                                                                                                                            N-PSDB; ABJ05564.
                                                                                                                      WO200259377-A2
                                                                                                   Unidentified.
                                  14-NOV-2002
                                                                                                                                        01-AUG-2002
                 ABT07721;
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a blological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention

9; Page 372; 414pp; English.

Claim

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

Alignment Scores:

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927
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                              SerLeuGlnThrSerTyrValPheLeu
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                 Percent Similarity:
Best Local Similarity:
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                                  Query Match:
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Query Match: DB:

Gaps:

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BP

ADB80503 standard; DNA; 927

RESULT

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SerLeuGlnThrSerTyrValPheLeu

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US-10-774-176-7 (1-9) x ABX76333 (1-927)

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that medulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a meanmal having lung cancer by administering a medulatory compound identified. The methods are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                 lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinfilammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                                                                                                                                                         cancer-associated polynucleotide #197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 336; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2001; 2001US-0284770P.
10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0330666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
                                                                                      ABX76333 standard, DNA; 927 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOSB-) EOS BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                  02-APR-2003
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                                                                                                                                                                            ABX76333;
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                                                                                                                                                                                                                                                                                                                                                             Lung
RESULT 7
                                                 ABX7633
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cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.

Location/Qualifiers

Homo sapiens

Key

1. .927 /\*tag=

WO2002102235-A2

27-DEC-2002.

(EOSB-) EOS BIOTECHNOLOGY INC

WPI; 2003-167431/16. P-PSDB; ADB80504. Mack DH, Gish KC;

27-AUG-2001; 2001US-0315287P. 05-SEP-2001; 2001US-0317544P. 13-NOV-2001; 2001US-0350666P. 12-APR-2002; 2002US-0372246P.

18-JUN-2002; 2002WO-US019297. 18-JUN-2001; 2001US-0299234P.

Ovarian cancer-associated transcript #34.

04-DEC-2003 (first entry)

ADB80503;

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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymuclecited that selectivel hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting mode of therapy, chemotherapy or radiation therapy, in selecting mode of therapy, detectining tumour prognosis, early detection of pre-cancerous lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and as vaccines. This sequence corresponds to one of the nucleic acids used for the detection method of the invention.
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

927

Length: Matches: Conservative: Mismatches:

15.7 43.00 100.0%

Percent Similarity: Best Local Similarity:

Alignment Scores: Pred. No.:

nvention.

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diseases such as angiogenic or fibrotic disorders, and to methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                         AAD56198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                           fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; ettinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or
                                                                                                                                                                                               Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glynne R, Hevezi PA;
3, Zlotnik A;
                                                                                                                                                                                                                   cancer; anglogenic disorder;
  60000
         Conservative:
Mismatches:
Indels:
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Wilson KE,
  Matches:
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                                        Gaps:
                                                                           1 SerLeuGlnThrSerTyrValPheLeu 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seful for diagnosing, prognosing or to nucleic acid in a biological sample.
                                                          (1-927)
                                                                                                                                                                                                                   differential expression;
                                                                                                                                     ADN38723 standard; cDNA; 927 BP
                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0340376P.
2002US-034731P.
2002US-0347349P.
2002US-0355250P.
2002US-0356714P.
2002US-0356714P.
2002US-035077P.
2002US-0370110P.
2002US-0370110P.
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R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0396839P.
2002US-0397775P.
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2001US-0334393P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0397845P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-2002; 2002US-0409450P
                                                        US-10-774-176-7 (1-9) x ADB80503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-468649/44.
P-PSDB; ADN38724.
   Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                 WO2003042661-A2
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08-JAN-2002;
10-JAN-2002;
13-PSB-2002;
20-FSB-2002;
20-FSB-2002;
29-MAR-2002;
04-APR-2002;
04-APR-2002;
05-JUN-2002;
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22-JUL-2002;
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Mack DH,
                                                                                                                                                        ADN38723;
                                                                                                                            ADN38723
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of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; p53 pathway; Leucine rich repeat capricious related protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
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43.00
100.0%
100.0%
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Francis-Lang H, Friedman
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Best Local Similarity:
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polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antilnflammatory; cardiant; haemostatic; neuroprotective; anorectic; noctropic; immunosuppressive; osteopathic; antiparkineonian; cancer; antilnfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopolatic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopolesis; wound healing; angiogenesis; ds.
                                                                                                                     Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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2001US-0275235P.
2001US-0275578P.
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2001US-0275601P.
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2001US-0277239P.
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2001US-0278894P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV8a coding sequence.
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43.00
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100.0%
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12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
16-MAR-2001;
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20-MAR-2001;
20-MAR-2001;
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Casman SJ;
SA, Vernet CAM;
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                                 2001US-0280233P.
2001US-0280802P.
2001US-0280802P.
2001US-028104P.
2001US-0281675P.
2001US-0283675P.
2001US-0287444P.
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2001US-0299303P.
2001US-0299310P.
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2001US-0318462P.
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2001US-0332271P.
2001US-0332272P.
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2001US-0294889P.
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P-PSDB; ABP70071.
                                 30-MAR-2001;
02-APR-2001;
02-APR-2001;
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31-OCT-2001;
14-NOV-2001;
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14-NOV-2001;
                                                             02-APR-2001;
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03-MAY-2001;
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30-MAY-2001;
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18-JUN-2001;
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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is sury number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, cardiovascular

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.

Claim 16; Page 114-115; 619pp; English.

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disturbances associated with obesity, metabolic syndrome X or wasting distrates associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. weurogenesis, call differentiation, call poliferation, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in
fertility, bronchial asthma, AIDS, dyslipidemia, metabolic
                                                                                                                                                                                                                                       therapeutic or diagnostic methods
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

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1156
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                         Conservative:
Mismatches:
Indels:
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Matches:
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                                                                  US-10-774-176-7 (1-9) x ABV99349
        20.1
43.00
100.0%
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                                  Best Local Similarity:
                         Percent Similarity:
Alignment Scores:
Pred. No.:
                                        Query Match:
DB:
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(1-1156)

ABK87175 standard; cDNA; 1260 BP ABK87175; RESULT 12 ABK8717 ઠ 셤 CCCCX8X44444X88X4X4X4X6X8X44444X8XXXXXXXXCCCCX

cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4. (first entry) 07-OCT-2002

Peline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal call; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.

ВÞ. Pelis

/product= "5T4 protein" Location/Qualifiers 1. .1260 /\*tag= a

WO200238612-A2

16-MAY-2002.

13-NOV-2001; 2001WO-GB005004

13-NOV-2000; 2000WO-GB004317.

(OXFO-) OXFORD BIOMEDICA UK LID,

Carroll M; Drury N, Myerв К,

WPI; 2002-557449/59.

P-PSDB; AAU98694.

Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat. Claim 4; Page 68; 68pp; English.

The present invention relates to the isolation of canine and feline concofoctal leucine-rich glycoproteins known as F14, and the polymucleotide sequences encoding them. The F14 proteins are expressed in a significant proportion of tumours. The sequences of the invention are

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useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also he used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New major histocompatibility complex class I peptide epitopes from human 574 tumor-associated antigen, useful for preventing and/or treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel Major Histocompatibility Complex (MHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                    Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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/product= "Feline 5T4 antigen protein"
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                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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provides a polyapitope string comprising the 5T4 epitope; a nucleic acid sequence encoding the 5T4 epitope or a polyapitope string of the 5T4 epitope, a vector system capable of delivering the 5T4 epitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope, a polyepitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope, a polyepitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising the presence of the 5T4 epitope or ties encoding nucleic acid; a method comprising the 5T4 epitope in conjunction with an MHC class of molecule. The 5T4 epitope has cytostatic activity. The vaccine is pecifically recognising the 5T4 epitope in conjunction with an MHC class of particularly cancer. The detection method is useful for diagnosing or particularly cancer. The detection method is useful for diagnosing or presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease, and for detecting the progression of a cancercous disease.
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class I peptide epitope of the 5T4 antigen. The invention further
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/product= "Feline 5T4 antigen protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        5T4 antigen coding DNA of the invention.
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P-PSDB; ADB97455.
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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for detecting the presence of a peride or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the human 5T4 tumour-associated antigen ({\sf TAA}). The TAA 5T4 is a glycoprotein which is widely expressed in
                                                                                                                                                                                                                                                                               Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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                                                              Disclosure, Page 49; 63pp; English.
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carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen [tashed] can be used to elicit an immune response, preferably CIL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ellard FM;
                                                                                                                                                     Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                     TCCTGCAAACCTCTTATGTCTTCCTG 1077
                                                                                                                                                                                                                                                                           Gaps:
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/product= "5T4"
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Best Local Similarity:
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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a disease pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune disease, cancers, central nervous system disorders including Parkinson's disease, gastrointestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                            Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK87174 standard; cDNA; 1263
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P-PSDB; AAU98693.
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Query Match:
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell composition for the prevention and/or proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in disgnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes canine 574 protein
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Seguence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;

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     Length:
Matches:
Conservative:
Mismatches:
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Alignment Scores:
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US-10-774-176-7 (1-9) x ABK87174 (1-1263)

1051 TCCCTGCAGACTTCTTATGTCTTCCTA 1077 1 SerLeuGlnThrSerTyrValPheLeu 9 셤 ò

RESULT 18 AAA27059

(first entry) AAA27059

AAA27059 standard; DNA; 1281 BP

22-AUG-2000

Mouse 5T4 tumour-associated antigen gene.

Mouse, TAA, tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;

Mus musculus.

WO200029428-A2.

25-MAY-2000

99WO-GB003859. 18-NOV-1999; 

99GB-00017995. 98GB-00025303 99GB-00001739 18-NOV-1998; 30-JUL-1999; 17-JAN-1999

(OXFO-) OXFORD BIOMEDICA UK LTD.

Myers KA; ΜM, Carroll

WPI, 2000-387735/33.

Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.

Example 2; Page 78; 79pp; English.

The present sequence encodes the mouse 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system expected a comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a
carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathway; Leucine rich repeat capricious related protein;
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                                                                                                                                                                                                             Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1069 TCCCTGCAGACTTCCTATGTCTTCCTA 1095
                                                                                                                                                                                                                                                                                                                                                               Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                    US-10-774-176-7 (1-9) x AAA27059 (1-1281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD56199 standard; DNA; 1331 BP
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15-FRB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human LRRCAPS related DNA #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2002; 2002WO-US033540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-421410/39.
                                                                                                                                                                                                                                                                                                 Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                    Alignment Scores:
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       888888888888888
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the printed specification but has been obtained in electronic format from the US Patent Office at ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.

Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;

2020 9 0 0

Length: Matches: Conservative: Mismatches:

37.7 43.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

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Indels:

TCCCTGCAAACCTCTTATGTCTTCCTG 1147

1121

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ACC51052 standard; cDNA; 2053 BP

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(1-2020)

US-10-774-176-7 (1-9) x ADJ56299

SerLeuGlnThrSerTyrValPheLeu

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composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA differentially expressed in MYCN activated cells SegID 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numan; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
                                                                  Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ56299 standard; cDNA; 2020 BP.
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(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.

03-JUL-2002; 2002WO-US021338

WO2003003906-A2 Homo sapiens

16-JAN-2003.

Human bladder cancer associated cDNA sequence SEQ ID NO:192.

(first entry)

12-JUN-2003

ACC51052;

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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that $80 \% identical to a contacting a biological sequence that $80 \% identical to a condectively hybridises to a sequence that $80 \% identical to a concectively hybridises to ACC51059. ACC50951 to ACC51059 encode the human bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is cancer-associated transcript in a cell from a patient. The method is compounds that modulate bladder cancer, such as hormones or antibodies. The mucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 296; 307pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                            03-JUL-2001; 2001US-0302814P.
03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666F.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-201532/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mack DH, Aziz N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABR48236.
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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymuclocide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protonon concern that is amplified in neuroblastoma cells and is common in small concern in hybridisation assays to detect expression of nucleic as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymuclecide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in

New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the

Claim 1; SEQ ID NO 105; 27pp; English.

cancer.

Shohet JM

Plon SE,

Stuart SG, Nuchtern JG,

WPI; 2003-635698/60.

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WO2003035831-A2
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                                                                                                                                                                                                                              invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; attilifiammatory; autiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lession; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                         U; 0 Other;
                                                                                                                                      Length:
Matches:
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Mismatches:
Indels:
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                                                      461 A, 602 C, 499 G, 491 T,
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and/or antisense/inhibition applications
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2001US-0290492P.
2001US-0339245P.
2001US-0350666P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX76332 standard; DNA; 2053
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P-PSDB; ABU56603.
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                                                         Sequence 2053 BP;
                                                                                                                                                                                                                              Best Local Similarity:
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for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benden or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapoutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system modulating a purified Leucine rich repeat, capticious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity where a citizen activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                            (1-2053)
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15-PEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human LRRCAPS DNA #11.
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Mismatches:

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                                                  Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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gene therapy. The present sequence is human LRRCAPS DNA
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                                                                                                                                                                                                                                                                                                          (1-2053)
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01-MAR-2002; 2002US-0361196P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prancis-Lang H, Priedman L;
                                                                                                                                                                                                                                                                                                     US-10-774-176-7 (1-9) x AAD56197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-421410/39.
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                    Alignment Scores:
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2053 9 0

Length: Matches: Conservative:

38.4 43.00 100.0%

Percent Similarity:

Alignment Scores: Pred. No.:

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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                            Human; differential expression; cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a
                                                                                                                                                                                                                                                                                                                                   retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:39.
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A;
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3, Zlotník
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Wilson KE,
               Indels:
                                                                                                                                                                                                                                                                                                                            inflammatory disease; autoimmune disease;
                                                                                                       TCCCTGCAAACCTCTTATGTCTTCCTG 1161
                                                                                      σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for diagnosing, prognosing or ti
a nucleic acid in a biological sample.
                                                                                      SerLeuGlnThrSerTyrValPheLeu
                                                         (1-2053)
                                                                                                                                                                           standard; cDNA; 2053 BP
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R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0347349P.
13-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355077P.
20-FEB-2002; 2002US-0359077P.
24-APR-2002; 2002US-0359077P.
12-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0370216P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0335394P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
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                                                         US-10-774-176-7 (1-9) x AAD56200
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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Mack DH,
                                                                                                                  1135
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the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart diseasing antibodies and methods are useful for diagnosing, prognosing and treating theroaclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
by detecting a nucleic acid at least 80% identical to those of
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

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Hillan KJ, Polakis P, Polson A, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; tumour-associated antigenic target; TAT; cell death; tumour; cancer; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tumour-associated antigenic target (TAT) cDNA sequence #53.
                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                    1135 TCCCTGCAAACCTCTTATGTCTTCCTG 1161
                                                                                                                                                                                   Gape:
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; 2002US-0419008P.
; 2002US-0426847P.
; 2003US-0484959P.
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u TD, Zhang Z;
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                                                                                     Percent Similarity:
Best Local Similarity:
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15-NOV-2002;
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Alignment Scores:
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The present invention relates to the isolation of human tumour-associated

Claim 1, SEQ ID NO 53; 319pp; English.

polypeptide, use treating cancer.

New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or

WPI; 2004-257144/24. P-PSDB; ADL06552.

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antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which the binds. The antibody is useful for preparing a composition for diagnosing or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark H, Jackman J, Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                      Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other,
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                                                                                                                                                                                                                                                                                             US-10-774-176-7 (1-9) x ADL06473 (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipsoriatic cDNA sequence #180.
                                                                                                                                                                                                                                                                                                                                                                                                                   ADN03961 standard; cDNA; 2053 BP
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Best Local Similarity:
Query Match:
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                                                                                                                                                                       Alignment Scores:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN03961;
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                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wa ID;
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 27
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(first entry)

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Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
               ACN38510 standard; cDNA; 2053 BP.
                                                                       18-NOV-2004
                                           ACN38510;
                according to prognosts by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of classifying a breast cancer patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
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                                                                                                                                                                                                                                                                                           ds; breast cancer; prognosis; gene expression; diagnosis.
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     marker used in the method of the invention
                                                                                                     TCCCTGCAAACCTCTTATGTCTTCCTG 1161
                           Gaps:
                                                                                                                                                                                                                                                                Breast cancer prognosis marker #1305.
                                                                                    SerLeuGlnThrSerTyrValPheLeu
                                                         US-10-774-176-7 (1-9) x ADN03961 (1-2053)
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                                                                                                                                                                           ADR25444 standard; DNA; 2053 BP
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Best Local Similarity:
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                                                                                                                                                                                                        ADR25444;
             Query Match:
DB:
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The Invention relates to Annah Cumour associated antigenic target (IATY) oblypeptides, and their related mucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide acquences at least 80% identical to the TAT nucleic acids and polypeptides and polypeptides and polypeptides and polypeptides and polypeptides and polypeptides a peptide or organic acid; an antibody specific for a TAT polypeptide; fusion proteins comprising a TAT nucleic acids, an antibody specific for a TAT polypeptides, nucleic acids, and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, are acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, lung cancer, cancer, bladder cancer, pancreatic cancer, cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human tumour-associated antigenic target (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
Tumour-associated antigenic target; TAT; human; overexpression; catumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                gene therapy; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-347921/32.
P-PSDB; ABM80804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004030615-A2.
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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US-10-774-176-7 (1-9) x ACN38510 (1-2053)

2053 9 0 0 0

Matches: Conservative: Mismatches: Indels:

38.4 43.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

.. 90

Query Match: DB:

1135 TCCCTGCAAACCTCTTATGTCTTCCTG 1161

SerieuGlnThrSerTyrValPheleu 9

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RESULT 29

US-10-774-176-7 (1-9) x ADR25444 (1-2053)

Length:

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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a particular disease, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals or affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, well as Parkinson's and Alzheimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, noctropic, antimand and antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is contracted and average of the presence of a therapeutic compound and accounts and average of the presence of a therapeutic compound and accounts and accounts and average of the presence of a gene that is
                                                                                                                                                                                                                                                                                                                             disease signature; neuropsychiatric; neurodegenerative; schizophrenia;
bipolar affective disorder; BAD; autism; Parkinson's;
Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contacted with the test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laeng P;
                                                                                                                                                                                                                                                                                                           human; 88; multi-parameter high throughput screening; MPHTS
                                                                                                                                                                                                                                                                Human cDNA of an exemplary efficacy gene for BAD SegID174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hook D, Klimczak LJ,
                        1135 TCCCTGCAAACCTCTTATGTCTTCCTG 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; SEQ ID NO 174; 39pp; English.
1 SerleuGlnThrSerTyrValPheleu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans D,
                                                                                                                               ADV35098 standard; cDNA; 2053 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PSYC-) PSYCHIATRIC GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2001; 2001US-0299151P.
07-SEP-2001; 2001US-0317828P.
25-SEP-2001; 2001US-035150P.
14-NOV-2001; 2001US-033934P.
18-JAN-2002; 2002US-0349936P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0361834P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2002; 2002US-00175523
                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Altar CA, Brockman JA,
Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI, 2004-118903/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-2002;
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                                                                                                                                                                          ADV35098;
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Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;

2053

Length:

38.4

Alignment Scores: Pred. No.:

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal control of (II) is useful in gene therapy techniques to restore normal control of generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the consisting analysis, genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to produce other types of data and products dependent on DNA and no acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #22979.
                 Conservative:
Mismatches:
Matches:
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                                                                           Gaps:
                                                                                                                US-10-774-176-7 (1-9) x ADV35098 (1-2053)
                                                                                                                                                                                                                                                                   AAS87175 standard; cDNA; 2338 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
43.00
100.0%
100.0%
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABG22988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-0CT-2001.
                                                                                                                                                                                                                                                                                                          AAS87175;
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                                                                                                                                                                                                                                 RESULT 31
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       Human; full length cDNA; cDNA synthesis; oligo-capping;
                2338
9
0
0
0
                                           Conservative:
Mismatches:
Indels:
                Length:
Matches:
                                                                                                                                                                              1392 TCCCTGCAAACCTCTTATGTCTTCCTG 1418
                                                                                                                                                                                                                                                                                                                                                       Human full-length cDNA, SEQ ID NO: 2864.
                                                                                             Gaps:
                                                                                                                                                          SerleuGlnThrSerTyrValPheleu 9
                                                                                                                            (1-2338)
                                                                                                                                                                                                                                                         AAK94253 standard; cDNA; 2359 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000EP-00114089
                                                                                                                            US-10-774-176-7 (1-9) x AAS87175
               44.5
43.00
100.0%
100.0%
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-524255/58.
                                        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1130094-A2.
gnment Scores:
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                                                                                                                                                                                                                                                                                           AAK94253;
                                                                                                                                                                                                                           RESULT 32
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2359 9 0 0

Length: Matches: Conservative: Mismatches: Indels:

43.00 100.0% 100.0%

Percent Similarity: Best Local Similarity: Query Match:

Pred. No.:

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                       signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii S, Kawai Y;
S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 2864; 1340pp; English.
                                                                           1474 TCCCTGCAAACCTCTTATGTCTTCCTG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                       Full length human cDNA clone SeqID 2864.
                                               σ
                                             1 SerLeuGlnThrSerTyrValPheLeu
US-10-774-176-7 (1-9) x AAK94253 (1-2359)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T,
na T, Nagai
                                                                                                                                                                                          ADL30831 standard; cDNA; 2359 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                   oligo-capping method; ss; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-001183865.
07-JUL-2000; 2000RP-00114089.
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                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-204755/20.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                          human; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wakamatsu A,
                                                                                                                                                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                          ADL30831;
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                                                                                                                                                                   ADL3083
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Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Octe: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K, Ishli S, Kawai Y,
K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                                                                                                                            Human full-length cDNA, SRQ ID NO: 2866
                                                                                                                                                                                                                                                                                                                                                                                                                        T, Isogai T,
iyama T, Nagai
                               AAK94254 standard; cDNA; 2361 BP.
                                                                                                                                                                                                                                                                                                                          08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                                                                            07-JUL-2000; 2000EP-00114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wakamatsu A, Sugiyama T,
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB, AAM93334
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                             EP1130094-A2
                                                                                              06-NOV-2001
                                                                                                                                                                                                                                                            05-SEP-2001
                                                              AAK94254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from BPO
                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830
RESULT 34
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2361 9 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-774-176-7 (1-9) x AAK94254 (1-2361) 45 43.00 100.0% 100.0% Percent Similarity: Best Local Similarity: gnment Scores: Query Match: DB:

1476 recerceadacererrarererrecae 1502 SerLeuGlnThrSerTyrValPheLeu 9

8

ADI26162 standard; cDNA; 2361 AD126162;

RESULT 35

AD126162

BP.

(first entry) 22-APR-2004

se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmuno disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematoeus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS. Human cDNA encoding protein that promotes STAT6 activation #64 Ishizawa K; Muramatsu S, Honda G, 26-DEC-2002; 2002JP-00377326. 27-DEC-2002; 2002JS-0436467P. 15-MAX-2003; 2003JP-00137505. 16-MAY-2003; 2003US-0470836P. 05-JUN-2003; 2003WO-JP007123 05-JUN-2002; 2002JP-00164257, 06-JUN-2002; 2002US-0385912P. Sugahara T, Matsuda A, (ASAH ) ASAHI KASEI KK WPI; 2004-122214/12. P-PSDB; ADI26163. WO2003104277-A2 Homo sapiens. 18-DEC-2003 

New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. diabetes and cancer

Claim 4; SEQ ID NO 127; 1368pp; English

The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression a activity of the corporation. The nucleic acid is useful for diagnosing a disease or compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening composition. Compositions, antibodies and antisense molecules are useful corposition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allowed in for the treating diseases. Compositions are also useful in rheumatoid or treating diseases. Compositions are also useful in rheumatoid arthritis, osteoarthitis, systemic lupus erythematosus, sepsis, asthma, allergic thinitis, ischaemic heart diseases, subarachnoid hasmorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activities, distinct or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive human and an arthritis, and an arthritis or inhibition of STAT6. The present sequence represents a human and an arthritis and all preventing disease associated with excessive human and an arthritis and preventing disease associated with excessive human and an arthritis and preventing disease associated with excessive human and an arthritis and preventing disease associated with excessive human and an arthritis and preventing disease associated with excessive human and an arthritis and preventing disease associated with excessive human and an arthritis and preventing disease associated with excessive human and an arthritis and preventing the protein has effectively useful for accepting human and an arthritis and preventing dis activation or inhibition of STAT6. The present sequence represhuman cDNA encoding a protein which promotes STAT6 activation.

506 A; 684 C; 638 G; 533 T; 0 U; 0 Other; Sequence 2361

00000 Conservative: Mismatches: Indels: Length: Matches: Gaps: 100.0% 45 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

US-10-774-176-7 (1-9) x ADI26162 (1-2361)

se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

encoding protein that promotes STAT6 activation #63.

22-APR-2004 (first entry)

Human cDNA

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This invention relates to a novel primers useful for synthesising full length CDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
                                                                                                                                                                                                                               human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawai Y;
T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi K, Ishii S,
K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 2866; 1340pp; English.
               1476 TCCCTGCAAACCTCTTATGTCTTCCTG 1502
                                                                                                                                                                                             Full length human cDNA clone SegID 2866.
1 SerLeuGlnThrSerTyrValPheLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T, Nishikawa T, Isogai T,
Wakamatsu A, Sugiyama T, Nagai
                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                oligo-capping method; ss; gene.
                                                                                            ADL30833 standard; cDNA; 2361
                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000RP-00114089.
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                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000; 2003EP-00025638
                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                              EP1396543-A2.
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                                                                                                                                                              20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                10-MAR-2004.
                                                                                                                             ADL30833;
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for screening The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The mucleic acid is useful for disquosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, the profit diseases, inflammation, autoimmune diseases, diabetes, dispersiplidaemia, infections disease and cancers. Compositions are useful for treating disease ascolated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischeemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATE activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a human cDNA encoding a protein which promotes STATE activation. 

2361 9 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

45 43.00 100.0% 100.0%

Best Local Similarity:

Query Match:

Percent Similarity

Alignment Scores:

Pred. No.:

ò g ADI26160 standard; cDNA; 2557 BP

RESULT 37 ADI26160 ID ADI26:

US-10-774-176-7 (1-9) x ADL30833 (1-2361)

New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.

Claim 4; SEQ ID NO 125; 1368pp; English.

diabetes and cancer

Ishizawa K;

Sugahara T, Matsuda A, Honda G, Muramatsu S,

WPI; 2004-122214/12.

P-PSDB; ADI26161

(ASAH ) ASAHI KASEI KK

06-JUN-2002; 2002US-0385912P. 26-DEC-2002; 2002US-0037732C. 27-DEC-2002; 2002US-043647P. 15-MAY-2003; 2003US-0013750S. 16-MAY-2003; 2003US-0470836P.

05-JUN-2003; 2003WO-JP007123

WO2003104277-A2.

18-DEC-2003

Homo sapiens

2002JP-00164257

05-JUN-2002;

BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other; Sequence 2557

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               Matches:
Conservative:
Mismatches:
        Length:
       49.2
43.00
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                         Percent Similarity:
Best Local Similarity:
Alignment Scores:
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or ascreptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for grodein composition, a transformant for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for treating a disease associated with STAT6 activation such as
                                                                                                                                                                                                                                                                                                           ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autodimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal transducer and activator of transcription 6 activation noting purified protein, for diagnosing and treating disease ociated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                              Human cDNA encoding protein that promotes STAT6 activation #62.
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                                                                                                   1624 TCCCTGCAGACTTCCTATGTCTTCCTA 1650
Indels:
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               Gaps:
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2002JP-00377326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASAH ) ASAHI KASEI KK
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associated
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Query Match:
DB:
                                                                                                                                               RESULT 38
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allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STATS activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, athmat allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATS

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypoptides encoded by the genes. Antibodies (Ab) raised against the optypoptides encoded by the genes. Proteins, Ab and cells that carry a gene-containing vector are used to select compounds that andulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Iuminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The
activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a human cDNA encoding a protein which promotes STATE activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danchin A;
                                                                                           Sequence 2557 BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;
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Conservative:
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Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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ACP67367 17
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Continuation (7 of 7) of ACPG5386 from base 600001 (Photorhabdus luminescens nucleotide WP Sequence split into 7 fragments LOCUS ACPG5386 Accession Acf65386
WP ACPG5386_1 10000 10000
WP ACPG5386_1 100000 310000
WP ACPG5386_2 200001 310000
WP ACPG5386_3 300001 410000
WP ACPG5386_4 400001 510000
WP ACPG5386_5 600001 700779
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57 fragments LOCUS ACF67367 Accession Acf67367
genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that ser sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                        Sequence 14952 BP; 3174 A; 3899 C; 4409 G; 3470 T; 0 U; 0 Other;
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WP Sequence split into 57
WP ACPG 367 01
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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent of office at the fire sequence. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomanna, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of homologous photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake the contract of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 565 BP; 128 A; 153 C; 157 G; 127 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou Y, Kovalic DK, Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SerLeuGlnThrSerTyrValPheLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-7 (1-9) x ADX45743 (1-565)
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                                                                                                                                                                                                                                                                                                                       28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999; 99US-00304517.
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100.0%
77.8%
86.0%
                                       protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-180133/17.
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Best Local Similarity:
                                                                                                                                                                             US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                improving yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIU J.
ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAO Y.
                                                                                                         Unidentified.
                                                                                                                                                                                                                                                      19-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 44
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ID AAT7
XX
AC AAT7
       The invention also relates to a peptide array comprising two or more nucleic acid probes.

The invention also relates to a peptide array comprising two or more isolated polypeptide, an isolated acid sequence, a compound that binds to a polypeptide, an isolated acid sequence, a compound binds to a polypeptide, which is prepared by immunizing a host animal composition comprising the polypeptide or its antigen binding the polypeptide or its antigen binding fragment and collecting calls from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of sereening for anticancer activity, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid. A mucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody and detecting the presence or absence of cancer cells in an individual which involves contacting cells from the cancer cells and the antibody where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cells in an individual or for inhibiting expression of a CA gene in a cells in an individual or for inhibiting expression of a CA gene in a cells in an individual or for inhibiting expression of a CA gene in a cells in an individual or for inhibiting expression of a CA gene in the interaction of a cells in the cancer and for inhibiting expression of a CA gene in the cancer of a cancer of a cells in the cancer and the cancer associated genomic DNA of a cancer and a cancer a
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                                                                                                                                                                                                                                                                                                                                                                                                cancer associated nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117730 BP; 32629 A; 25620 C; 25334 G; 34147 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a nucleic acid array for detecting a cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant full length insert polynucleotide seqid 20483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                comprises two or more nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 70; 198pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16982 CTTCAGACTTCATATATTTTTTT 16959
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                                           23-SEP-2004; 2004WO-US031617.
                                                                                                            23-SEP-2003; 2003US-00669920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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100.0%
87.5%
88.4%
                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid array useful
                                                                                                                                                                                                                                                      Morris DW, Malandro MS,
                                                                                                                                                                                                                                                                                                                       WPI; 2005-273395/28.
                                                                                                                                                                             (CHIR ) CHIRON CORP.
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Percent Similarity:

Query Match:

Alignment Scores:

21-APR-2005

ADX45743;

RESULT 43 ADX45743

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the invention

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Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel sequences which are useful for preparing composition for diagnosing or treating carcinomas. These sequence are also useful in gene therapy. The present sequence is human CCND1 carcinoma associated (CA) gene. This sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid encoding carcinoma associated protein,
                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid and its encoded protein, useful for preparing a composition for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30346 BP; 6484 A; 8431 C; 8729 G; 6702 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CCND1 carcinoma associated gene, SEQ ID NO:980.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                         23-OCT-2001; 2001US-00004113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2001; 2001US-00035832.
                                                                                                                   22-OCT-2002; 2002WO-US033835
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37.00
100.0%
87.5%
86.0%
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                                                                                                                                                                                                                                      Engelhard EK, Morris DW;
                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                           WPI; 2003-421412/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                      WO2003035837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003057146-A2
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    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                            01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; da.
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    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a leptin receptor (OB-R) protein, OB-Rb. The OB-R can be used to treat obesity, optionally in conjunction with a treatment for diabetes, high blood pressure and high cholesterol, or in ossmetic compositions for reducing body weight. It may also be used in agriculture to produce leaner food animals, e.g. beef cattle, swine poultry, sheep. An antibody specific for OB-R can be used to measure the presence of OB-R in a sample, optionally in vivo, while the nucleic acid molecule encoding OB-R can be used to detect defects in the OB-R polypeptide associated with obese phenotypes, or diagnostically to massure its encoded RNA and protein in nutritional disorders. The nucleic acid molecule can be used in gene therapy, or the antisense nucleic acid molecule, can be used to treat weight loss e.g. associated with AIDS, cancer or anorexia nervosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinoma; gene therapy; carcinoma associated gene; CA; CCND1; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leptin receptor, OB-R, polypeptide - useful to treat obesity, optionally in conjuction with treatment for diabetes, high blood pressure and high
                                                                        Murine, leptin receptor, OB-R, obesity, diabetes, high blood pressure, high cholesterol; body weight, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2848 BP; 785 A; 596 C; 623 G; 829 T; 0 U; 15 Other;
                                    Murine leptin receptor aplice variant OB-Rb encoding cDNA.
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Conservative:
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Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                            Ioffe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; Page 98-99; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-774-176-7 (1-9) x AAT75704 (1-2848)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD56099 standard; DNA; 30346 BP
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                                                                                                                                                                                                                                                       97WO-US001010
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37.00
88.9%
88.9%
86.0%
16-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              Lee G,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-385338/35.
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Best Local Similarity:
                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                           16-JAN-1996;
14-FEB-1996;
                                                                                                                                                                          W09726335-A1
                                                                                                                                                                                                                                                       16-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                            Priedman JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholesterol.
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                                                                                                                                                                                                                24-JUL-1997.
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Query Match:

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The invantion relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host calls comprising a CA nucleic acid, a polypeptide (sepecially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or direct consequence of the effects of proviral integration into host proteoncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular thereby account sequence acids, proteins and antibodies are also useful as therefore a specially seart of the protein and antibodies are also useful as present sequence of the invention. Note: The complete sequence data for this patent of the printed specification, but was obtained in all particul forms.
useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                           Claim 1; SEQ ID NO 980; 245pp; English
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Sequence 30346 BP; 6484 A; 8431 C; 8729 G; 6702 T; 0 U; 0 Other;

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human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                      4000
    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                              Gaps:
                                                                                    CTTCAAACCAGCTATGTATTTATT 406
                                                            US-10-774-176-7 (1-9) x ADA02461 (1-30346)
                                                                           2 LeuGlnThrSerTyrValPheLeu 9
                                                                                                                          ADB72200 standard; DNA; 30346 BP
    1.54e+04
37.00
100.0%
87.5%
86.0%
                                                                                                                                                          04-DEC-2003 (first entry)
                              Best Local Similarity:
                                                                                                                                                                         Human CCND1 gene
                     Percent Similarity
Alignment Scores:
                                                                                                                                          ADB72200;
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                                     Query Match:
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2001US-00798586. 2001US-00004113. 2001US-00052482.

02-MAR-2001; 23-OCT-2001; 08-NOV-2001; 20-DEC-2001;

2001US-00034650 2001US-00997722

30-NOV-2001;

Engelhard EK;

Morris DW,

(SAGR-) SAGRES DISCOVERY

26-DEC-2001; 2001WO-US051291

WO2003008583-A2.

30-JAN-2003

Homo sapiens

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The invention comprises human and mouse cancer-associated nucleic acid sequences. The cancer associated nucleic acids of the invention are useful for screening for anticancer activity in a potential drug, as well as detecting, diagnosing, preventing and treating cancers (e.g. lymphoma, leukaemia, or breast cancer). The present sequence represents a cancer-
                                                                                                                              The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating
                                                                                                                                                                                                                   carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cancer-associated proteins and nucleic acids, useful for screening for anticancer activity in a potential drug, or for detecting, diagnosing, preventing and treating cancers, e.g. lymphoma, leukemia or
                                               recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; cancer-associated nucleic acid; screening; cancer; lymphoma; leukaemia; breast cancer; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                    Sequence 30346 BP; 6484 A; 8431 C; 8729 G; 6702 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       30346
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Mismatches:
                                                                 cancers, neoplasm, adenocarcinoma, or sarcomas.
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Matches:
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                                                                                                  Claim 1; SEQ ID NO 28; 2304pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 CTTCAAACCAGCTATGTATTTATT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-7 (1-9) x ADB72200 (1-30346)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlnThrSerTyrValPheLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CCND1 genomic DNA sequence.
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               WPI; 2003-239337/23.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morris DW;
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Matches:

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene; ds; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
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                                                           Sequence 30346 BP; 6484 A; 8431 C; 8729 G; 6702 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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associated nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAAACCAGCTATGTATTTATT 406
                                                                                                                                                                                                                                                                                                                                                               US-10-774-176-7 (1-9) x ADE82932 (1-30346)
                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlnThrSerTyrValPheLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABD33387 standard; DNA; 176594 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine cancer-associated (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2003; 2003WO-US040081.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morris DW, Malandro MS;
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                                                                                                                                                                                                         Percent Similarity:
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176594

Length:

1.12e+05

Alignment Scores: Pred. No.:

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The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL70633. The cdps sequences can calculate from those given in ABL70627 to ABL70633. The cdps sequences encode corn tassel-derived polypepides (CDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, calculated and semilatoral markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to concept equality equality isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid sequences from DNA libraries, in nucleic acid determine homology of known sequences, as guery sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to concept and the degree of similarity between two (or more) nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel purified corn tassel-derived polynucleotide useful for determining
                                                                                                                                                                                                                                                                                                                                                                                                                        Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                      Corn tassel-derived polynucleotide (cdps) SEQ ID NO:4788.
 C4400
                   Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4788; 201pp; English.
                                                                               Gaps:
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                                                                                                                x ABD33387 (1-176594)
                                                                                                                                                      1 SerieuGlnThrSerTyrValPheLeu
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                                                                                                                                                                                                                                                                     ВР
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                                                                                                                                                                                                                                                                     ABL75414 standard; cDNA; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00294093
                                                                                                                                                                                                                                                                                                                                              14-MAY-2002 (first entry)
37.00
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(ITOL/) ITO L Y.
(SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lalgudi RV, Ito LY,
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                     Percent Similarity:
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SQ Sequence 199 BP; 33 A; 42 C; 51 G; 73 T; 0 U; 0 Other;

d. No.:	87	Length:	199
re:	36.00	Matches:	7
cent Similarity:	100.0	Conservative:	
t Local Similarity:	87.5	Mismatches:	0
ry Match:	83.7	Indels:	0
1	9	Gaps:	0

US-10-774-176-7 (1-9) x ABL75414 (1-199)

1 SerleuGlnThrSerTyrValPhe 8 දු දු

Search completed: April 25, 2006, 12:35:21 Job time : 340.3 secs

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AXO25013 Sequence
AX825168 Sequence
AX82513 Sequence
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AX82153 Sequence
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BD249731 Polypepti
AX025011 Sequence
AX316085 Sequence
AX316085 Sequence
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AX361915 Homo sapi
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AX361915 Sequence
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AX361917 Homo sapi
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AC12829 Homo sapi
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AX822164
AX821513
AX821513
AX025011
AX149553
AX16086
AX467371
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AL105366
CR225725
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AP001808
AC105320
AC012417
AC124407
AC124400
AC102094
BX323822
AC152094
BX32822
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Ygapext
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us-10-774-176-7.p2n.rge

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81.4 181292 14 81.4 181307 5 81.4 181322 8	81.4 182157 19 81.4 182157 18 81.4 182209 8 81.4 18220 9 81.4 18220 9 81.4 18231 9 81.4 18231 19	81.4 182883 9 81.4 183113 14 81.4 183227 9 81.4 183338 14 81.4 183445 14 81.4 183478 9	81.4 183503 14 81.4 183503 14 81.4 183761 14 81.4 184043 14 81.4 184165 14 81.4 184463 9 81.4 184463 9 81.4 18465 5	35 81.4 185321 14 AC026153 35 81.4 185501 8 AC133781 35 81.4 185608 8 AC037126 35 81.4 186074 8 AC027126 35 81.4 1861074 8 AC025661 35 81.4 186107 9 AL591390 35 81.4 186126 14 AC134752 35 81.4 18642 8 AC024168 35 81.4 18644 9 AC12228 35 81.4 187043 9 AC083895 35 81.4 187043 9 AC083895 35 81.4 187043 9 AC083895 35 81.4 187043 9 AC083895 35 81.4 187043 9 AC083895	81.4 188027 14 81.4 188335 9 81.4 188318 9 81.4 188789 14 81.4 188946 9 81.4 18986 9	65 bp DNA linear PAT Sequence 29022 from Patent W00210449. C0559387. C0559387.1 GI:41525814 Mus musculus Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buts musculus Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buts Manmalla; Eutheria; Buarchontoglires; Glires; Rodentia; Boiurognathi; Muroidea; Muridae; Murinae; Mus. Sciurognathi; Muroidea; Muridae; Mus. Bollgonucleotide library for detecting rna transcripts an variants that populate a transcriptome Patent: W0 0210449-A 29022 07-PEB-2002; Compugen Inc. (US) Location/Qualifiers 165
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 3 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0029428-A 3 25-MAY-2000;
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BIOMEDICA LTD (GB)
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PAT 14-DEC-2001

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
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MHC class I peptide epitopes from the human 5t4 tumor-associated
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AX821548
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AX821533
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Felis sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
                                                                                                                                                                                                                                                                                  PAT 12-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mack, D.H., Gish, K.C. and Afar, D.
Methods of diagnosis of breast cancer, compositions and methods of screening for medulators of breast cancer.
Patent: WO 02059377-A 57 01-AUG-2002;
EOS Biotechnology, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Sequence 57 from Patent W002059377.
AX829164.1 GI:39838931

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Patent: WO 0238612-A 3 16-MAY-2002;
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AX467373.1 GI:21900603
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Homo sapiens
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43.00
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REFERENCE

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REFERENCE AUTHORS TITLE JOURNAL

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PAT 15-SEP-2000
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W., Bllard, P.M. and Myers, K.A. Antibodies
Antibodies
Patent: WO 0136486-A 14 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                         CALROLLING
POLYPEPLIGE
PACENT: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="5T4"
                                                                                                  DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 14 from Patent W00136486.
AX149553
                                1051 TCCCTGCAACCTCTTATGTCTTCCTG 1077
                                                                                               AX025011 1263 bp
Sequence 1 from Patent W00029428.
AX025011
AX025011.1 GI:10184932
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                 SerLeuGlnThrSerTyrValPheLeu
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AX025011
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1 (bases 1 to 1263)

Carroll,M.W. and Myers,K.A.
Polypeptide

LO Patent: JP 2002530060-A 1 17-SEP-2002;
OXFORD BIOWEDICA L.TD

OS Homo sapiens (human)

PN JP 2002530060-A/1

PN 19 2002530060-A/1

PN 19 2002530060-A/1

PN 18-NOV-1999 JP 2000582415

PR 18-NOV-1999 GB 9917995.4

PR 18-NOV-1999 GB 9917995.4

PR 18-NOV-1999 GB 9917995.4

PC C12N15/00,

PC C12N15/00,

PC C12N15/00

CC Polypeptide

FW Key

L. 1263

FT Source

Loganism='Homo sapiens (human)'.
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            Carroll, M.O., Harrop, R.O. and Kingsman, S.O. MHC class II peptide epitope of 5t4 antigen Patent: WO 03068815-A 1 21-AUG-2003; Oxford Blomedica (UK) Limited (GB)
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Matches:
Conservative:
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/db_xref="taxon:9606"
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BD249731
BD249731.1 GI:33059501
JP 2002530060-A/1.
Homo sapiens (human)
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Musuculus Butheria; Butheria; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathii, Muridae; Mus.

1 (Dases 1 to 1281)

2 Carroll, M.W. and Myers, K.A.

Polypeptide

OX FORD BIOMEDICA LTD

OX FORD BIOMEDICA LTD

OX FORD BIOMEDICA LTD

OX Mus musculus (mouse)

PN JP 2002530060-A/2

PN JP 2002530060-
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Location/Qualifiers
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Gaps:
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Sequence 2 from Patent WO0029428.
AX025012
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/organism="Mus musculus"
                                                                               Gaps:
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JP 2002530060-A/2.
Mus musculus (house mouse)
Mus musculus
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Mus musculus
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BD249732
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Canis sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT 16-JUL-2002
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 105-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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    1263
/organism="Canis sp."
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    .1263
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Indels:
Gaps:
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Sequence 1 from Patent EP1160323.
AX316086.1 GI:17899278
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AX467371
                                                                                                  SerLeuGlnThrSerTyrValPheleu 9
                                                          US-10-774-176-7 (1-9) x AX149553 (1-1263)
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                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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REFERENCE AUTHORS TITLE JOURNAL

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AX467371

REPERENCE AUTHORS JOURNAL

FRATURES

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TLABLĄGLPHIRVPLDNNPWCDCHMADMYTWLKETEVVQGKDRLTCAYPEKMRNYL
LELNSADLDCDPILPPSLĄTSYVFLGIVLALIGAIFLLYLYLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYBINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                              Myers, K.A.
Direct Submission
Submitted (16-DBC-1993) Myers K. A., Paterson Institute for Cancer
Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="Anchorage of the protein to the cell membrane"
                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                       1 (bases 1 to 2053)
Myers,K.A., Rahl-Saund,V., Davison,M.D., Young,J.A., Cheater,A.J.
and Stern,P.L.
Isolation of a cDNA encoding 5T4 oncofetal trophoblast
glycoprotein. An antigen associated with metastasis contains
blodine-rich repeats
J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="placenta"
/clone lib="lambda gt11 library of J. Milan"
/2.372
/product="LRR N-terminal flank"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2053
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373. .966
Product="Leucine rich repeat region"
/label=LRRs
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Matches:
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                                                                                                                                                                                                                                                                                                                           1. .2053
/organism="Homo sapiens"
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/db xref="taxon:9606"
/sex="female"
               5T4 gene; 5T4 oncofoetal antigen.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-774-176-7 (1-9) x HS5T4OA (1-2053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=C-flank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label=N-flank
                                                                                                                                                                                                                                    (bases 1 to 2053)
    GI:435654
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                                                                                             Hominidae, Homo.
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misc_RNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 2 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
                                                                          Polypeptide
Patent: WO 0029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Homo sapiens 5T4 gene for 5T4 oncofoetal antigen.
Z29083
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Mismatches:
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Conservative:
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Matches:
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/db_xref="taxon:10090"
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/db xref="taxon:10090"
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                                                                                                                     BIOMEDICA LTD (GB)
Location/Qualifiers
                                                             Carroll, M.W. and Myers, K.A.
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MTVLPAGAFARQPPLADLAVIALSGNHLKEVGAGAFEHLPGIERLDISHNPLTNISAF
TFAGSNVSVSTPSPLLELILNHIVPPEDQRQNGSFEGWVAFEGWVAALRSGLALRGL
HHLELASHRFYLPRDLLDQLPSLKHUDLRNNSLVSLYSTSTRNLTHLESLHLEDNAL
KYLHSTLAERQCIAHVRYLDNNPWYCDCYWADWYSWLKETEVVPDKARLTGPER
MRNRGLDLTSSDLODATLEQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPSLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bul27282 2359 bp DNA linear PAT 18-SEP-2002
Primer for synthesizing full-length cDNA and use thereof.
BD127282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mpgagsrqpsagdgrlrlarlalvllgwysasapsslpsssts
paaplasgsagpppaercpaacecseaartykcynrnllevpadlppyvrnlflung
2 (bases 1 to 2333)
Buchman, V.L.
Direct Submission
Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 97S,
UK
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2713 22-JAN-2002; HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                     product="5T4 oncofetal antigen homolog"
protein id="AAP21770.1"
/db xref="G1:6650212"
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0 0 0 0
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Matches:
Conservative:
Mismatches:
                                                                                                                                                              1. 2333
/organism="Rattus norvegicus"
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/tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
Gaps:
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1. .2333
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                                                                                                                                             Location/Qualifiers
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JP 2002017375-A/2713
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JP 2002017375-A/2713.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                  /gene="5T4"
364. .1644
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2315. .2320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-NOV-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: trop@sanger.ac.uk
Sanger Xenopus troppicalis EST/CDNA project.
This sequence is from a Kenopus Gene Collection (XGC) library, from a library constructed by Aaron M. Zorn. CDNA was prepared from RNA extracted from gastrula embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
                                                                                                                                                                                                                                                                    Xenopus tropicalis

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;

Amphibia, Batrachia, Anura; Mesobatrachia, Pipoidea; Pipidae;

Xenopodinea, Xenopus; Silurana.

1. (bases i to 2183)

Amaya, E., Ashurst, J.L., Bonfield, J.K., Croning, M.D.R., Davies, R.M., Francis, M.D., Garrett, M., Glichrist, M.J., Grafham, D.V.,

Volgt, J. and Zorn, A.M.

Direct Submission
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                                                                                                                                                  VRT 03-NOV-2004
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1 (bases 1 to 233)
Ninkina,N.N. and Buchman,V.L.
Structure and expression of the rat 574 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA, APO63939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="texon:8364"
/db_cxref="texon:8364"
/clone="TdesO20h08"
/clone="TdesO20h08"
/clone="tdesO20h08"
/dev_stage="gastrula" (stage 10.5-13 mixed)"
                                                                                                                                       Zenopus tropicalis finished CDNA, clone TGas020h08.
CR855786
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Host: Escherichia coIi XL1-blue.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                                                  1135 TCCCTGCAAACCTCTTATGTCTTCCTG 1161
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                           SerLeuGlnThrSerTyrValPheLeu 9
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-7 (1-9) x CR855786 (1-2183)
                                                                                                                                                                                                             CR855786.1 GI:55295318
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43.00
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Query Match:
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.. No.:

ORIGIN

SOURCE

REFERENCE AUTHORS TITLE

DEFINITION

RESULT 21

8

AP063939

ACCESSION

VERSION

PEATURES

ORIGIN

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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Gubmitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK074786 2359 bp mRNA linear PRI 03-SEP-2002 Homo sapiens CDNA FLJ90305 fis, clone NT2RP2000694, highly similar to Homo sapiens 574 oncofetal trophoblast glycoprotein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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mRNA from NT2 neuronal precursor cells after 2-weeks
retinoic acid (RA) induction"
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Mismatches:
Indels:
Gaps:
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Mismatches:
Indels:
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                                         Length:
Matches:
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/db_xref="taxon:9606"
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/cell line="NT2"
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2 (bases 1 to 2359)
Isogai,T. and Otsuki,T.
Direct Submission
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            Alignment Scores:
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KEYWORDS
SOURCE
ORGANISM
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                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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TITLE
JOURNAL
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AK074786
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/ DOOT 27 (APP 1958 1."

/ DOOT 27 (APP 1958 1.")

/ DOOT 27 (APP 1958 1.")

/ DO ARE 27 (APP 1958 1.")

/ DOOT 27 (A
PD 22-JAN-2002
PP 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI TOSHIO, OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI SHIII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC CI2NIS/09, C07K14/47, C07K16/18, C12NI/15, C12NI/19, C12NI/21, C12NIS/ PC
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                                                                                                                                                                                                                                                                                                                  CC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                         (424). . (1572). Location/Qualifiers
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Matches:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity:
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DB:
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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CQ782724

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FEATURES

ORIGIN

2359 0 0 0 0

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Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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AUTHORS
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                                                                                         BD127283 2361 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD127283
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
JP 2002017375-A/2714
22-JAN-2002
07-JUL-2000
JP 200253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C (12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N1S/00,C12NS/00 CC Primer for synchesizing full-length cDNA and use thereof FH Key Location/Qualifiers

T CDS (456). (1685).
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Butherla, Buarchontoglires, Primates, Catarrhini, Hominidea, Homo.

1 (Jases 1 to 2361)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
                                                                                                                                                                                                                                                                                                         Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2714 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Sequence 2866 from Patent EP1396543.
CQ782726
                 1474 TCCCTGCAAACCTCTTATGTCTTCCTG 1500
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 1 SerLeuGlnThrSerTyrValPheLeu 9
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JP 2002017375-A/2714.
Homo sapiens (human)
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Best Local Similarity:
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AFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
SNHFLYLPRDVLAQLPSLERHIJLSNNSLVSLTYVSFRNLTHLESILHLEDNALKYLHNG
TLAELQGLPHIRVFLDNNPWVCDCHMADMYTWLKETEVVQGKDRLTCAYPEKMRNYL
LELNSADLDCDPILPPSLQTSYVFLIVLALIGAIFLLYLYLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYRINDPRLTNLSSNSDV"
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AFSGSNASVSAPSPLVELILINHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
SNHPLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Patent: WO 03104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                             Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2866 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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/organism="Homo sapiens"
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426_.1688
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Seguence 127 from Patent WO03104277.
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LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHWEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK074790 2361 bp mRNA linear PRI 09-JUL-2005 Homo sapiens cDNA FLJ90309 fis, clone NT2RP2000903, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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DNA Res. 12, 117-126 (2005)
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Mismatches:
Indels:
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Homo sapiens (human)
Homo sapiens
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Matches:
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Ratus norvegicus (Norway 181)

Ratus norvegicus (Nordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroldae; Muridae; Murinae; Ratus.

1 (bases 1 to 2361)

Sistrauberg, R.L., Feingold, B. A., Grouse, L.H., Derge, J.G., Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKernan, R.J., Mulking, W., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Madan, A., Rodrigues, S., Sanchez, A., Whithing, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M. Schein, J. B., Rocker, L. Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E., Butterfield, Y.S., Argenences

Nast, Manna, M. Schein, J.E., Jones, S.J. and Marra, M. A. Schein, J. B., R. Schein, J. B., Rettennences CDNA sequences

Nast, M. Schein, J. E., Schein, J. E., Schein, J. Bost, J. Schein, J. Bost, R. S., J. Schein, J. Schein, J. Bost, R. Schein, J. Schein, J. Bost, R. S., J. Schein, J. Schein, J. Bost,
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web aite: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
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mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Rhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maslello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
            Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richarde, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richarde, S., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skallska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Grimwood, J., Sand Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 26 Row: m Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-SBP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="synonyms: M6Pl,
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427. 1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/gene="TPBG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2379)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                              TITLE
                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Linta et http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143.
1. .2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trainiation="Megagsrqpsagdgrlrlarlarlarlgwysasapssslpsssts
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Paaflasgrapppladlarvalsgrmtkevgagaffellfpglrldlshnpltnlsaf
Tragsrvsystpsptlllerlilmhivppeddrongsfrgwyargewyarlarglalrhil
Hhlelasnhflylpprdlpslkhldlrnnslvslltyasfrnuthleslhiednal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVIJINSTIJAEMOGIAHVRVPIDNNPMVCDCYMADMVSMIKETEVVPDKARLTCAPPEK
MRNRGILDDIJSSDLDCDATLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMBGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2379 bp mRNA linear PRI 29-JUN-2004 Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317 IMAGE:4138906), complete cds.
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1 (bases 1 to 2379)

Strausberg, R.L., Feligold, R.A., Grouse, L.H., Derge, J.G.,

Altschul, S.P., Zeeberg, B., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, P.,

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="Tpbg protein"
(protein id="AAH87011.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="GeneID:83684"
db_xref="RGD:621453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="synonym: 5T4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="RGD:621453"
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BC037161.2 GI:33872201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="Tpbg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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43.00
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Best Local Similarity:
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DB:
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KRYWORDS
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckerrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Teurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFAGSNASVSAPSPLEELILMHIVPPEDORONGSFEGMVAPEGMVAAALRSGIALRGI
TCLELASNHFLFLPRDILAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KVINSTLEAGMGLAHVKPELDNNPWYCDCYAADMVAMLKETEVVPDKARLTCAFPEK
MRNEGLIDLMSSDLOCDAVLPOSLOTSYVEKSIVYLIGIALIGAIFLLVLYLNRKGIKKWM
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānblation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSVPSSSTS
PAAFLASGSAQPPPAERCPAACECSEAARTVKCVNRNLLEVPADLPPYVRNLFLTGNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="COG4886; Region: COG4886, Leucine-rich repeat (LRR)
                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LRRCT; Region: Leucine rich repeat C-terminal
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/note="Vector: pCMV-SPORT6"
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Conservative:
Mismatches:
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(db xref="CDD:COG4886"
1299. .1415
/gene="Tpbg"
                           Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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Sequencing Center (NISC),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="Tpbg"
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Best Local Similarity:
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Riausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bossak, S.A., McRwan, P.J.,
McKernan, K.J., Malek, J.A., Qunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Whiting, M., Nadan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2423 bp mRNA linear ROD 21-OCT-2003 Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 MRGE:5353871), complete cds.
                        LAVLPAGAFARRPPLAELAALNISGSRLDEVRAGAFEHLPSIRQLDLSHNPLADLSPF
APSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELA
SNHFLYLPRDVIAQLPSLRHLDLSNNSLVSLTYVSFRNITHLESIJHLEDNALKVLHNG
                                                                                                   TLAELGGLPHIRVFLDNNPWVCDCHMADMYTMLKETEVVQGKDRLTCAYPEKMRNRYL
LELNSADLDCDPILPPSLQTSYVFLGIYLALIGAIPLLVLYLNRKGIKKMMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
APPLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Submitted (15-SE2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
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Hashimoto, K., Kusuda, J. and Sugano, S.
Direct Submission

Submitted (18-MAR-2014)

Infectious Diseases, Division of Genetic Resources; 23-1, Toyama

1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan

(R-mail:khashi@mih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)

The International consortium for macaque cDNA sequencing and analysis oonsists of: Department of Virology and Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan, Division of Genetic Resources, National Health Research Institute, Taipei, Taiwan; Dispartment of Molecular Biology, Academia Shinca, Taipei, Taiwan; Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA; Center for Information
                                                                                                                                                                                                   AB168308 2714 bp mRNA linear PRI 18-JUN-2005 Macaca fascicularis testis cDNA clone: QtsA-11109, similar to human trophoblast glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osada, N., Hirata, M., Tanuma, R., Kusuda, J., Hida, M., Suzuki, Y., Sugano, S., Gojobori, T., Shen, J.C.-K., Wu, C.I. and Hashimoto, K. Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey CDNAs
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oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                         /mol_type="unassigned DNA"
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556_ .1836
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Stat6 activation gene
Patent: WO 03104277A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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Stat6 activation gene
Patent: WO 03104277A 123 18-DEC-2003;
Asahi Kasel Kabushiki Kaisha (JP)
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Sequence 123 from Patent W003104277.
AX961912
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AX961914
AX961914.1 GI:40881324

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                        1470 TCCCTGCAGACTTCCTATGTCTTCCTA 1496
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/gene="5T4"
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/gene="5T4"
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/gene="5T4"
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/gene="5T4"
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                                                                       Hominidae; Homo.
    Homo sapiens
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                                                                                 Vector: pWE186-FL3 (Acc.No. AB009864)
R. Sitea: Drail (CACTGTGTG)
R. Sitea: Drail (CACTGTGTG)
R. Sitea: Drail (CACTGTGTG)
R. Sitea: Drail (CACTGTGTG)
R. Sitea: Acc.No. About the control of the care of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biology, National Institute of Genetics of Japan, Mishima, Japan. Clone distribution: clone distribution information can be found at: http://www.nih.go.jp/yoken/genebank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 15-APR-2005
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5T4 Gene; 5T4 oncofetal trophoblast glycoprotein. Homo sapiens (human)
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/dev_stage="adult"
764._.2026
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Matches:
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Mismatches:
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QtrA: temporal lobe right
QflA: frontal lobe left
QmoA: medulla oblongata
QbsA: brain stem
QcrA: occipital lobe right
QtsA: testis
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/mol type="mRNA"
/db xref="taxon:9541"
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db_xref="GI:67967900"
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGIRRLDLSHNPLTNLSAF
VPAGSNAAVGAPSPLEELILNHIVPPENOKOMGAFEGHVAFRGWVAAALRSGLALRGL
TRLELASHNPLPLPRDLLAGDJPSLYVLDLRNNSLVSLTYASFRNLTHLESILHLENDAL
KVLHNSTLAEMQGLAHTVYPLDNNPWVCDCYWADWYAMLKETEVVDBARLLYGCAFPER
MRNRGLLDLNSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWH
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Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BK, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                    King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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/db_xref="InterPro:IPR001591"
/db_xref="WG1:1341264"
/db_xref="WG1:1341264"
                                                                                                                                                                                                                            Mus musculus 5T4 oncofetal trophoblast glycoprotein gene
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AJ012160.1 GI:3805948
5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Mus musculus (house mouse)
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 Indel8:
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/strain="129/Sv"
/db_xref="taxon:10090"
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3108. 3113
/bound_molety="Sp1"
                                                                                              SerLeuGlnThrSerTyrValPheLeu 9
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/gene="5T4"
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/gene="5T4"
3779. .5059
/gene="5T4"
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Direct Submission

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Dec 15, 2000 this sequence version replaced gi:11558491.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromesome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.aanger.ac.uk/HGP/Chr6

RRD: 492P14 is from the library RPCI-3 constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm

VECTOR: pCYPAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSJ492P14 12-MAY-2005
Human DNA sequence from clone RP3-492P14 on chromosome 6q13-15
Contains a single stranded DNA binding protein pseudogene, the TPBG
gene for trophoblast glycoprotein (5T4-AG) and a CpG island,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                      'product="5T4 oncofetal trophoblast glycoprotein"
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NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV*
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Matches:
Conservative:
Mismatches:
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HTG; CpG island; TPBG.
Homo sapiens (human)
Homo sapiens
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/gene="5T4"
5759. .5764
/gene="5T4"
                                                                                         3866. .5056
/gene="5T4"
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/gene="5T4"
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AL121977
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as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                                                                                                               ROD 21-JUN-2005
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Submitted (21-JUN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On May 4, 2005 this sequence version replaced gi:61656412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-MAY-2005) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 167046) Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                               ACI58516 167046 bp DNA linear ROD 21-JUN-
Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
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Contact: submissions@watson.wustl.edu
                                                                                                                    Center project name: M_BB0511A23
Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi, Muridae, Murinae, Mus.
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                                                                        US-10-774-176-7 (1-9) x HSJ492P14 (1-121909)
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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AC158516.2 GI:63025421
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Wilson, R.K.
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AC158516/c
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AFSGSNASVGAPSPLVELILNHIVPPEDERQNRSFEGWVVAALLAGRALQGLRRLELA
STRYFZVLPROVLAQLPSLRHLDLSNNSLVSLTYVSFRALTHLESLHLEDNALKYLHNG
TLAELQGLPHIRVFLDNNPWVCDCHRADMYTMLKETEVVQGKDRLTCAYPERWRNYL
LELNSPALDCDPILPSELQTSYVPTGIVLALICAIFLLYLYLNRKGIRKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV*
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BF314984 BI196133 BI562387 BM069633 BM670613
match: cDNAs. 2.4420536.1 Z29083.1"
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codon start=1
except on the rare occasion of the clone being a YAC.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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109639. .116836
gene="TPBG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE.
AC128294.3 GI:25083347
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rutus norvegicus
                  Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                          The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CSTBL/6J mouse spleen and/or brain genemic DNA. The Clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
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16685. 16712
/note="Sequence derived from PCR product of genomic DNA"
31565. 31779
/note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46721. .46808
/note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of the clone.
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Gebregeorgis E., Geer K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harvalak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Hollins, B., Howells, S., Hune, J., Hodgeon, A., Hogues, M., Hollins, B., Howells, S., Hune, J., Hodgeon, R., Johnson, R., Liu, J., Liu, M., Liu, Y., Lebow, H., Lorado, R.J., Lews, J., Lews, J., Lews, J., Lews, J., Lews, J., Lorgacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Mangum, B., Mangum, B., Mangum, B., Mangum, B., Martiner, G., Mandartne, M., Mandadartne, M., Monte, S., Mores, S., McLeod, M.P., Mortin, K., Martin, R., Martinez, E., Mankhiney, S., McLeod, M.P., Morkell, T.Z., Meenen, E., Morris, K., Martin, K., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, M., Morris, S., Morris, S., Morris, S., Morris, S., Manker, G., Minja, E., Mundasa, M., Murphy, M., Naris, L., Lu, Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Polidetter, A., Polidetter, A., Polidetter, A., Rosie, M., Rosie, M., Richards, S., Riggs, F., Reilly, B., Reilly, M., Ren, Y., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Savery, G., Scherter, S., Soret, G., Shataman, S., Shen, H., Steinle, M., Strong, R., Shor, Y., Valas, R., Shor, J., Walfer, R., Willen, S., Warren, J., Walfer, R., Willen, W., Waller, M., Waller, R., Willen, W., Waller, R., Willen, J., Waller, R., Willen, J., Waller, R., Willen, J., Waller, R., Willen, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausenn, A., Weiss, R., Merse, R., Holt, R., Weiss, R., Merse, R., Holt, R., Weiss, R., Merse, R., Weiss, R., Weiss, R., Weiss, 
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ICE 3 (bases 1 to 210237)

RRS Rt Genome Sequencing Consortium.

Submitted (19-MOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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On Nov 19, 2002 Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Expense and Whole Genome Shotgun Sequence ordered as scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold by Sized gaps filled with NS to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of Whole genome Shotgun sequence reads. Both end sequences and Whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GZGV
Center clone name: GZGV
Center clone name: CH230-176H20
Assembly program: Phrap; version 0.990329
Consensus quality: 201781 bases at least Q30
Consensus quality: 203921 bases at least Q30
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Center code: BCM
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Direct Submission
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REFERENCE
AUTHORS
TITLE
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                                                                               NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
unordered pieces.
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1 (bases 1 to 239076)

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Aydeqii, M., Baca, B., Baden, H., Baladaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Consensus quality: 205310 bases at least Q20
Bstimated insert size: 205531; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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AC106962.5 GI:25139469
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Conservative:
Mismatches:
Indels:
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/mol_type="genomic DNA"
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complement(206062..206961)
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Best Local Similarity:
Query Match:
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AC106962/c
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Bryant, N. Bungay, C., Burca, F., Burca, L., Cacader, N., Carter, N., Carter, N., Carter, N., Carter, N., Carter, N., Carter, C., Cayola, M., Carter, N., Carter, C., Cayola, M., Care, N., Carter, N., Clacko, J., Chacko, J., Davil, R., Panig, T., Panig, P., Panig, C., Panig, C., Panig, C., Panig, C., Panig, R., Davil, B., Cartia, A., Garner, T., Garza, M., Gebregeorgis, E., Gerk, G., Hamilton, C., Hamilton, R., Harnandez, R., Habel, S., Hiddun, S. L., Hodgson, A., Hollish, B., Howells, S., Haldun, S. L., Hodgson, A., Harnandez, R., Jacob, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Jackson, L., Jackson, R., Johnson, B., Johnson, R., Manigh, P., Martin, R., Martin, R., Mani, J., Manigh, R., Manier, P., Maris, S., Munidasa, M., Murin, M., Mallow, P., Maris, S., Munidasa, M., Murin, S., Pani, R., Perez, J., Peraz, J., Peraz, R., Perez, R., Perez, R., Pennen, E., Phazzo, M., Oulxor, J., Pennen, E., Phazzo, M., Oulxor, J., Pennen, R., Rayler, R., Miner, G., Minja, R., Mayu, M., Martin, R., Reilly, M., Ren, Y., Reigh, R., Rives, C., Davilor, C., Scherer, S., Scott, G., Shateman, S., Shan, H., Savery, G., Scherer, S., Socki, C., Wallson, W., Villasana, D., Waldor, M., Walde, R., Walder, R., Walder, R., Martin, R., Martin, R., Marti Direct Submission

Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dases 1 to 239076)

Bat Genome Sequencing Consortium.

Direct Submission

Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:22857070.

The sequence in this sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequence contigs will be indicated in the feature Calderon, B. Bryant, N., Buhay, C., Burch, P., Burrell, K., (bases 1 to 239076) Worley, K.C. Direct Submission Unpublished

------ Genome Center Center: Baylor College of Medicine

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Direct Submission

L. Submitted (129-2015) National Institutes of Health, Mammalian Direct Submission

M. Submitted (129-2016-2015) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Will Talbot

CDNA Library Preparation: Dr. Yutaka Suzuki and Dr. Sumio Sugano

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casawant, T.L.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKernan, F.J.,
McKernan, K.J., Malek, J.A., Gask, S.H., McKernan, F.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
M.D. 1977027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
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of 2500 embryos"
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            AUTHORS
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                      * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* Consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 1713)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Matches:
Conservative:
Mismatches:
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from base 200001 (AL353584 Homo sapiens chromosome X (
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Homo sapiens chromosome X clone RP11-466G5, 17 unordered pieces.
AL445194
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 26, 2001 this sequence version replaced gi:10716446.
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                    Gaps:
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Homo sapiens (human)
Homo sapiens
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RSLRSLDLSNNQLAVIHPRAFTVQSRMLRBLALSRALYNHSSVMDLATSLRWSSLSDL
LYLDLSSNGLVPLPSGI FCHLVGLRRLQLGRNSI VSI HNGTFTGLDRLQELDLTHNAL
RTLRBEALKELBQLHSARLHLADNPFTCTCDI BPFAAMLNGSRGQVVDI EGLTCAFPV
ALHNTSLLTVSDLELGCHKAGDSDNLALQTSVYPLGIVLGFVGLMFLFVLYLNRKDIK
KRI YDMRDACREVWEGYHYRYEI DSDPRLSQVSSTADV"
                                                                                                                                                                                                                                                                                                                                                                                               nduy/825 11-JUN-2003
Danio rerio YF-296 mRNA for hypothetical protein, complete cds.
AB097825
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Furutani-Selki,M.
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DLRDIPSGIPGYTRNIPITGNHISQIGPESFQGLENVTNLSLSNNRISEVKSHTFSSL
RSLRSLDLSNNQLAVIHPRAFTVQSRMLREIMSRALYNHSSVMDLAATSLRWSSLSDL
LVLDLXSRGLVFLPSGIFCHLVGLRRLQLGNNSIVSINSTFGLDHLQRLDLTHNAL
RTLARBALKELRQLHSARLHLADNPFTCTCDIRPFAAWLNGSRGQVVDIBGLTCAPPV
ALHNTSLLTVGDLEGCHKAGBSDNLAALQTSYVPLGIVGFVGLMFLFVLYINRKDIK
KRIYDMRDACREVWEGYHYRYEIDSDPRLSQVSSTADV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished

(bases 1 to 1765)

Yoda, H., Kondoh, H. and Purutani-Seiki, M.

Direct Submission

Submisted (10-DEC-2002) Makoto Purutani-Seiki, ERATO Kondoh

Differentiation Signaling Project, JST; Kawara-machi 14, Yoshida,

Sakyo-ku, Kyoto 606-8305, Japan

(B-mail::furutanie:ki@msi.biglobe.ne.jp, Tel:81-75-771-9362,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An expression pattern screen for genes involved in induction of posterior nervous system of zebrafish
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protein_id="BAC77539.1"
db_xref="G1:31580870"
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1. .1765
/gene="YF-296"
                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                    1 SerLeuGlnThrSerTyrValPheLeu 9
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Location/Qualifiers
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/gene="YP-296"
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Danio rerio
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TITLE

Pred. No.:

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ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 42

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AB097825

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Fragment_chain:2"
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Quality coverage: 3.46x in Q20 bases; sum-of-contigs Quality coverage: 2.78x in Q20 bases; agarose-fp
                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                               12531: contig of 12531 bp in length 12631: gap of 100 bp 17456: contig of 4825 bp in length 17556: gat of 100 bp 19714: contig of 2158 bp in length 19814: gap of 100 bp 26971: gap of 100 bp 31635: contig of 4664 bp in length 26971: gap of 100 bp 31735: gap of 100 bp 37319: contig of 5584 bp in length 37419: gap of 100 bp 53243: contig of 5584 bp in length 37419: gap of 100 bp 53243: contig of 100 bp 532443: contig of 100 bp 542443: contig of 100 bp 542443: contig of 100 bp 5424443:
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90669: 94p of 100 bp
90669: 94p of 100 bp
96363: contig of 5634 bp in length
96463: 94p of 100 bp
108198: contig of 11735 bp in length
108298: 94p of 100 bp
119566: 94p of 100 bp
119666: 94p of 100 bp
122309: contig of 2643 bp in length
122409: 94p of 100 bp
131711: contig of 9302 bp in length
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fragment.chain:1"
17557...19714
/note="assembly_fragment:00751
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/db_xref="taxon:9606"
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12632._.17456
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Cambrited (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
Clone Sep 9, 2000 this sequence version replaced gi:9943980.

The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:
Bm:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human achromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL139114 13-MAY-2005
Human DNA sequence from clone RP11-328C23 on chromosome
9p22.3-24.1, complete sequence.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                          4000
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Mismatches:
Indels:
53344 . .58752
/note="assembly fragment:00257
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fragment chain:2"
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Matches:
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Sehra, H.
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Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
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JOURNAL
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                                                                                                                                                                                                                                                                      regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                         RP11-328C23 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all
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Mus musculus chromosome 1, clone RP24-188H2, complete sequence
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Mus musculus chromosome 1, clone RP24-188H2
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Mismatches:
Indels:
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                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VBCTOR: pBACe3.6
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                       Web site: http://www.sanger.ac.uk
http://www.Banger.ac.uk/HGP/Chr9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="p22.3-24.1"
/clone="RP11-328C23"
                                                                                                               Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="9"
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40.00
100.0$
: 88.9$
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                                                                    Center code: SC
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Best Local Similarity:
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DB:
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No.:
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
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AUTHORS
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Direct Submission

Direct Submission

Direct Submission

Charles Street, Cambridge, MA 02141, USA

# (bases 1 to 178603)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Brickson, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B. Hall, J., Horton, L., Hulme, W., Illev, I., Gandon, D., Maccean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Landers, T., Levine, K., Lindalad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maccathy, M., Meldrim, J., Meneus, L., Miyova, T., Micol, R., Norbu, C., O'Comnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasawy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, V., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalnoun, J., Zambek, L., Dibmitted (12-JTN-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacCaenld, P. Major, J., Marquis, N., Matthews, C., McCarthy, M., McGwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seman, J., Rosetti, M., Spencer, B., Stange-Thomann, N., Stojanovic, N. Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Waman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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repeat\_region

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Center: Broad Institute of MIT and Harvard
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181. .422
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complement (1091. .1251)
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complement (1252. .1465)
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complement (5033 .5160)
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complement (9584. .9684)
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complement (1631. 1722)
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2503. 2609
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522. Ref
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omplement(7321. .7474)
rpt_family="81_MM"
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243. .7265
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2627. .2703
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rpt_family="(GAA)n"
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929 _ 6052
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                                                                                                          Location/Qualifiers
1. .178603
                                                                                                                                                                                                          clone="RP24-188H2"
                                                                                                                                                                                chromosome="1"
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AC116853 188514 bp DNA linear ROD 19-OCT-2004
Mus musculus chromosome 1, clone RP24-400M20, complete sequence.
AC116853
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mus musculus chromosome 1, clone RP24-400M20
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/rpt family="ID B1"
complement (15412. .15449)
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15789. .15823
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complement(15323. .15334)
/rpt_family="BlF"
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complement (15948. .16077)
/rpt family="B1 MM"
complement (16201. .16272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="B1F"
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complement(16362, .16466)
/rpt_family="Bl_MM"
complement (10088. .10193)
/rpt_family="PB1D9"
complement (10940. .11043)
/rpt_family="L3"
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13704. 13925
/rpt_family="B3"
13959. 14090
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[2049], .12093
                                                                                                                       /rpt_family="(TG)n"
13265. .13317
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Mus musculus
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5083. .15166
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                                                                          .11882
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AC116853
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TITLE JOURNAL

REFERENCE AUTHORS

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Contact: sequence submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                Clone lib="RPCI-24 Male Mouse BAC"
          Web site: http://www-seg.wi.mit.edu
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complement(1429. .1622)
/rpt family="HALL"
/rpt family="HALL"
                                                                                                                                                                                                                                                                        organism="Mus musculus"
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466. .3503
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/rpt_family="B3"
{054. .4157
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complement(1825..1838)
/rpt_family="B4A"
complement(1839..1957)
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/db_xref="taxon:10090"
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complement (1958. .1998)
/rpt family="B4A"
1999. .2037
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complement(2086, .2655)
/rpt_family="Lx2"
2655, .2810
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complement (516. 566)
/rpt_family="B2 Mm2"
complement (632. 804)
/rpt_family="B2 Mm1"
complement (874. 1020)
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/rpt_family="U2"
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4437. .4467
/rpt_family="AT_rich"
4691. .4744
                                                                                                     Center project name: L25620
Center clone name: 400_M_20
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/rpt_family="B3"
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'rpt_family="(CAAA)n"
856. .2947
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984. .3211
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family="(TTTG)n"
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/rpt_family="B2_Mm2"
                                                                                                                                                                                                           Location/Qualifiers
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5128. .5323
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complement (1178. .1
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811. .2855
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Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macdenald, P., Major, J., Marquis, M., Matthews, C., Macdonald, P., Major, J., Marquis, M., Matthews, C., Macdonald, P., Major, J., Marquis, M., Matthews, C., Micol, M., Minga, V., Murphy, T., Naylor, J., Mquyen, C., Nicol, R., Olver, J., Poterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Staley, R., Schauer, S., Schupback, R., Stans, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (Dases 1 to 188514)

Birren, B., Wusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, J., S., Dooke, P., Comum, S., Collymore, A., Cooke, P., Corum, B., Cander, J., S., Dooley, K., Dorris, L., Brickeon, J., Raro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B. Hall, J., Horton, L., Hilme, M., Illev, I., Levine, R., Lindblad-Took, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., Macdonald, P., Major, J., Manning, J., Mathews, C., Macdonald, P., Major, J., Mihova, T., Micol, R., Mabbitt, R., Murphy, T., Naylor, J., Welly, C., Nguyen, C., Nguyen, T., Micol, R., Machan, C., Senmor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Senman, S., Severy, P., Saith, C., Spencer, B., Stange-Thomann, N., Stoham, S., Stubbe, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Volamer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Suban, S., Subanission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/MIT Center for Genome Research
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On Oct 19, 2004 this sequence version replaced gi:50726824.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catenses, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AL353584; the clone sequenced to the right is AC020674. Actual start of this clone is at base position 1 of RP11-462H12; actual end is at base
                                                                                                                                                                                                               University, 4444 Forest Park Avenue, St. Louis, Mashington 6 (bases 1 to 213793)
Waterston, R.
                          Direct Submission
Submitted (29-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MM 03108, USA
5 (bases 1 to 213793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jul 29, 2000 this sequence version replaced gi:7631007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
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Center code: WUGSC
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Contact: sapiens@watson.wustl.edu
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137.322
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1021..1146
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                                                                                                                                                                                                     Waterston, R.
Direct Submission
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Homo sapiens BAC clone RP11-462H12 from X, complete sequence.
AC019212
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4 (bases 1 to 213793)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grewal, N., Drone, K., Laplant, Y. and Le, T.
The sequence of Homo sapiens BAC clone RP11-462H12
Unpublished
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Matches:
Conservative:
Mismatches:
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1 (bases 1 to 213793)

10 Suston, J. B. and Materston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt family="B4" (8125) (rpt family="B4" (8335) (rpt family="Lt" (rpt family="Lt" (8580) (rpt family="
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/rpt family="LiM4"
complement (6282 . .6422)
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complement (6423 . .6468)
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complement (7338. .7445)
/rpt family="Bl_MM"
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[ement (8)^^
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Best Local Similarity:
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Pred. No.:

DEFINITION ACCESSION VERSION

RESULT 48

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AC019212

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KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL

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32897. .35332

/rpt family="RRVI"

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1 (Dases 1 to 64140)

Birren, B., Linton, L., Nusbaum, C. and Lander, R.
Homo sapiens chromosome 18, clone RP11-35013
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Norbu.C., Netterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Rette,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talains,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,N., Travers,N., Vessiliev,H.,
Vel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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C 808																																																													

us-10-774-176-6.p2n.rng

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The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKF2psG611313 activity. The methods are useful for treating cancer, e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be
                                                                                                    Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for inhibition of DKFZp5661133 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; expression profile; solid tumour; mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                                                                                                                                                                                         Sequence 246 BP; 77 A; 49 C; 59 G; 61 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 30; SEQ ID NO 47; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solid tumour prognosis gene seqid 2116.
                                                                                                                                                                                                                                                                          used in the method of the invention.
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23-JAN-2004; 2004US-0538246P.
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Immerman F, Dorner AJ;
                                                                          WPI; 2003-577534/54.
              (CHIR ) CHIRON CORP
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Best Local Similarity:
Query Match:
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(STRA/) STRAHS A.
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peripheral blood
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                                            Hansen R;
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Adb86278 Human sec
Acf56385 Human sec
Acf56692 Human sec
         AC£4435 Human sec
Acc04627 Human sec
Acc04024 Human sec
Acd21129 Human sec
Acd20822 Human sec
Acf07218 Human sec
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Acf77874 Human sec
Acf46272 Human sec
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Acf86036 Human sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; cytostatic; gene therapy; DKFZp5661133 activity inhibitor; breast cancer; differential expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast cancer differentially expressed gene product #47.
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ADB66278
ACF5638
ACF56692
ACF55171
ACF55171
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ADD06008
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ADC01711
ACC7775
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ACC7775
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ACF47175
ACF4543
ACF45947
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ACF48659
ACP38659
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ACD86036
ACF76032
ACF60932
ACH05819
ADA82970
ACF56078
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            Homo sapiens.
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   ADK11641;
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4 4 6

A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.

WPI; 2004-804779/79.

Disclosure; Page; 111pp; English

08-JAN-2003; 2003WO-US000657. 08-JAN-2002; 2002US-0345637P.

WO2003057926-A1.

RESULT 1 ADK11641 17-JUL-2003

Slonim DK;

Twine NC,

/note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids"

misc\_feature

/\*tag= c/fnote= mgiven in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids"

207. .216 /\*tag= d

misc\_feature

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The invention describes a method comprising comparing an expression profile of at least one gene, where the fast one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood monomclear cells (PBMGs) of a first class of patients as compared to PBMGs of a second class of patients, where cot patients as compared to PBMGs of a second class of patients, where cot patients and second classes of patients have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, and patients who have the solid tumour, and where the majority of the first class of patients has a second clinical outcome. Also described are: a system comprising (i) a memory or a cutcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at class one gene in a peripheral blood sample of a patient who has a solid tumour, (ii) at least another storage medium including data that the expression profile of the reference expression profile, and (iv) a processor capable of executing the companies on profile, and (iv) a processor capable of executing the companies on profile, and (iv) a processor capable of executing the class of patients where solid tumour prognosis genes is differentially expressed in thical outcomes of the patients; and an another accord class of patients as compared to pages. Where comprising outcomes of the patients; and an another expression profile of patients and except of protein array are useful for prognosis genes of patients and second class of patients and second class of patients as compared to page.

The method, system, and array are useful for prognosing and treating gene of the invention. Note: The sequence data for this pateent dat not form part cot the invention. Note: The sequence data for this
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Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-774-176-6 (1-9) x ADU11677 (1-475) 31.6 40.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: 8

AAA27060 standard; DNA; 901 BP AAA27060 RESULT 3 

AAA27060;

(first entry) 22-AUG-2000

Canine 5T4 tumour-associated antigen gene.

Canine; TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer; Canine;

Canis sp.

/\*tag= a /product= "5T4 antigen" 51. .74 Location/Qualifiers /\*tag= misc\_feature

Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors. /\*tag= e
/note= "given in the specification but does not seem to
/note= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids"
351. .361 /\*tag= f
/orde= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids" /\*tag= h /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" 572. .583 /\*tag= k /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" 784. .801 /\*tag= 1
/note= "given in the specification but does not seem to
be part of the coding sequence and does not encode any
corresponding amino acids" /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /\*tag= g /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" /note= "given in the specification but does not seem to be part of the coding sequence and does not encode any corresponding amino acids" (OXFO-) OXFORD BIOMEDICA UK LTD. 98GB-00025303. 99GB-00001739. 99GB-00017995. 99WO-GB003859 422. .436 497. .511 644. .653 /\*tag= /\*tag= Carroll MW, Myers KA; WPI; 2000-387735/33. P-PSDB; AAY94351. WO200029428-A2. misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature 18-NOV-1999; 18-NOV-1998; misc\_feature misc\_feature misc\_feature 27-JAN-1999; 30-JUL-1999; 25-MAY-2000 

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                                    The present sequence encodes the canine 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been human or murine 5T4 gene sequence. The 5T4 antigen to octor containing the human or murine 5T4 gene sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used
                                                                                                                                                                              elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
                                                                                                                                                                                                                        Sequence 901 BP; 178 A; 246 C; 212 G; 153 T; 0 U; 112 Other;
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              Disclosure, Page 78-79; 79pp; English.
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09-APR-2001; 2001US-00829472.
09-APR-2001; 2001US-028269B.
04-MAY-2001; 2001US-0288590P.
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Claim 9; Page 372; 414pp; English.

cancer nucleic acids.

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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer calls dor detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABTO763 - ABTO7761 represent the 69 breast cancer-associated gene sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0334370P.
29-NOV-2001; 2001US-0334370P.
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P-PSDB; ABU56604.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX76333;
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DB:
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transcript in a cell from a patient, comprising cancering a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer caspociated polymucleotides and polypeptides are used for identifying a compound that modulates a lung cancer—associated polypeptide, for inhibiting proliferation of a lung cancer—associated polypeptide, for inhibiting proliferation of a lung cancer—associated polypeptide, for inhibiting proliferation of a lung cancer—associated polypeptide, for cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful cor treating lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis The genes, polyuncleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                    The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological
patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927
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Mismatches:
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Matches:
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                                                Claim 22; Page 336; 453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB80503 standard; DNA; 927 BP
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2001US-0315287P.
2001US-0317544P.
2001US-0350666P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2001;
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12-APR-2002;
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DB:
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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                     The invention relates to a method of detecting an ovarian cancer-
sasociated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
and as vaccines. This sequence corresponds to one of the mucleic acids
used for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                        Claim 10; Page 297; 332pp; English.
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(BOSB-) EOS BIOTECHNOLOGY INC.
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21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
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40.00
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                                                                    WPI; 2003-167431/16
                                  Gish KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                    P-PSDB; ADB80504
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comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a candidate p53 pathway-modulating agent for treating cancer
                  Human; p53 pathway; Leucine rich repeat capricious related protein;
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                                            LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                          21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                  22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                       Belvin M, Schleithoff L, P]
Francis-Lang H, Priedman L;
                                                                                                                                                                                                                                                                                                                                                             (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-421410/39.
                                                                                                                                  WO2003035831-A2
                                                                                        Homo sapiens.
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DB:
The invention relates to mucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a confident by defecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attenned other conditions such as psoriasis, ischaemia, heart disease, attenned other conditions such as psoriasis, ischaemia, heart disease, attenned other conditions such as soriasis, include the may necessary diseases, autonoment diseases, attenned the acids in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                         Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a nucleic acid sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                           Afar D, Aziz N, Ginsburg WM, Mack DH, Murray R, Watson SR,
                14-DEC-2001; 200108-0340376P.
08-JAN-2002; 2002U8-034731PP.
10-JAN-2002; 2002U8-034734PP.
08-PEB-2002; 2002U8-0355250P.
13-PEB-2002; 2002U8-0355250P.
29-MAR-2002; 2002U8-0358977P.
29-MAR-2002; 2002U8-0368097P.
12-APR-2002; 2002US-0368097P.
05-JUN-2002; 2002US-0368697P.
                                                                                                                                                                                                                                                                                                                                                                                                         Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                       2002US-0397775P.
                                                                                                                                                                                                                                                                                                                   2002US-0409450P
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22-JUL-2002; 2
09-SEP-2002; 2
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Plowman GD, Funke RP, Lioubin MN,

The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent agent and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; notropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertiilty; rerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; dlabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other; 60000 60000 Conservative: Mismatches: Indels: Gaps: Length: Matches: 763 GCCCTGATAGGCGCTATTTTCCTCCTG 789 o 1 AlaLeuileGlyAlailePheLeuLeu US-10-774-176-6 (1-9) x AAD56198 (1-973) ABV99349 standard; DNA; 1156 Human NOV8a coding sequence. (first entry) 71.4 40.00 100.0\$ 100.0\$ Best Local Similarity: Percent Similarity: Alignment Scores: 27-JAN-2003 ABV99349; RESULT 9 ABV99349 ò 셤 

AAD56198 standard; DNA; 973

RESULT 8

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Human LRRCAPS related DNA #5.

(first entry)

07-AUG-2003 AAD56198;

AAD56198
ID AAD5
XX
AC AAD5
XX
DT 07-P
XX

US-10-774-176-6 (1-9) x ADN38723 (1-927)

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Casman SJ; RA, Vernet CAM;

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99127-ABV99555 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disquences and proteins are useful for treating, preventing or disquences and proteins are useful for treating, concer, neurodegenerative disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or disagnostic methods
                                                                       Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli RA, Vernet CAM, Pena CEA, Burgess CE, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE, Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                    New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; feetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                               Claim 16; Page 114-115; 619pp; English.
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 03-JAN-2002; 2002US-0345705P. 08-MAR-2002; 2002US-00093463.
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                                             (CURA-) CURAGEN CORP.
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Best Local Similarity:
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Query Match:
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bronchial asthma, dyslipidemia, metabolic disturbance, neurogenesis, metabolic syndrome X; wasting disorder; cell differentiation, gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
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2001US-0287424P.
2001US-0288066P.
2001US-0288342P.
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2001US-0275579P.
2001US-0275601P.
2001US-0276000P.
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2001US-0294889P.
2001US-0294899P.
2001US-0299027P.
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2001US-0274281P.
2001US-0274322P.
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2001US-0276994P.
2001US-0277239P.
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2001US-0291190P.
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2001US-0338092P
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21-MAR-2001;
22-MAR-2001;
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26-MAR-2001;
27-MAR-2001;
                                                         Homo sapiens.
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04-DEC-2001;
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02-APR-2001;
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03-MAY-2001;
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16-MAY-2001;
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31-OCT-2001;
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                                                                                                                   19-SEP-2002
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5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.

Unidentified

Key

/product= "Feline 5T4 antigen protein"

WO2003068816-A1

21-AUG-2003.

Location/Qualifiers 1. .1260 /\*tag= a

Redchenko I;

Carroll M, Kingsman S, WPI; 2003-637141/60.

P-PSDB; ADB97520.

(OXFO-) OXFORD BIOMEDICA UK LTD.

13-FEB-2002; 2002GB-00003419. 13-FEB-2003; 2003WO-GB000670

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the professed leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tisgues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, useful in preparation of vaccine for treating preventing cancer in a subject, preferably a dog or cat.
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Matches:
Conservative:
Mismatches:
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                                                                                                                        /*tag= a
/product= "5T4 protein"
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                                                            Location/Qualifiers
1. .1260
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                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2000; 2000WO-GB004317.
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40.00
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Best Local Similarity:
Query Match:
DB:
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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 574 antigen. The invention further class I peptide epitope string comprising the 574 epitope; a uncleic acid sequence encoding the 574 epitope or a polyepitope string of the 574 cpitope; a vector system capable or a polyepitope string of the 574 epitope is a cell pulsed with the 574 epitope, a polyepitope of the 574 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease or a pubject by administering the vaccine; an agent capable of binding specifically to the 574 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 574 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of specifically recognishing the 574 epitope in conjunction with an WHC class or specifically recognishing the 574 epitope in conjunction with an except system or cell is useful in the prevention and/or treatment of a disease, comprising the 574 epitope or its encoding nucleic acid and the vector of particularly cancer. The detection method is useful for diagnosing or particularly cancer. The detection method is useful for diagnosing or presence of the 574 epitope or its nucleic acid. The T cell line or clone controlled in the manufacture of a medicament for treating and/or preventing a disease. This polynucleotide sequence represents the felline correct of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New major histocompatibility complex class I peptide epitopes from human 5T4 tumor-associated antigen, useful for preventing and/or treating a disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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Mismatches:
Indels:
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Matches:
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Best Local Similarity:
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DB:
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Major Histocompatibility Complex class I peptide epitope; MHC;

Feline 5T4 antigen DNA

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lmmunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;

Human; TAA; tumour-associated antigen; anti-tumour; cytostatic;

5T4 tumour-associated antigen gene.

Human

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Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
The invention relates to a Major Histocompatibility Complex (MHC) class of II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognishing a peptide epitope in conjunction with an MHC molecule, for disgnosing or monitoring the presence of a peptide connucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polymucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                                                                                                gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Major Histocompatibility Complex class II peptide epitope of 574, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
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                                                                                                                                                                                                                                                                                        /product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                            Location/Qualifiers
1. .1260
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 49; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kingeman S;
                                                                                          DNA encoding feline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD BIOMEDICA UK LTD
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                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                WO2003068815-A2.
                                                                                                                                                                                            Unidentified
                                                    04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2003
                  ADB97452:
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The present sequence encodes the human 5T4 tumour-associated antigen

Example 2; Page 78; 79pp; English.

(OXFO-) OXFORD BIOMEDICA UK LTD.

Carroll MW, Myers KA; WPI; 2000-387735/33.

98GB-00025303. 99GB-00001739. 99GB-00017995.

30-JUL-1999; 27-JAN-1999;

99WO-GB003859

18-NOV-1999; 18-NOV-1998;

25-MAY-2000

WO200029428-A2 Homo sapiens.

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CTAA). The TAA ST4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metaetessis in colorectal and gastric cancer. ST4 antigen may be therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The ST4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single chain antibody, ScPv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                         Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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40.00
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100.0%
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Best Local Similarity:
Query Match:
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60

Length: Matches: Conservative: Mismatches: Indel8:

95.7 40.00 100.0% 100.0%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores:

.. 9

1087 GCCCTGATAGGTGCCATTTTCTTACTG 1113

AAA27058 standard; DNA; 1263

RESULT 13 AAA27058

22-AUG-2000 (first entry)

AAA27058;

1 AlaLeuIleGlyAlaIlePheLeuLeu

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US-10-774-176-6 (1-9) x ADB97452 (1-1260)

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Canis sp.

25-MAY-2001

Myers KA;

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynuclocides sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell conformation in facing the conformatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The coll call may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).

The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
proliferative disorder; infection; inflammatory condition;
                       cancer immunotherapy; foetal cell; maternal blood; cytostatic;
foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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Gaps:
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/*tag= a
/product= "5T4 protein"
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                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 67; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                          13-NOV-2001; 2001WO-GB005004.
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Best Local Similarity:
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                                                                                                                                                                                                                                                   WO200238612-A2
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                                                                                      Canis sp.
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cell
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                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA27059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, partidontal diseases, cardiopulmonary diseases, cardiovaccular diseases, gastrointestinal disorders, infections, diabetes, Helicobacterelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Mismatches:
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                                                            Location/Qualifiers
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                                                                                                                /*tag= a
/product= "5T4"
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                                                                                                                                                                                                                                                                      13-NOV-2000; 2000WO-GB004317.
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P-PSDB; AAB83839.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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1263 9 0 0 0 0

ABK87174;

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RESULT 15 ABK87174

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Lioubin MN,

Funke RP,

Mouse;

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA differentially expressed in MYCN activated cells SegID 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; differential expression; transactivator; proto-oncogene; neuroblasioma; small cell lung cancer; cytostatic; gene therapy; ss; MYCN activated cell.
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                                                                                                                                                                                                                                                                    Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 75-76, 99pp, English.
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                                                                                                                                          22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                   21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                    Belvin M, Schleithoff L, P
Francis-Lang H, Friedman L;
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Best Local Similarity:
Query Match:
                   WO2003035831-A2
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                                                          01-MAY-2003
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the mouse 574 tumour-associated antigen carcinomas but has a lycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours aben induced were inculated with a virus expression vector containing the present sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                            .mmunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; d8.
                                                      TAA; tumour-associated antigen; anti-tumour; cytostatic;
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Matches:
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               Mouse 5T4 tumour-associated antigen gene
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99GB-00001739.
99GB-00017995.
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                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                    18-NOV-1999;
                                                                                                                                                                                                                                                                                                             .8-NOV-1998;
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Homo sapiens

AAD56199

RESULT 17 AAD56199

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Query Match: DB:

2001US-0310099P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymouleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protoconcedent is amplified in neuroblastoms cells and is common in small concers. The present invention describes these cDNA molecules cas useful for in hybridisation assays to detect expression of nucleic cids (or complementary nucleic acids) in a present in a given sample, as specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymouleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the DYA patent Office at
                                                                                                                   New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bladder cancer associated cDNA sequence SEQ ID NO:192.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009
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Conservative:
Mismatches:
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                                                                                                                                                                           Claim 1, SEQ ID NO 105, 27pp, English,
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                                                                           Plon SE,
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 23-FEB-2001; 2001US-0270784P
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                                                                          Stuart SG, Nuchtern JG,
                     (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
                                                                                                WPI; 2003-635698/60.
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                                                                                                                                                        cancer.
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC5095). ACC50951 to ACC51059 encode the human bladder cancerassociated proteins given in ABR48146 to ABR48342). Bladder cancerassociated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancerassociated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer and in screening and diagnostic methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                              Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 296; 307pp; English
                                                                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC
                           2001US-0343705P.
2001US-0350666P.
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                                                                                      12-APR-2002; 2002US-0372246P
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P-PSDB; ABR48236.
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Best Local Similarity:
                                                                                                                                                                                                               Mack DH, Aziz N;
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03-AUG-2001;
08-NOV-2001;
13-NOV-2001;
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                                                                                                                                                                                Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                              Claim 22; Page 335; 453pp; English.
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                     10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-03373246P.
                                                                                              (EOSB-) EOS BIOTECHNOLOGY INC
            2001US-0284770P
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40.00
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                                                                                                                                             WPI; 2003-093161/08.
P-PSDB; ABU56603.
                                                                                                                      Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                      Aziz N,
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DB:
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway—modulating agent for preparing composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                         Funke RP,
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Mismatches:
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                                                                                                    21-OCT-2002; 2002WO-US033540.
                                                                                                                                                    22-OCT-2001; 2001US-0338733P
                                                                                                                                                                         15-FEB-2002; 2002US-0357600P
01-MAR-2002; 2002US-0361196P
                                                                                                                                                                                                                                                                                                                                   Francis-Lang H, Friedman L;
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15-FEB-2002; 2002US-0357600P
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                                                                                                                                                                                                                                                      (EXEL-) EXELIXIS INC
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WO2003035831-A2
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                                                  01-MAY-2003
                                                                                                                                                                                                                                                                                                         Belvin M,
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RESULT 2.
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                                                                                                              comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, differential expression, cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
inflammatory disease; autoimmune disease;
                                                                                                   Identifying a candidate p53 pathway-modulating agent for treating cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
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                                             Lioubin MN,
                                                                                                                                                                                                                                                                                                 Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                             Funke RP,
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Matches:
Conservative:
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                                             Plowman GD,
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                                                                                                                                                 Disclosure, Page 76-77, 99pp; English.
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2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
01-MAR-2002; 2002US-0361196P.
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                                           Belvin M, Schleithoff L, P
Francis-Lang H, Priedman L;
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40.00
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                      (EXEL-) EXELIXIS INC.
                                                                              WPI; 2003-421410/39.
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29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
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DB:
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as anglogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; antibodies for drug targeting;
and methods of screening for modulators of acids, polypeptides,
antibodies and mucleic acids. The mucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
attherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumour-associated antigenic target (TAT) cDNA sequence #53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gish KC, Glynne R, He Wilson KE, Zlotnik A;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 39; 1385pp; English
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Mack DH, Murray R, Watson SR,
2002US-0347349P.
2002US-0355250P.
2002US-0356714P.
2002US-0359077P.
                                                                                                                                                                                                                                                                                                                                                                                                          (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                         20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0370110P.
                                                                                                                                                                                         12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                   05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
                                                                                                                                                                                                                                                                                22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
                                                                                                                                                                                                                                                                                                                                             09-SEP-2002; 2002US-0409450P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-468649/44.
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Best Local Similarity:
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                                                                13-FEB-2002;
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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of
                                                                                                                                                                                                                                              New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                          Jackman J, Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; breast cancer; prognosis; gene expression; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast cancer prognosis marker #1305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                  25-SEP-2003; 2003WO-US030907
                                                                   25-SEP-2002; 2002US-0414006P
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                                                                                                                                        Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-593473/57.
                                                                                                                                                                                             WPI; 2004-305105/28
                                                                                                    (GETH ) GENENTECH
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Best Local Similarity:
                                                                                                                                                                                                               P-PSDB; ADN03962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004065545-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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 08-APR-2004
                                                                                                                                          Bodary S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR25444;
                                                                                                                                                                                                                                                                                      mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of human tumour-associated antiganic target (TAT) polymucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for represents or treating tumours and cancer. The present sequence represents a human TAT CDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                        Polson A, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody that binds to a tumor-associated antigenic target (TP polypeptide, useful for preparing a composition for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1, SEQ ID NO 53, 319pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-6 (1-9) x ADL06473 (1-2053)
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                                                                                                                                                                                         21-AUG-2002; 2002US-0405645P.
23-SER-2002; 2002US-0413192P.
15-OCT-2002; 2002US-042008P.
15-NOV-2002; 2002US-0426847P.
02-JUL-2003; 2003US-0484959P.
                                                                                                                                                                                                                                                                                                                                    Desauvage PJ, Frantz G, Hil
Spencer SD, Wu TD, Zhang Z;
cancer; cytostatic; gene; ss
                                                                                                                                        19-AUG-2003; 2003WO-US025892
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P-PSDB; ADL06552.
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Best Local Similarity:
Query Match:
DB:
                                                                   WO2004016225-A2
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                                                                                                                                                                           19-AUG-2002;
                                  Homo sapiens
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The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; disgnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
genes in a cell sample taken from patient, to control levels
                                                                                                                                                                                                                                                       Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
                                  Disclosure; SEQ ID NO 1305; 226pp; English.
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN38510 standard; cDNA; 2053 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-347921/32.
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                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
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The Invention Feature to the diagnosis of and their related uncleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide equences at least 80% identical to the TAT nucleic acid and polypeptide or organic polypeptides; expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancer, liver cancer, bladder cancer, lung cancer, cancers such as breast cancer, colorectal cancer, lung cancer, oversian cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central neces as hybridisation probes, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acids may further be represents a TAT nucleic acide invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; se; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.
invention relates to human tumour-associated antigenic target (TAT)
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PSYC-) PSYCHIATRIC GENOMICS INC.
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25-SEP-2001, 2001US-0325150P
14-NOV-2001, 2001US-0333047P.
18-JAN-2002, 2002US-0349936P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-2002; 2002US-0361834P.
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Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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WPI; 2004-118903/12

P-PSDB; ABG22988.

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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a patticular disease, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals of affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiarric and neurodegenerative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as well as Parkinson's and Alzheimer's disease. Accordingly, the compounds of this invention exhibit various activities including neuroleptic, continually continual activities including neuroleptic, and antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is differentially expressed in the presence of a therapeutic compound and represents an exemplary efficacy gene for bipolar affective disorder, given in an exemplary efficacy gene for bipolar affective disorder,
                  Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell contacted with the test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #22979.
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Matches:
Conservative:
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                                                                                                                        Example 6; SEQ ID NO 174; 39pp; English
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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DB:
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BX1X5X5X5X5X5X5X5X5X5X5X5X5X5X5
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WPI; 2001-639362/73

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supporting in tissue, as molecular weight markers and as a food cuppeptide in tissue, as molecular weight markers and as a food suppoptide in tissue, as molecular weight markers in medical imaging of sites expressing (II) il) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences the invention. Note: The sequence data for this printed specification, but was obtained in
                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;
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Matches:
Conservative:
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                                                                                                                                Claim 1; SEQ ID NO 22979; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Best Local Similarity:
                                                                                             biodiversity.
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The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                         830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; medicine; signal transduction; glycoprotein; transcription;
Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                      Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
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Matches:
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-0013865.
07-JUL-2000; 2000EP-00114089.
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P-PSDB; ADL30832.
                                              WPI; 2001-524255/58.
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Best Local Similarity:
Query Match:
DB:
                                                              P-PSDB; AAM93333
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ADL3083
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 Primers useful for synthesizing full length cDNA clones and their use
             oligonucleotide primers (830 cDNAs) useful for synthesizing full
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K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                          Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Matches:
Conservative:
Mismatches:
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                                                            Example 1; SEQ ID NO 2864; 1340pp; English.
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la T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Wakamatsu A, Sugiyama T,
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                                length human cDNAs
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Best Local Similarity:
Query Match:
DB:
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X44X8X0000000000X8
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for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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Other; 0,0 638 G; 533 T; 0 Sequence 2361 BP; 506 A; 684 C;

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SE; gene; human; signal transducer and activator of transcription 6; STA76; immunogen; STA76 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; systemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal transducer and activator of transcription 6 activation
                                                                                                                                                                                                                                                                                      Human cDNA encoding protein that promotes STAT6 activation #64.
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               2361
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              Length:
Matches:
Conservative:
Mismatches:
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                                                                Indels:
                                                                                                                                          Claim 4; SEQ ID NO 127; 1368pp; English.
                                                                             Gaps:
                                                                                                                              1 AlaLeulleGlyAlallePheLeuLeu 9
                                                                                                     US-10-774-176-6 (1-9) x AAK94254 (1-2361)
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                                                                                                                                                                                                         BP
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2002US-0436467P.
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              196
40.00
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P-PSDB; ADI26163.
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                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003104277-A2
                                      Percent Similarity:
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27-DEC-2002;
15-MAY-2003;
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06-JUN-2002;
Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                  AD126162;
                                                                Query Match:
DB:
              No.:
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of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthitis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATG activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATG. The present sequence represents a
useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an surigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATE activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease and the STATE activation are useful for treating disease and the STATE activation and or prevention for the broad of the STATE activation and or prevention for the broad of the STATE activation and or prevention for the broad of the STATE activation and or prevention for the broad of the STATE activation and or prevention for the broad of the STATE activation and or prevention for the state of the STATE activation and or prevention for the state of the STATE activation and or prevention for the state of the STATE activation and or prevention for the state of the STATE activation and or prevention and the state of the STATE activation and the processing the state of the STATE activation and the processing the state of the STATE activation and the processing the state of the STATE activation and the processing the state of the STATE activation and the processing the state of the stat
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T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human cDNA encoding a protein which promotes STAT6 activation
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K, Kojima 8
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Matches:
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Wakamatsu A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
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Claim 4; SEQ ID NO 125; 1368pp; English.

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, encoding proteins that are associated with signal transduction, for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
                          Example 1, SEQ ID NO 2866; 1340pp; English.
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se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                           Human cDNA encoding protein that promotes STAT6 activation #63.
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          2361
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         Length:
Matches:
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2002US-0436467P.
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27-DBC-2002; 2002U9-0436467P
15-MAX-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
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                                                                                                                                                                                                                                     (first entry)
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P-PSDB; ADI26161.
                                              Best Local Similarity:
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                                   Percent Similarity:
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Alignment Scores:
Pred. No.:
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DB:
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New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.

diabetes and cancer.

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful of the hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic thinking, isoheemic heart diseases, subarachnoid hasmorrhage, viral hepatitis and AlDS. The protein has efficient promoting STAT6 activity. The protein has essociated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                human cDNA encoding a protein which promotes STAT6 activation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                activation or inhibition of STAT6
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2002UP-00377326.

2002US-0436467P.

2003UP-00137505.

2003US-0470836P.
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26-DEC-2002;
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15-MAY-2003;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                              The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves adminiatering the protein for its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression a activity of the corporation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening composition. Compositions, antibodies and antisense molecules are useful corposition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allowed in inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthitis, soluentic lupus erythematosus, sepsis, asthma, allergic thinitis, ischaemic heart diseases, subarachnoid heemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive human and allergic activation or inhibition of STAT6. The present sequence represents a human and a protein and antise of the present sequence represents a human and and antise of the present and antise of the 
                                                                                                                                                                                 New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding a protein which promotes STAT6 activation.
                                                    Ishizawa K;
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                                                    Muramatsu S,
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                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 123; 1368pp; English
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                                                    Honda G,
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                                                    Matsuda A,
(ASAH ) ASAHI KASEI KK
                                                                                                    WPI; 2004-122214/12.
P-PSDB; ADI26159.
                                                                                                                                                                                                                                                                     diabetes and cancer
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Best Local Similarity:
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                                                    Sugahara T,
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ADP ADP
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polymocleotides. The invention also relates to antibodies against the polymocleotides. The invention also relates to antibodies against the polymoptides, amethod of generating vaccines for producing the polymoptides, a method of generating a compound for the ability to bind a P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis, a polymoptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymocleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polymucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene mapping; tissue profiling;
ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to new Proteus mirabilis polypeptides and
                                                                                                                                                                                                                                                   New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or biocontrol agents for plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer related polynucleotide SEQ ID NO 548.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                  (GENO-) GENOME THERAPEUTICS CORP.
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99US-0128706P
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P-PSDB; ADF06409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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  09-APR-1999;
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(ABN27253-ABN33262)

invention relates to an isolated polynucleotide

with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for gene therape. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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Sequence 567 BP; 171 A; 135 C; 195 G; 66 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches:

103 38.00 100.0% 88.9% 95.0%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

Indels:

Gaps:

188 GCTCTTCTAGGCGCCATCTTCCTCCTC 162

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ADO35702 standard; DNA; 1101

RESULT 40

AD035702

26-AUG-2004 (first entry)

ADO35702;

1 AlaLeuIleGlyAlaIlePheLeuLeu

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US-10-774-176-6 (1-9) x ABN60925 (1-567)

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The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polynegide, to detect differentially expressed genes correlated with a cancercus state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapputic and disgnostic purposes. The polynucleotide is useful for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                            New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth.
                                                                                                                                                                                                                         directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Labat I;
                                                                                            Claim 1; SEQ ID NO 548; 883pp + Sequence Listing; English
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Кавват А,
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Zhang G,
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38.00
100.0%
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95.0%
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Scott BM,
                       WPI; 2002-241905/29
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Best Local Similarity:
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Lamson G,
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mouse; murine; cancer; psoriasis; ulcerative colitis; inflammation; ischaemic heart disease; thrombosis; immune disorder; bacterial disorder; viral disorder; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                          New mouse nucleic acid molecules and polypeptides, useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischemic heart disease or thrombosis.
                                                                                                                                                                                                                                                                                                                                      Kamiya M;
                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y,
                                                                                                                                                                                                                                                                                                                                      Hestir K,
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 375; 263pp; English.
                                                                                                                                                                                                                                                                                                                   (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                           Novel mouse gene sequence #375.
                                                                                                                                                                                                   2002US-0426916P.
2002US-043115BP.
2002US-0431445P.
2003US-0431660EP.
2003US-0476621P.
2003US-0476632P.
2003US-0485217P.
2003US-0485359P.
                                                                                                                                                                                                                                                                                                                                       Lee E,
                                                                                                                                                                                 24-OCT-2003; 2003WO-US033948
                                                                                                                                                                                                                                                                                              2003US-0493356P
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                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-431966/40.
                                                                                                                                         WO2004046310-A2
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08-JUL-2003;
08-JUL-2003;
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                                                                                                                                                                                                                                                                                             08-AUG-2003;
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                                                                                                                                                                                                               04-DEC-2002;
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Human; cytostatic; gene expression; gene mapping; tissue profiling; gene therapy; cancer; tumour; gene; ss.

Human cancer related polynucleotide SEQ ID NO 892

New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth.

Claim 1; SEQ ID NO 892; 883pp + Sequence Listing; English

, Reinhard C, Randazzo F; Pot D, Labat I;

Sudduth-Klinger J, ing G, Kassam A, P

Zhang G,

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Garcia Scott BM,

۵,

Sacobedo

Lamson G,

WPI, 2002-241905/29.

(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.

16-AUG-2001, 2001WO-US025840 16-AUG-2000, 2000US-0226326P

WO200214500-A2 Homo sapiens

21-FEB-2002.

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The invention comprises 744 novel mouse DNA sequences (genes). The DNA sequences of the invention are useful for treating cancer, psoriasts, ulcerative colitis, inflammation, ischaemic heart disease, thrombosis, immune disorders, bacterial disorders and viral disorders. The present ordate presents a mouse DNA sequence of the invention. NOTE: The present present DNA sequence is not shown in the specification, but has been retrieved from the WIPO website.
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Sequence 1101 BP; 216 A; 332 C; 355 G; 198 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
                                                Indels:
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        220
38.00
100.0%
88.9%
95.0%
                                     Best Local Similarity:
                            Percent Similarity:
Alignment Scores:
                                              Query Match:
DB:
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US-10-774-176-6 (1-9) x ADO35702 (1-1101)

394 GCCTGCTCGGAGCCATTTTCCTCCTC 420 σ 1 AlaLeulleGlyAlallePheLeuLeu

ACA28481 standard; DNA; 951 BP RESULT 41 셤 ò

Prokaryotic essential gene #10138 (first entry) 19-JUN-2003 ACA28481;

Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

Clostridium botulinum.

WO200277183-A2

03-OCT-2002,

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

(BLIT-) BLITRA PHARM INC

Zyskind JW; Xu HH; Haselbeck R, Ohlsen KL, Yamamoto R, Porsyth RA, Haselbeck R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02 P-PSDB; ABU24611.

screening ដ New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 16351; 1766pp; English.

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding The invention relates to an isolated nucleic acid comprising any one of ACA28481

ACA284

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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway compound for cellular proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the growth of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation in cisolate candidate molecules for rational card discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, continued for proliferation in cells other than S. aureus, S. typhimurium, continued for proliferation in cells other than S. aureus, S. typhimurium, continued for proliferation of the printed specification, but was obtained in cellettown and continued in the printed specification, but was obtained in the printed for the printed specification, but we seem the printed specification and the printed specification and the
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Mismatches:
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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(GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly 8. agalactiae and 8. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bilogolasical sample. (I) is used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus, GAS, GBS; group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V, Margarit Y RosI, Grandi G, Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225 BP; 77 A; 49 C; 40 G; 59 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 3929; 4525pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-10-774-176-6 (1-9) x ABN70062 (1-225)
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN69887 standard; DNA; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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36.00
100.0$
77.8$
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
P-PSDB, ABP29431.
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2002
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Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN69887;
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DB:
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ABN69887
ID ABN69887
XX
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenee), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN6604-ABN71526 and actibacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to detect Streptococcus in a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromeography, immunoassays, and distinguishing/identifying
                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225 BP; 77 A; 47 C; 41 G; 60 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #22978.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GCTATTTTGGGAGCTATCTTTTTACTG 72
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                                                                                                                                                                                                                       Claim 7; Page 3906; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-774-176-6 (1-9) x ABN69887 (1-225)
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631
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36.00
100.0%
77.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus proteins
WPI; 2002-352536/38.
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Best Local Similarity:
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                                 P-PSDB; ABP29256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
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                                                                                                          The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cetivity of (II) in or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of supplement. (II) and its binding partners are useful for treating disorders of supplement. (IC) and (II) and (II) are useful of medical imaging of supplement. (IC) and (II) and (II) are useful for treating disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this coding sequences of the invention. Note: The sequence data for this cefter, wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                        U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Photorhabdus luminescens nucleotide sequence #10464.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                                                      Claim 1; SEQ ID NO 22978; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACF71997 standard; DNA; 681 BP.
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36.00
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P-PSDB; ABG22987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                               biodiversity.
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and related species, to study polymorphisms, for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymeptides encoded by the genes. Antibodies (Ab) raised against the collympetides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that the genes in plants, andulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Compinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The combinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The cherapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens and ab are also useful care sensitive to P. luminascens-coded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. C. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens
                                                                                                                                                                                                                                            Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                 Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteus mirabilis infection; bacterial infection; antibacterial;
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                                                                 Kunst F,
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Matches:
Conservative:
Mismatches:
                                                                     Glaser P, Frangeul L,
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                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 10464; 1205pp; French
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                     Taourit S,
                                                                                                                                                                              WPI; 2003-148459/14.
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Best Local Similarity:
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                                                                     Duchaud B, T
Buchrieser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
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Query Match:
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Page 32

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The invention relates to new Proteus mirabilis polypeptides and polymerlectides. The invention also relates to antibodies against the polypeptides, amethod of generating the polypeptides, amethod of specifications the polypeptides, amethod of polypeptides and polypeptides with a method of polypeptides and amethod for the ability to bind a P. mirabilis and polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drags or as bio-control agents for plants. This sequence represents a Proteus mirabilis polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caspase; caspase cleavage site; green fluorescent protein; GFP; FRET; fluorescent resonance energy transfer; fusion protein; identification; caspase inhibitor; apoptosis; neurodegenerative disease; stroke; Alzheimer's disease; reamentic brain injury; stabelmenta-reperfusion injury; graft-versus-host disease; autoimmune disorder; inflammatory disease; neuronal damage reduction;
                                                                                                                  New Proteus mirabilis polypeptides and polynucleotides, useful as reagants for disagness of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green fluorescent protein (GFP) encoding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 687 BP; 211 A; 127 C; 152 G; 197 T; 0 U; 0 Other;
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(GENO-) GENOME THERAPEUTICS CORP.
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                                                                   WPI; 2003-895291/82.
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                                                                                   P-PSDB; ADP07361
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                                   Breton GL;
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The present invention describes a fusion protein (I) comprising of a donor green fluorescent protein (GFP) that is an ultra-bright GFP and an acceptor GFP linked by a peptide comprising at least one caspase cleavage site. AAB51201 to AAB51225 represent specifically claimed caspase cleavage site. AAB51201 to AAB51225 represent specifically claimed caspase cleavage site peptide sequences from the present invention. The fusion protein is useful in fluorescent resonance energy transfer (FRET) and in the identification of activators or inhibitors witch can be used in the identification of caspase inhibitors which can be used in treating approals, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, traumatic brain injury, stroke, ischaemia-reperfusion injury, graft-versus-host disease and autoimmune disorders. These caspase inhibitors may also be used in clinical trial for treatment of inflammatory diseases or reduction of neuronal damage in a rabbit model of bacterial meningitis. The present invention
                                                                                       New fusion protein comprising an ultra-bright donor and an acceptor green fluorescent protein linked by a peptide having at least one caspsse cleavage site, for identifying activators or inhibitors of caspase in living cells or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Locus specific targeting fragment; eukaryotic cell; homologous recombination; endogenous mismatch repair; gene function; gene expression; over-producer clone; high protein production; therapeutic target discovery; pharmacological compound screening; protein manufacturing; mismatch repair protein; green fluorescent protein; GPP; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aequorea victoria green fluorescent protein (GPP) DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 922 BP; 322 A; 164 C; 170 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cassady R, Nicholson D;
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/product= "Aequorea victoria GFP"
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   Tawa
                                      2001-070966/08.
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                                                      P-PSDB; AAB51230
Xanthoudakis S,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 10241; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3222 BP; 800 A; 823 C; 837 G; 762 T; 0 U; 0 Other;
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  11-JUL-2000; 2000US-00614150
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                                                                                     Venter JC, Adams M,
                                                                                                                               WPI; 2001-656860/75
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P-PSDB; ABB61149.
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Best Local Similarity:
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  This invention relates to a novel method for the introduction of a locus specific targeting fragment into the genome of a eukaryotic cell through homologous recombination and comprises the inhibition of endogenous mismatch repair of the cell. The locus specific targeting fragment is a polynucleotide comprising at least one promoter, a selectable marker and 5' and 3' flanking regions of 20-120 nucleotides. The 5' and 3' flanking regions of 20-120 nucleotides. The 5' and 3' flanking regions of a selected portion of the genome of the cell. The method of the invention may be useful for introducing a locus specific targeting fragment into the genome of a cell through homologous recombination. This may be useful for studying gene function, gene expression and generating over-producer clones for high protein production. In addition, the invention may be useful for therapeutic target discovery, pharmacological compound screening and protein manufacturing. The present sequence is the DNA sequence of Aequorea victoria green fluorescent protein (GPP) which was used as a reporter element during the exemplification of the method of the invention
                                                                                                                                                                                                                               Introducing a locus specific targeting fragment into the genome of a cell through homologous recombination by inhibiting endogenous mismatch repair of the cell and introducing a locus specific targeting fragment into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 10241.
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pharmaceutical; gene; ss.
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17-JAN-2003; 2003WO-US001361
                                      18-JAN-2002; 2002US-0349565P
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                                                                                (MORP-) MORPHOTEK INC
                                                                                                                           Grasso L, Kline JB,
                                                                                                                                                                     WPI; 2003-646070/61.
P-PSDB; AAO27520.
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Pred. No.:
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Claim 1, SEQ ID NO 10238; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in cluidating cell signalling and cell-cell interactions in higher cukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1640-ABL3011), expressed DNA sequences (ABL01840-ABL1675) and the encoded proteins (ABS57737-ABS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences ###X#X666666665X8

Sequence 8737 BP; 2394 A; 1869 C; 1894 G; 2580 T; 0 U; 0 Other;

8737 7 2 0 0 Length:
Matches:
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Mismatches:
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Gaps: 6.22e+03 36.00 100.0% 77.8% 90.0% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

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Search completed: April 25, 2006, 12:37:14 Job time : 323.3 secs

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AP006840_77
CP000083_11
SME591789
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PAT 14-DEC-2001

COMMENT

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Pissipedia, Canidae,
Canis.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Methods of diagnosis of breast cancer, con
screening for modulators of breast cancer
Patent: WO 02059377-A 57 01-AUG-2002;
EOS Biotechnology, Inc. (US)
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Sequence 3 from Patent EP1160323.
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                            18-NOV-1999 JP 2000582415
18-NOV-1998 GB 9825303.2,27-JAN-1999 GB 9901739.4 PR
JUL-1999 GB 9917995.4
MILLS WILLIAM CARROLL, KEVIN ALAN MYERS
C12N15/09,A61K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,C07K19/00,
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Polypeptide
Patent: WO 0029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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RESULT 4 AX025013

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Pred. No.:

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Felis catus (cat)
Felis Catus (cat)
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Bukaryota; Metazoa; Chordata; Craniata; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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PD1ypeptide.
BD249731
BD249731.1 GI:33059501
JP 2002530060-A/1.
Homo sapiens (human)
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Felis sp.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis
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Sequence 1 from Patent W003068816.
AX821533 1 GI:39724929
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Sequence 3 from Patent W00238612.
AX467373 GI:21900603
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PAT 08-JUN-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160323-A 1 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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AX316086
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           Polypeptide
OXFORD BIOMEDICA LID
OX Homo sapiens (human)
PD 2002530060-A 1 17-SEP-2002;
OXFORD BIOMEDICA LID
OS Homo sapiens (human)
PN JP 2002530060-A/1
PD 17-SEP-2002
PP 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9825303.2,27-JAN-1999 GB 9901739.4 PR 30-JUL-1999 GB 9917995, XEVIN ALAN MYERS
PC CIZNIS/09, A61K39/00, A61K48/00, A61P35/00, CO7K14/065, PC CIZNIS/00, CC CO7K19/00, PC CIZNIS/00, PC CIZNIS/00
PC POLYPEPTIGE
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Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LID (GB)
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Sequence 1 from Patent W00029428.
AX025011 GI:10184932
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Carroll, M.W. and Myers, K.A.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Patent: WO 0029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
          Location/Qualifiers
1. .1281
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Sequence 2 from Patent WO0029428.
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LOCATION/Qualifiers
                                                 Location/Qualifiers
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Mus musculus
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AX316087
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AX025012
                                                 PEATURES
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                         PAT 16-JUL-2002
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muridae, Murinae, Mus.
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002,
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1263
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                                                               1090 GCCCTGATAGGCGCTATTTTCCTCCTG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1090 GCCCTGATAGGCGCCATCTTCCTACTG 1116
                                                                                                                      AX467371 1263 bp
Sequence 1 from Patent W00238612.
AX467371
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                        US-10-774-176-6 (1-9) x AX316086 (1-1263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BD249732.1 GI:33059502
JP 2002530060-A/2.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                               AX467371.1 GI:21900602
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BD249732
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Cancer

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/vcvc...
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/db_xref="InterPro::IPR00161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="transmembrane peptide"
/standard_name="transmembrane region"
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                                                                                        Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                      Myers, K.A., Rahl-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.
and Stern, P.L.
glolation of a CDNA encoding 5T4 oncofetal trophoblast
glycoprotein. An antigen associated with metastasis contains
leucine-rich repeats
J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-DEC-1993) Myers K. A., Paterson Institute for (Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta"
/clone_lib="lambda gtll library of J. Milan"
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|product="Leucine rich repeat region"
|label=LRRB
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/product="LRR C-terminal flank"
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/label=N-flank
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Matches:
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/db_xref="taxon:9606"
/sex="female"
Z29083
Z29083.1 GI:435654
ST4 gene; ST4 oncofoetal antigen.
Homo sapiens (human)
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2 (bases 1 to 2053)
Myers, K.A.
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misc_RNA
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                        Carroll, M.W. and Myers, K.A.

5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BP 1160313-A 2 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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PB Corporation (NY) (US)
Location/Qualifiers
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Matches:
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HELIX RESEARCH INSTITUTE
OF Homo sapiens (human)
PN JP 2002017375-A/2713
PD 22-JAN-2002
PP 72-JAN-2002
PP 77-JUJ-2000 JP 200253172
PP 77-JUJ-2000 JP 200253172
PP 77-JUJ-2000 JP 200253172
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifier
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                               1 (bases 1 to 2359)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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                                       buls/282
Primer for synthesizing full-length cDNA and use thereof.
BD127282
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JP 2002017375-A/2713.
Homo sapiens (human)
Homo sapiens
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               RESULT 21
BD127282
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                                                                                                                     Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA, complete cds.
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paaplasgsaqpppaercpaacecsbaartvkcvnrnllevpadlppyvrnlflugnq
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HELLASNHFLYLPRDLLDQLPSLKHDLRNNSLVSLTYASFRNLTHLESIHLEDNAL
KVLHNSTLAEWQGLAHVRYLDNNPWVCDCYMADMVSWLKETEVVPDKARLTCAFPEK
MRNRGLLDLTSSDLDCDATLPQSLCYSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPSLTNLSSNSDV"
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Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat.)
Sattus norvegicus
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="5T4 oncofetal antigen homolog"
'protein id="AAP21770.1"
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Ninkina,N.N. and Buchman, V.L.
Structure and expression of the rat 5T4 gene
Unpublished
(bases 1 to 2333)
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tissue_type="cerebellum"
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gene="5T4"
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US-10-774-176-6 (1-9) x HS5T4OA (1-2053)
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Buchman, V.L.
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SHINICHI KOJIMA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomice Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (S-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-396) NEDO human cDNA sequencing project supported by Ministry of Sconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                             / trains a tion="MPGGCSRGPAAGDGRLRLARLALVILGWVSSSSPTSSASSFSSS APFLASAVSAQPPLPDGCPALCECSEAARTVKCVNRNLTBVPTDLPAYVRNLFLTGNQ LAVLPAGAPARPPLPSLRQLDLSHNPLTGNQ LAVLPAGAPARPPLPSLRQLDLSHNPLADLSPP RESSNASVASPSPLVELLIAMI VPPEDERQNRSPEGWVVAALLAGRALQGLRRLELA SNHFLYLPRDVLAQLESLRHLDLSNNSLVSLTTVSRVNLTHLESLHLBLHLBDLARVLHNGTLARLQGLPHIRVPLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKMRNRUL LELNSADLDCDPILPPSLQTSVVFLGIVAALIGAIFLUVLYLNRGIKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND AND A TIMEAR PLASS DE MENA LINEAR PRI 03-SEP-2002 HOMO BADIENS CDNA FLASO305 fis, clone NT2RP2000694, highly similar to Homo Bapiens 5T4 oncofetal trophoblast glycoprotein gene. AR074786
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004; Research Association for Biotechnology (JP) Location/Qualifiers
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Isogai, T. and Otsuki, T.
Direct Submission
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83 2361 bp DNA linear PAT 18-SBP-2002 for synthesizing full-length cDNA and use thereof.
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TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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/note="cloning vector: pMB18SFL3
note="cloning vector: pMc18SFL3
retinoic acid (RA) induction"
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YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
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Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2714 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 202017375-A/2714
PD 22-JAN-2007
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JP 2002017375-A/2714.
Homo sapiens (human)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Location/Qualifiers
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Sequence 2866 from Patent BP1396543.
CQ782726
CQ782726.1 GI:45502669
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ARSGSNASVSARSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGIRRLELA
SNHFLYLPRDVLAQLPSLARHDLSNNSLVSLTYVSFRILTHIBSLHLEDNALKVLHNG
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RDHMEGYHYRYEINADPRLTVLSSNSDV"
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Homo sapiens cDNA FLJ90309 fis, clone NT2RP2000903, highly similar
LO Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
AK074790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mpggcorgpaagdgrlrlarlalvllgwyssssptssasspss
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Yamamoto, J., Wakametsu, A., Kimura, K., Sakamoto, K., Hatano, N.,
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Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A.,
Okumura, K., Nagai, K., Sugano, S. and Isogai, T.
Signal Sequence and Keyword Trap in silico for Selection of
Full-Length Human CDNAs Encoding Secretion or Membrane Proteins
from Oligo-Capped CDNA Libraries
Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene Stat6 activation gene Patent: WO 03104277-A 127 18-DBC-2003; Asahi Kasei Kabushiki Kaisha (JP)
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Homo sapiens (human)
Homo sapiens
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24 This clone was selected for ful length sequencing because it passed the following selection criteria: matched mENA gi: 13929143.
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TFAGSNVSVSTPSPLIELILAHIVPPEDQRQNGSFEGAVAFEGAVAAALRSGLALRGI
HHLELASHNFTYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
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paaflasgsaqpppaercpaacecseaartvkcvnrnllevpadlppyvrnlfltgnq
                                                                                                                                                            Submitted (02-DEC-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
42 (19888 1 to 2361)
Director MGC Project.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364. .1644
/gene="Tpbg"
/codon_start=1
                                                                                                                                                                                                                                                                                                     Contact: MGC help desk
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                                                                                                                                           Direct Submission
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Best Local Similarity:
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PUBMED
REFERENCE
AUTHORS
TITLE
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COMMENT
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ENKARYOKO NOVEGETOUS

SCHUKORATOLS

MARTINE MULDIGES; Chordata; Vertebrata; Buteleostomi;

Mammalla; Butherla; Buarchontoglires; Glires; Rodentia;

Sciuropatchi; Muroidea; Muridae; Murinae; Rattus.

1 (Dases 1 to 2361)

S trausborg, R.L., Peingold, R.A., Grouse, L.H., Derge, J.G.,

KAUSBORT, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K.,

HOPKINS, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Habeh, P.,

Distchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, W.M., B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Bouffard, G.G., Blakesley, R.W., Touchman, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
                                               Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba, 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-32-3975, Fax:81-438-52-3986) WEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- £ 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCUBYUII 2361 bp mRNA linear ROD 13-DEC-2004 Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="NT2"
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/clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3
note="cloning vector: pME18SFL3
retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2361
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2000903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-774-176-6 (1-9) x AK074790 (1-2361)
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BC087011.1 GI:56268819
  Isogai, T. and Otsuki, T. Direct Submission
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Best Local Similarity:
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DB:
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DEFINITION

37161

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eurachontoglires; Glires; Rodentia; Sciurognathi; Murcoidea; Murinae; Mus:

1. (Dases 1 to 2423)

2. (Dases 1 to 2423)

3. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Arange, C., Raha, S.S., Loquellamo, N.A., Peters, G.J., McKernan, K.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J., Mallahy, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodersen, M., Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APFLASAVGAPPLEDOCPALCEGEAARTYKKVVNRNLTEVFTDLERYYNLELTGNO
LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLFSLRQLDLSHNPLADLSPF
AFSGSNASVSAPSPLVELILMHIVPRDBRQNRSFBEMVVAALLAGRALGGLRRLELA
THFYLLPRDVLAQLPSLRHDLSNNSLVSFTYVSFRNLTHLESLHLEDNALKVLHNG
TLAELQGLPHIRVFLDNNPWYCDCHWADNVTWLKFTEVVGGODRLTCAYPEKRNRVL
LELNABADLOCDPILPSELQTSYYPLGIVLAIGAIFLLTGXYPEKRNRVL
LELNABADLOCDPILPSELQTSYYPLGIVLAIGAIFLLTGXYPEKRNRVL
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 BC059198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="5T4 oncofetal trophoblast glycoprotein"
/protein_id="AAH3161.1"
/db_xref="EGI:2271383"
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/db_xref="MIM:190920"
                                                                                                                          tissue type="Muscle, rhabdomyosarcoma"
/clone lib="NIH MGC 17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2379
9
0
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/db.xref="GeneID:7162"
/db.xref="MIM:190920"
/organism="Homo sapiens"
|mol_type="mRNA"
| Mol_type="maxon:9606"
| Arcf="taxon:9606"
|clone="MGC:15317_iMaGE:4138906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                       'note="Vector: pOTB7"
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                          gene="TPBG"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1. (bases 1 to 2379)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mulahy,S.J., Bosak,S.A., McEwan,P.J.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,R.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:22713382.
On Aug 19, 2003 this sequence version replaced gi:22713382.
On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov
Contact: nisc_mgc@nhgri.nih.gov
Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Valan,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Tucchamar,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 26 Row: m Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717. Location/Qualifiers
                                                                                                            BC037161 29-JUN-2004
Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:18317
IMAGE:4138906), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-SBP-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   1471 GCTCTGATAGGCGCTATTTTCCTCCTC 1497
                                                                                                                                                                                                                                                                           BC037161.2 GI:33872201
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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PUBMED REFERENCE AUTHORS TITLE

REMARK COMMENT

JOURNAL

TITLE

Bource

FEATURES

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VFAGSNASVSAPSPLEELILMHYVPPEDQRQNGSFEGWVAFEGWVAALLRSGLALRGL
TRLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLBSLHLBDNAL
KVIHNSTLASWGLAHVYRPLDNNPWYCDCYMADMVAMLKETEVVPDKARLTCAPPEK
MRNEGLDLNSSDLDCDAVLPGSLOTSYVFLSIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTULSSNSDV"
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSVPSSSTS"
                                                     Region: COG4886, Leucine-rich repeat (LRR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene Patent: WO 031104277-A 123 18-DEC-2003; Asahi Kasei Kabushiki Kaisha (JP) Location/Qualifiers
                                                                                                                          1299. .1415
/gene="Tpbg"
/note="LRRCT; Region: Leucine rich repeat C-terminal
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                                                                  protein [Function unknown]" /db xref="CDD:COG4886" 1299...1415
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Sequence 123 from Patent WO03104277.
AX961912
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Matches:
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/db_xref="taxon:10090"
556..1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1509 GCTCTGATAGGCGCTATTTTCCTCCTC 1535
                                                                                                                                                                                                                           /db xref="CDD:smart00082"
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|protein_id="CAF06465.1"
|db_xref="G1:40881323"
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                                 /gene="Tpbg"
/note="COG4886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Mankeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MGC:68145 IMAGB:5353871"
/tissue type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
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paaplasgsaqpppaercpaacecseaartvkcynrnlleypadlppyvrnlflgnq
wtvlpagaparqpplladlealnlsgnhlkeycagafehlpglrrldlshnpltnlsap
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TCELEASMHTLELPRDLLAQDPSLRYTLILRNNSLYSLYTASPSRNLTHESELHEBNAL
KVLHNSTLAEMÇGLAHVKVFLDNNPWYCDCTWADMVARLKETEVVPDKARLTGREPER
MRNRGLLDLNSSDLDCDAVLPQSLQTSYVPLGIVLALIGAIFLLVLYINRKGIKKWH
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalsky, U., Smailus, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                Direct Submission
Submitted (15-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                fene Collection (MGC), Cancer Genomics Office, National Cancer.
institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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/product="Tpbg protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym: 5T4"
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PEATURES

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PAT 14-JAN-2004

DEFINITION

RESULT 32

AX961914 LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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Direct Submission

Direct Submission

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Direct Submission

Direct Submission

Infectious Diseases, Division of Genetic Resources; 23-1, Toyama

1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan

1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan

(E-mail:khashi@mih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)

The International consortium for macaque cDNA sequencing and
analysis consists of: Department of Virology and Human Genome

Center, Institute of Medical Science, The University of Tokyo,
Tokyo, Japan; Division of Genetic Resources, National Institute of
Infectious Diseases of Japan, Tokyo, Japan; National Health
Research Institute, Taipel, Taiwan; Institute of Molecular Biology,
Academia Sinica, Taipel, Taiwan; Department of Ecology & Evolution,
University of Chicago, Chicago, IL, USA; Center for Information

Clone distribution: clone distribution information can be found at:
http://www.nih.go.jp/yoken/genebank/
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R. Sitel: Draill (CACTGTGTG)
R. Sitel: Draill (CACTGTGTG)
R. Sitel: Draill (CACCATGTGTG)
R. Sitel: Draill Strand CDNA was primer and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments A.1.Skb.The Sfil-digested PCR product was cloned into distinct Draill sites of pWE18S-FL3. XhoI sites just outside the Draill sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Libraries were made from:
QCCE: cerebellum cortex
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/note="unnamed protein product; Homo sapiens trophoblast
glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3"
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                             Osada, N., Hirata, M., Tanuma, R., Kusuda, J., Hida, M., Suzuki, Y., Sugano, S., Gojobori, T., Shen, J.C.-K., Wu, C.I. and Hashimoto, K. Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs
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/dev_stage="adult"
264 _ 2026
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                                                                                                                                                                                                                                               3 (bases 1 to 2714)
Hashimoto, K., Kusuda, J. and Sugano, S.
Direct Submission
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AB168308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / LTAIN ALL COME "MECAGESROPSAGDGRIRILARILALVILGWVSASAPSSSVPSSSTS
PADFLASGSAQPPARRCPAACRCSRAARTVKCVNRNILEVPADLPPYVRNILFILTGNO
WTVLPAGAFARQPPLADLEALNILGGRHILKEVCAGAFEHLPGILRLDISHNPLTNILSAF
WTVLPAGARASVSAPEPLERLILAHI VPPEDQRQNGSFEGAVAFEGAVAAALRSGIALRGI
TRIELASNHFLPLPERDLIAQILPSILXTDLRNNSLVSITYASFRNITHLESLHILEDNAL
KVIHNSTLASMGAGATVKPFLDNNPWVCDCYMADMYAMLKETEVVPDKARLTCAFPEK
MRNRGILDIANSSDLOCDAVLPGSLOTSYVPATIVALIGAIFLLVYLNRKGIKKWMH
NIRDACRDHWGGYHYRYRINADSNSDV"
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DNA sequences of macaque genes expressed in brain or testis and its
evolutionary implications
Unpublished
                                                                                                                                                                                                                                                   PAT 14-JAN-2004
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K.
Stat6 activation gene
Patent: WO 03104277-A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                                                                                                                                                                                                                                   linear
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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Matches:
Conservative:
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                                                                                                                                                                                                                                                        DNA
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Sequence 125 from Patent WO03104277.
AX961914
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                                               1663 GCTCTGATAGGCGCTATTTTCCTCCTC 1689
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    1 AlaLeuIleGlyAlaIlePheLeuLeu 9
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FEATURES

Query Match: DB:

8

No.:

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REPERENCE

JOURNAL

DEFINITION

AB168308 LOCUS

ACCESSION

us-10-774-176-6.p2n.rge

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SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLBSLHLBDNALKVLHNG
TABELGGEHRIRVFLDNNPWCDCHPNADMYTWLKETEVVQGKORLTCAYPEKRRNYL
LELNSADLDCDPILPPSLQTSYYFLGIYYALIGAIFLLYLYLNRKGIKKWMINIRDAC
RDHWEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus 5T4 oncofetal trophoblast glycoprotein gene.
LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
                                                                                                                                                                         /product="5T4 oncofetal trophoblast glycoprotein"
|5331. :5336
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5380. :5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Mus musculus (house mouse)
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Matches:
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                                                                                                                                                                                                                              5380. .5385
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Myers, K.A.
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Best Local Similarity:
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Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
AJ012159
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Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Homo sapiens (human)
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Biochim. Biophys. Acta 1445 (3), 257-270 (1999)
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Mismatches:
Indels:
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                                  Matches:
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db_xref="InterPro:IP
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              54.2
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                                          Percent Similarity:
Best Local Similarity:
Query Match:
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Alignment Scores:
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            Pred. No.:
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HSA012159
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on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping droup. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP3-492P14 is from the library RPOI-3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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| Nocte="match: proteins: P81877 Q99LX9 Q9BWW6 Q9CYZ8 Q9D6L4
Q9P038 Q9Y4T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a MAC.

1. 121909
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/product="trophoblast glycoprotein"
/note="match: BGTs: AA149121 AA152323 AA565852 AA643734
/note="match: AW71072 AW662538 BE260089 BF306457 BF306926
BF314984 BI196133 BI562387 BM069633 BW670613
match: cDNAs: AJ420536.1 Z29083.1"
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codon_start=1
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|standard_name="OTTHUMP00000016786"
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109639. .116836
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/mol_type="genomic DNA"
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP3-492P14"
/clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: vega@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                   /product="514" Oncolectal trophoblast glycoprotein:
/protein id=(AAA)9311.1"
/db_xref="G1:3805949"
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/db_xref="InterPro:IPR00372"
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/db_xre
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121909 bp

DNA

linear PRI 18-MAY-2005

Human DNA sequence from clone RP3-492P14 on chromosome 6q13-15

Contains a single stranded DNA binding protein pseudogene, the TPBG

gene for trophoblast glycoprotein (5T4-AG) and a CPG island,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                 product="5T4 oncofetal trophoblast glycoprotein"
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AL121977.11 G1:11863678
AL121977.11 G1:11863678
HTG: CpG island; TPBG.
Homo sapiens (human)
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1 (bases 1 to 121909)
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/gene="5T4"
3866. .5056
/gene="5T4"
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/gene="5T4"
5759. .5764
/gene="5T4"
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TITLE
JOURNAL
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LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPP
AFSGSNASVSAPSPLVELILANHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLEKLA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
                                                                          TLAELGGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVGGKDRLTCAYPEKMRNYVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIPLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV*
APPLASAVSAQPPLPDQCPALCECSBAARTVKCVNRNLTBVPTDLPAYVRNLFLTGNQ
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Submitted (19-WAR-2005) Genome Sequencing Center, 4444 Forest Park
Submitted (19-WAR-2005) Genome Sequencing Center, 4444 Forest Park
Submitted (19-WAR) Genome Sequencing Center, 4444 Forest Park
3 (Dases 1 to 167046)
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Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
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1 (Dases 1 to 167046)
Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
2 (Dases 1 to 167046)
Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC158516 167046 bp DNA linear ROD 21-JUN Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
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On May 4, 2005 this sequence version replaced gi:61656412.
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Matches:
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                          /locus_tag="RP3-492P14.1-001"
121909
                                                                                                                                                                              /locus_tag="RP3-492P14.1-001
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Drafting center: WIBR
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/gene="TPBG"
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Direct Submission
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AC158516 AC117768
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Best Local Similarity:
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                                                                                                                                        polyA_signal
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AC158516/c
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.
This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleoting repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is This sequence was finished as follows unless otherwise noted: minima]

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated. MAPPING INFORMATION

http://genome.wustl.edu

SOURCE INFORMATION:

The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

16685.\_.16712\_\_\_\_\_/note="Sequence derived from PCR product of genomic DNA" 31565. .31779 This sequence is the entire insert of the clone. Location/Qualifiers 1. .167046 /organism="Mus musculus" /mol\_type="genomic DNA" /db\_xref="taxon:10090" /chromosome="9" /clone="RP24-511A23" /clone\_lib="RPCI-24" misc\_feature source FEATURES

/note="Unresolved simple sequence repeat." 46721. .46808 /note="Unresolved simple sequence repeat." 142336. .142347 ungure unsure ungure

/note="Sequence derived from one plasmid subclone." ORIGIN

00000 Length: Matches: Conservative: Mismatches: Indels: 4.83e+03 40.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Aliqnment Scores: Query Match: Pred. No.:

US-10-774-176-6 (1-9) x AC158516 (1-167046)

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RESULT 38

210237 bp DNA linear HTG 19-NOV-2002 Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE. AC128294.3 GI:25083347 AC128294/C LOCUS DEFINITION ACCESSION VERSION

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft, sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 210237: contig of 210237 bp in length.
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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/db xref="taxon:10116"
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                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sclurognathi; Muroldea; Muridae; Murinae; Rattus.
           HTGS_DRAFT; HTGS_FULLTOP.
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COMMENT

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS REFERENCE

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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On Nov 20, 2002 this sequence version replaced gi:22857070.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/reat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234710: contig of 234710 bp in length 234810: gap of unknown length 235924: contig of 1114 bp in length 237314: contig of 1290 bp in length 237314: gap of unknown length 237414: gap of unknown length 239076: contig of 1662 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
           Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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                                                                                                                                               AC106962 239076 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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AC106962.5 GI:25139469
HTG; HTGS_PHASE1; HTGS_PULLTOP.
Rattus norvegicus (Norway rat)
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                                                                                       RESULT 39
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Carachan, J., Caradyna, S., Graham, L., Grand-Pierre, N. Hafez, N., Farckson, J., Farchar, B., FritzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grahami, J., Grand-Pierre, N., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliaev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Macdonald, P., Major, J., Malonga, V., Murphy, T., Najor, J., Manyor, T., Nicol, R., Nishe, V., Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Fetta, R., Rise, C., Rogov, P., Romann, T., Nicol, R., Saeman, S., Severy, P., Somith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Voll, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Schwister, S., Schwister, 
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stofanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Lendet, Submission

AL Submitted (06-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Shiren, B., Nusbaum, C., Lander, B., Abouellei, A., Allen, N., Anderson, M., Anderson, B., Bodylaleris, B., Camarata, J., Chang, J., Choppel, Y., Collymore, A., Cock, A., Cooke, P., Corum, B., Bastien, V., Barckenn, S., Farchen, H., Barten, B., Mastie, M., Gage, S., Dooley, K., Dorley, K., Daris, J., Gardereland, J., Gardyna, S., Graham, L., Grand-Plerre, N., Hafez, N., Hafez, N., Hafez, N., Hafez, N., Mabbitt, R., Mochen, C., Macdonald, P., Marke, A., Kelle, C., Landers, T., McCarthy, M., Meldrim, J., Moneue, L., Mihova, T., Machuk, C., Machonen, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Norbu, C., O'Connor, T., Collyma, R., Saver, P., Smith, C., Spenar, S., Schupba, M., Sever, P., Smith, C., Spenar, S., Schupba, M., Talams, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, V., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Whaman, M., Subbitted (Basea Th, Sonet Basearch, 320 Charles Street, Cambridge, M., Shillson, B., Wu, X., Wilson, B., Mu, M., M., Milson, B.,
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seg.wi.mit.edu
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1. (bases 1 to 189710)
Birren, B., Nusbaum, C. and Lander, R.
Mus musculus chromosome 8, clone RP24-112G5
                                                                                                                                                                                                                                                                                                                                                                                  linear
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Patent: US 6605709-A 2522 12-AUG-2003;
Genome Therapeutics Corporation; Waltham, MA
Location/Qualiflers
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Matches:
Conservative:
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Sequence 2522 from patent US 6605709.
AR377516
                                                                                                                                                                                                       15622 GCTCTGATAGGCGCTATTTTCCTCCTC 15596
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown.
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complement(1. .404)
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complement (5372...5500)
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6490. 6613

frpt_family="CA)n"

7815. 8119

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8135. 8160

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8474. 8496

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864. 8895

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317. 3393

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Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Mlenga, V.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROD 28-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC158916 206384 bp DNA linear ROD 28-JUN
Mus musculus chromosome 8, clone RP23-18G2, complete sequence.
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Birren,B., Nusbaum,C. and Lander,B.
Mus musculus chromosome 8, clone RP23-18G2
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
/rpt family="B3"
complement (15667. .15808)
/rpt family="B3"
complement (15609. .15902)
/rpt family="PBID7"
complement (16250. .16371)
/rpt family="MIR"
complement (16394. .16777)
/rpt family="MIR"
                                                                                                                                                                                                                                                                                                                         /rpt family="(TTG)n"
complement(20388. 20801)
/rpt family="RWBRS"
20997. .21401
/rpt family="MTD"
complement(21435. .21581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="B3A"
21944. 21973
/rpt_family="(CA)n"
complement(22566. 22547)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                    rpt_family="(TTTA)n"
7091..17142
rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                     family="(TTAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-774-176-6 (1-9) x AC126539 (1-158710)
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                                                                                                                                                                                                                                               /rpt_family="A'
17143. .17214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC158916
AC158916.4 GI:68268153
                                                                                                                                                                                 .17089
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39.00
100.0%
88.9%
97.5%
                                                                                                                                                                'rpt_far
.7030.
                                                                                                                                                                                                                                                                                         /rpt_fa|
|7267.
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Best Local Similarity:
Query Match:
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ACCESSION
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AC158916
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
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TITLE

REFERENCE AUTHORS

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clone_lib="RPCI-23 Female Mouse BAC"
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4009. .14035
note="8ingle clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="MSTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="B1_MM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt family="AT rich"
omplement(10399. .10489)
rpt_family="B3A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ement (11029. .11217)
family="B2_Mm1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="(CAAA)n"
omplement(15431. .15592)
rpt_family="RSINE1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (18654. .18748)
/rpt_family="PB1D10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt family="L1 MM"
complement (8477. .8665)
/rpt family="URRLB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="AT_rich"
complement(11729. .13598)
                                                                                                                                                                                                                                                                                                                                                                                      /rpt family="(T)n"
complement (3661, 3723)
/rpt family="ID_B1"
4258, 4377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(CATA)n"
5541. .5693
/rpt_family="(CATATA)n"
5874. .5896
                                                             organism="Mus musculus"
                                                                                               Ltype="genomic DNA"
_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="B3"
complement(5019..5452)
rpt_family="MLT1F1"
468..5629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                omplement(6607. .6863)
rpt_family="B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :omplement(7583. .7625)
/rpt_family="L1"
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7306. .17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(TTTA)n"
complement(18822. .189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="GA-rich"
8267. .18290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .10661
family="(TCCC)n"
                                                                                                                                                                                                                                                                                   complement (1..67)
/rpt family="RSINE1"
1862. .1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="RMER20"
8161. .18237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(TG)n"
complement(18291...)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family="(CA)n"
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6851. .17099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="Lx2B"
7106. .17125
                                                                                                                                                                                                                             clone="RP23-18G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1"
3597. .15299
                                                                                                                                                                   chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5179. .16853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5302. .15324
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                                                                                                                                                                                                  map="8
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                                     source
FEATURES
             Phunkhang, P., Plerre, N., Rachupka, A., Kamasamy, U., Kaymond, C., Beanan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Scouptovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, W., Vasailiev, H., Venketaraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (24-MAR-2065) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA

Buren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allan, N., Anderson, M., Anderson, S., Azachchi, H.M., Barnai, N., Bartain, V., Bloom, T., Boguslavity, L., Boukhgalter, B., Commarta, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Cohepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Laffez, N., Erickson, J., Faro, S., Ferreira, P., PitzGerald, M., Asiefez, N., Hagopian, D., Hall, J., Horton, L., Hulme, W., Ilsev, I., Johnson, R., Johnson, R., Lindblad-Toh, Major, D., Major, J., Malming, Y., Matbitt, R., MacLean, C., Macdonald, P., Major, J., Malming, Y., Matbitt, R., Murby, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., Connor, T., O'Connor, T., O'Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boquisavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Bodde, S., Dooley, K., Dorris, L., Darris, L., Errickson, J., Farro, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Horton, L., Milme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., McCearhy, M., Meldrim, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., Naylor, J., Nguyen, T., Nicol, R., Norbu, C., Cornor, T., O'Donnell, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Venkatzraman, V.S., Viel, R., Vo, A., Wilson, B., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubmitted (21-APR-2005) Broad Institute of MIT and Harvard, 320 harles Street, Cambridge, MA 02141, USA (bases 1 to 206384)
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Contact: sequence submissions@broad.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Broad Institute of MIT and Harvard
   Rachupka, A
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Center clone name: 18_G_2
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Holling, H., Howells, S., Hulfk, S., Hume, J., Idlebrat, J., Jackbon, A., Jackbon, L., Lebow, H., Levan, C., Lewis, L., Liu, J., Kovar, C., Kraft, C.L., Lebow, H., Levan, C., Lewis, L., Lit, Z., Liu, J., Liu, W., Liu, Y., Londacre, S., Lopez, J., Liu, W., Liu, W., Liu, Y., Londacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Martinez, B., Mahned, M., Malloy, K., Martinez, E., Mantinez, B., Manda, P., Martin, R., Martinez, B., Mandiney, S., McLeod, M.P., McNeill, T.Z., Meenen, B., Mangum, A., Minosarljevic, A., Minort, G., Minidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parke, K., Pasternak, S., Paul, H., Perez, J., Peraz, L., Pall, S., Pall, H., Perez, A., Perez, L., Pall, S., Pall, H., Perez, A., Perez, L., Pall, S., Pall, H., Perez, A., Perez, L., Riggs, F., Reilly, B., Reilly, M., Ren, Y., Reeves, R., Reglar, M., Raggs, F., Riyes, C., Rodkey, T., Rojas, M., Rose, R., Reilly, B., Reilly, M., Ren, Y., Schert, S., Scotel, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svaele, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walden, M., Vera, V., Villasana, D., Walden, H., Woolen, H., Woler, K., Walden, Y., Yon, V., Williams, G., Willson, R., Waler, R., Wen, X., Wen, X., Weil, K., Walle, Y., Walght, D., Wright, D., Wright, R., Walers, S., Smith, D., N., Weinscock, G. and Gibbs, R.A., Smith, D.R., Woll, R., Smith, H.O., Weinscock, G. and Gibbs, R.A., Smith, D.R., Walle, R., Smith, H., D., Weinscock, G. and Gibbs, R.A., Smith, D.R., Smith, R., Weinscock, G. and Gibbs, R.A., Smith, D.R., Smith, R., Weinscock, G. and Gibbs, R.A., Smith, D.R., Weinscock, G. and Gibbs, R.A., Smith, D.R., Weinscock, G. and Gibbs, R.A., Smith, D.R., Smith, R. Wall, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Suministical (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:22857079.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/ratl/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project Information
Center project name: GOMX
Center clone name: GM23-138L4
Center clone name: GM23-138L4
Assembly program: Phrap; version 0.990329
Consensus quality: 196804 bases at least Q40
Consensus quality: 201135 bases at least Q20
Estimated insert size: 206652; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center code: BCM
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 208078)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208078 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-138L4, WORKING DRAFT SEQUENCE, 3
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldas, Muridae, Murinae, Rattus.
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HTG; HTGS PHASEI; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="L1_MM"
13836. .23885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="(TA)n"
complement(24389. .24575)
/rpt_family="B3A"
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complement (18970. .19179)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MYS_LTR"
25305. .25326
/rpt_family="AT_rich"
25819. .25941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-774-176-6 (1-9) x AC158916 (1-206384)
                                                                                                                                                                                                                           rpt family="CT-rich" 1677. .21730
                                                                                                                                                                                                                                                                                                                                                                                                                         'rpt family="RSINE1"
complement (23235. .2
                                                                                                                                                    /rpt_family="(CA)n" (03)2. .20436
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/rpt_family="B4"
19700. .19789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .24935
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39.00
100.0%
88.9%
97.5%
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24646.
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Best Local Similarity:
repeat_region
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AC107258/c
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SOURCE
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Raturota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidae, Murinae, Rattus.
1 (bases 1 to 241416)
Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Anin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Baldwin, N., Buhay, C., Burch, P., Burnell, K., Calderon, E.,
Cardenas, V., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cos, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Rattus norvegicus clone CH230-69E14, *** SEQUENCING IN PROGRESS
***, 6 unordered pieces.
                                                                                                                                                                                                                                             1 187677: contig of 187677 bp in length 8 187777: gap of unknown length 8 190426: contig of 2649 bp in length 7 190526: gap of unknown length 7 208078: contig of 17552 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC114100.4 GI:30579733
HTG; HTGS_HTGBL; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="GH230-138L4"
59079 . 62947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29752 GCTTTGATCGGGCTGTGTTTCTCCTC 29726
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/note="wgs_contig"
187678. 187777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_contig"
141848. .143914
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187778
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190527
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Best Local Similarity:
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DB:
                                                                                                                                                                                                                                                                                                                                                                                            Bource
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KEYWORDS
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Direct Submission

Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 241416)

SAt Genome Sequencing Consortium.

Direct Submission

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23268086.

The sequence in this sequence version replaced gi:23268086.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/ratk). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig estaffold that consists entirely of whole contigs within a contig estaffold that consists entirely of whole
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Plagg, N., Porbes, L., Garner, T., Garzer, P., Ferrandez, S., Finley, M., Plagg, N., Forbes, L., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Harnandez, R., Hanalton, K., Hamilton, K., Hamilton, K., Hamilton, K., Harnandez, R., Hines, S., Hiladun, S.L., Hodgson, A., Hogues, M., Harnandez, R., Hines, S., Hiladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jakebo, L., Jang, H., Johnson, B., Johnson, R., Jolivec, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Liu, W., Liu, Y., Land, H., Lorado, R., Lewa, J., Lewis, L., Liu, T., Liu, Y., Mar, J., Martin, R., Martinez, E., Malosa, M., Mallos, K., Maria, J., Martin, R., Martinez, B., Mangum, B., Mandawa, L., Loulseged, H., Lorado, R.J., Martin, R., Martinez, B., Manderis, S., McLeod, M.P., Morell, T.Z., Meenen, E., Manderis, S., McLeod, M.P., Morell, T.Z., Merrin, R., Martin, R., Reilly, R., Reilly, M., Ren, Y., Reuter, L., Perger, L., Farance, R., Reilly, R., Reilly, M., Ren, Y., Reuter, R., Reilly, R., Railly, M., Ren, Y., Reuter, R., Resper, R., Rose, R., Reille, R., Marcin, R., Saver, R., Saver, R., Thomas, S., Tingey, A., Tabor, P., Taylor, C., Taylor, C., Waigs, R., Warren, J., Zhou, J., Zhou, J., Yoon, V., Walle, R., Walle, R., Waller, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Marti
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Center code: BCM
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Center project name: GLLU
Center clone name: CH230-69E14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Genome Center
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Escobedo,J., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C.,
Randazzo,F., Lamson,G., Scott,B.M., Zhang,G., Kassam,A., Pot,D. and
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Kassam, A., Pot, D. and
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Human genes and gene expression products genes and gene expression products CHIRON CORPORATION (US); Hyseq Inc. (US)
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Sequence 892 from Patent WO0214500.
AX385964
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Homo sapiens
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     14
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Best Local Similarity:
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KEYWORDS
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DB:
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AUTHORS
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JOURNAL
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                                                                                                                                                      NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html). NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will.
Assembly program: Atlas 3.0;
Consensus quality: 180076 bases at least Q40
Consensus quality: 185112 bases at least Q30
Consensus quality: 189119 bases at least Q30
Estimated insert size: 187073; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                           1 223057; contig of 223057 bp in length 1058 223157; gap of unknown length 1158 234587; contig of 11490 bp in length 1158 234587; contig of 11430 bp in length 1588 234687; gap of unknown length 1688 235919; contig of 1232 bp in length 1692 23619; gap of unknown length 1602 236770; gap of unknown length 177 237470; gap of unknown length 1776 241416; contig of 125 bp in length 1776 241416; contig of 2641 bp in length 1676 24150; mol type="gaponic DNA" | mol type="gapon
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234588. .234687
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clone_end:T7"
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complement (150409.
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AP117351 Someones mobilis rrnB operon, partial sequence; RpfN (rpfN) gene, complete cds; rrnC operon, complete sequence; MexT), putative regulatory protain, dihydrodipicolinate synthetase (daph), hypothetical ABC transpoter permease protein, hypothetical ABC transpoter permease protein, hypothetical ABC transpoter permease protein, hypothetical ABC most), molybdenum transpote system protein (modD), and homocitrate synthase (nifV) genes, complete cds; and unknown genes.
LDVGENNHGGKPLIMYPCHGMGGNQYPEYTTQRDLRHNVGKQLCLRAGAGPVQLGECR
PRGQPTRVPPDEEWELTQDHLIKNHASRMCLTARGKHPAMAPCDPSDPHQLMSFT"
2286. .>3205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Zymomonas.

1 (bases 1 to 40133)

1 (bases 2 and Kang, H.S.
Sequence analysis of a 44F11 fosmid clone of Zymomonas mobilis ZM4
Dubblished
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Lee, J.S. and Kang, H.S.
Direct Submission
Submitted (DG-JAN-1999) Microbiology, Secul National University,
San 56-1 Shilimdong Gwanakgu, Secul 151-742, Korea
Location/Qualifiers
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/strain="ZM4"
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Zymomonas mobilis
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AF117351
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Gallus gallus mRNA for hypothetical protein, clone 1b1.
AJ851373
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TDSYLKDELDRYVKQLQIVPVVRQAERKGLITARLLCASVASGEVLIFLDAHGECFHG
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Submitted (12-OCT-2004) Caldwell R.B., GSF - Forschungszentrum,
Institut fuer Molevulare Strahlenbiologi, Ingolstaedter Landstr. 1,
D-85764 Neuherberg, GREMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caldwell, R. B., Kierzek, A. M., Arakawa, H., Bezzubov, Y., Zaim, J., Fiedler, P., Kutter, S., Blagodateki, A., Kostovska, D., Koter, M., Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J. M., Full-length cDNas from chicken bursal lymphocytes to facilitate gene function analysis Genome Biol. 6 (1), R6 (2005)
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                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (chicken)
Gallus gallus
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Caldwell, R.B.
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                                                                  Percent Similarity:
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Aa835779 Human car
Ade46473 Human car
Ad107891 Human car
Ab118534 Drosophil
Aax27723 B. lactof
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## ALIGNMENTS

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Bovine EST associated with lactation/muscle/fat deposition #5770.
     ABX40605 standard; cDNA; 343 BP.
                           20-PEB-2003 (first entry)
                ABX40605;
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Bovine; ss; RST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

Bos Taurus.

JS2002137139-A1

24-SEP-2001; 2001US-00960352.

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The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX4937, or complements of them. Also included are (i) in transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) where complementary nucleic acid permits the detection of the molecule; and (b) detection of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the complementary nucleic acid partern of a molecule acid is used for the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the sequence mapping, gene identification and analysis, cattle tris useful for genome mapping, gene identification and analysis, cattle consent sequence was not shown in the specification but was obtained in present sequence was not shown in the specification but was obtained in present sequence was not shown in the specification but was obtained in the patern of the molecule.
                                                                                                                                                                                                                                                                                                   New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                       Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 5770; 245pp; English
12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                       Byatt JC, Mathialagan N,
                                                                      (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                      WPI; 2003-110599/10.
                                                                                                                                                  (WARR/) WARREN W C.
                                                                                                                             (TAON/)
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Sequence 343 BP; 40 A; 146 C; 108 G; 49 T; 0 U; 0 Other;

Aliqnment Scores:			
Pred. No.:	1.23	Length:	343
Score:	44.00	Matches:	0
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Ouery Match:	100.0%	Indels:	0
ĎB:	60	Gaps:	0

US-10-774-176-5 (1-9) x ABX40605 (1-343)

PheLeuThrGlyAsnGlnLeuAlaval 9 179

8 셤 ACL56146 standard; cDNA; 505 BP ACL56146;

24-MAR-2005 (first entry) 

Differential expression; diagnosis; therapy; drug screening; cancer; neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;

Human colon cancer differentially expressed polynucleotide, SEQ ID:2281.

Feline; cat; oncofoetal leucine-rich glycoprotein; 574; tumour;

/product= "5T4 protein"

ø

1, .1260 /\*tag=

Key

(OXFO-) OXFORD BIOMEDICA UK LTD.

2002-557449/59.

P-PSDB; AAU98694.

13-NOV-2000; 2000WO-GB004317.

16-MAY-2002.

Location/Qualifiers

gb.

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Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                  cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
               cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                                                                                                                                    13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                                                                             WO200238612-A2.
                                                                                                                                             Felis
The invention relates to 9672 polymucleotides (ACL53866-ACL63537) which are differentially expressed in colon cancer cells. The invention also relates to vectors and host cells comprising a differentially expressed polymucleotide of the invention; a method for detecting a cancerous cell by detection of a gene product of the polymucleotides; a method for inhibiting a gene product of the polymucleotides; a method of treating an individual with cancer by administration of a modulator of a gene product of the polymucleotides; and an isolated antibody that specifically binds to a polymethedies, and methods are useful for the detection of cancerous cells; or the diagnosis, prognosis and management of cancer; for the diagnosis, prognosis and management of cancer; for the identification of therapeutic targets for cancer chemotherapy; and for the treatment of cancer, especially colon cancer and metastasized colon cancer, but also breast or pancreatic cancer. The polymucleotides colon cancer but also breast or pancreatic cancer. The polymucleotides cancer also useful as a source of probes or primers for use in diagnostic methods. The differentially expressed polymucleotides or their encoded concerned the prevention or treatment of cancer. The present sequence responses for the prevention or treatment of cancer. The present sequence responses diate for this differentially colon cancer. The present sequence or expressed in diagnostic but and a source of probe or primers for their encoded concerned as specifically claimed polymucleotide which is differentially expressed polymucleotide which is differentially expressed and each are also their encoded concerned as a second to the present sequence of expressed in colon cancer. The present sequence concerned and an each are also the present appears the present and an each and each an
                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides, which are differentially expressed in colon cancer cell, useful for treating cancer, e.g. colon cancer, breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 505 BP; 68 A; 202 C; 149 G; 85 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                          Garcia PD;
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2281; 97pp; English.
                                                                                                                                                                                                                                                          Bscobedo J,
                                                                                                                                                                                                                                                                                                                                                                     cancer, or pancreatic cancer.
                                                                                                                                           13-MAY-2004; 2004WO-US015421.
                                                                                                                                                                                03-JUN-2003; 2003US-0475872P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.93
44.00
100.0%
100.0%
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                                                                                                                                                                                                                    (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                             WPI; 2005-075421/08
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Best Local Similarity:
                                                                    WO2005000087-A2.
                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                        Randazzo F,
                                                                                                         06-JAN-2005
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DB:
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the proposition of solid sequences encoding them. The 574 proteins are expressed in a significant proportion of tumousts. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in disquance fix the for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in call culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The called may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes feline 5T4 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-774-176-5 (1-9) x ABK87175 (1-1260)
Claim 4; Page 68; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB97513 standard; DNA; 1260 BP
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100.0%
100.0%
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Best Local Similarity:
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DB:
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ID ADBS
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180 rrccrracceccaaccaecreecere 206

ABK87175 standard; cDNA; 1260

**ABK8717** 

07-OCT-2002 (first entry)

ABK87175;

PheLeuThrGlyAsnGlnLeuAlaVal

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US-10-774-176-5 (1-9) x ACL56146 (1-505)

σ

Gaps:

286 TTCCTCACCGGCAATCAGCTGGCCGTG 312

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ADB97452 standard; DNA; 1260 BP

1 PheLeuThrGlyAsnGlnLeuAlaVal

σ

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major histocompatibility complex class I peptide epitopes from human tumor-associated antigen, useful for preventing and/or treating a
                                                                                                                                                  Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1560
/*tsg= a
/product= "Feline 574 antigen protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redchenko I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002; 2002GB-00003419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2003; 2003WO-GB000670
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carroll M, Kingsman S,
                                                                                                   Peline 5T4 antigen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI, 2003-637141/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ADB97520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003068816-A1
                                                                                                                                                                                                                                                                Unidentified
                                                 04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-2003.
ADB97513;
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gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.

DNA encoding feline 5T4 protein.

04-DEC-2003 (first entry)

ADB97452;

Disclosure, Page 67; 73pp; English

The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 5T4 antigen. The invention further class I pervides a polypelicope string comprising the 5T4 epitope; a uncleic acid contains the 5T4 epitope in anticleic acid to a cell, a cell pulsed with the 5T4 epitope, a polypelitope of the 5T4 epitope nucleic comprising the above; a method for treating the 5T4 epitope nucleic comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising detecting the presence of the 5T4 epitope and the sort clone capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope or the sort clone capable of molecule. The 5T4 epitope has cytobetatic acid; the vaccine subject path is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for diagnosing or particularly cancer. The detection method is useful for diagnosing or particularly cancer. The detection method is useful for diagnosing or monitoring the brogression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone crossed in the manufacture of a medicament for treating and/or preventing a disease. 5T4 antigen coding DNA of the invention.

Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

Length: Matches: Conservative: Mismatches: Indels:

5.62 44.00 100.0\$ 100.0\$

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

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1260
0
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0
      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
      5.62
44.00
100.0$
100.0$
                              Similarity:
                     Percent Similarity:
Alignment Scores:
Pred. No.:
                                  Query Match:
DB:
                              Best Local
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US-10-774-176-5 (1-9) x ADB97513 (1-1260)

Trefredesaarcagecerg 312

PheLeuThrGlyAsnGlnLeuAlaVal 9

-286

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US-10-774-176-5 (1-9) x ADB97452 (1-1260)

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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognishing a peptide epitope in conjunction with an MHC molecule, for disagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polymucleotide sequence represents the DNA coding for the felline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                     Location/Qualifiers
1. .1260
/*tag= a /peline 574 antigen protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 49; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  Kingsman S;
                                                                                                                                                                                                                                                                                                                                                                                  (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002; 2002GB-00003420.
                                                                                                                                                                                                                                                                                                                   13-FEB-2003; 2003WO-GB000618
                                                                                                                                                                                                                                                                                                                                                                                                                 Carroll M, Harrop R,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-663795/62.
P-PSDB; ADB97455.
                                                                                                                                                                                                                                                     WO2003068815-A2
                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                      21-AUG-2003.
                                                                                                                                                                        Key
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Nucleotide sequence of canine 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK87174 standard; cDNA; 1263 BP
                                                                                       Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
ABK87174
ID ABK8
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes the human 5T4 tumour-associated antigen carcinomas but has a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targetting and immunotherapy. Mice in which tumours had been induced were incculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                    Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                          Human; TAA; tumour-associated antigen; anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                       Human 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheLeuThrGlyAsnGlnLeuAlaVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-774-176-5 (1-9) x AAA27058 (1-1263)
                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 78; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                            AAA27058 standard; DNA; 1263 BP
                                                                                                                                                                                                                                                                        (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                98GB-00025303.
99GB-00001739.
99GB-00017995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP89736 standard; DNA; 1263
                                                                                                                                                                                                             99WO-GB003859
                                                                   (first entry)
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44.00
100.0%
100.0%
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                                                                                                                                                                                                                                                                                              Myers KA;
                                                                                                                                                                                                                                                                                                                WPI; 2000-387735/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                    WO200029428-A2
                                                                                                                                                                                                                               18-NOV-1998;
27-JAN-1999;
30-JUL-1999;
                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                            MW,
                                                                                                                                                                                                            18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                   22-AUG-2000
                                                                                                                                                                                        25-MAY-2000
                                                 AAA27058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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                                                                                                                                                                                                                                                                                            Carroll
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DB:
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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, gestionteal diseases, cardiopulmonary diseases, ardiovascular diseases, gastrointestinal disorders infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
Single chain antibody; ScPv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bebbington CR, Carroll MW, Ellard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 26, 118pp, English.
                                                                                                                                                                                                                                                                         1. .1263
/*tag= a
/product= "5T4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1999; 99WO-GB003859.
15-PEB-2000; 2000GB-00003527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2000; 2000GB-00005071.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers KA;
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Human; p53 pathway; Leucine rich repeat capricious related protein;

LRRCAPS; cancer; gene therapy; ds.

21-OCT-2002; 2002WO-US033540.

WO2003035831-A2.

01-MAY-2003.

Homo sapiens

22-OCT-2001; 2001US-0338733P. 15-FEB-2002; 2002US-0357600P. 01-MAR-2002; 2002US-0361196P.

Human LRRCAPS related DNA #6.

07-AUG-2003 (first entry)

AAD56199;

AAD56199 standard; DNA; 1331 BP.

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RESULT 9
                                                    The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the professed in colynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaccutical composition for the prevention and/or treatment of tumours or other diseases associated with cell compositions in animals, proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                          Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                  cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                    /*tag= a
/product= "5T4 protein"
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1, Page 67, 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                                                                                                                              13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                   13-NOV-2001; 2001WO-GB005004
                                       (first entry)
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P-PSDB; AAU98693.
                                                                                                                                                                                                                                                             WO200238612-A2
                                       07-OCT-2002
                                                                                                                                                                                                                                                                                        16-MAY-2002
              ABK87174;
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Plowman GD, Funke RP, Lioubin MN,

Belvin M, Schleithoff L, P Francis-Lang H, Friedman L;

WPI; 2003-421410/39.

(EXEL-) EXELIXIS INC.

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent blased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheLeuThrGlyAsnGlnLeuAlaVal 9
                                                                                                              Disclosure; Page 75-76; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-774-176-5 (1-9) x AAD56199 (1-1331)
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Length: Matches: Conservative: Mismatches:

5.63 44.00 100.0\$ 100.0\$

Similarity:

Query Match

Percent Similarity:

Score:

Alignment Scores:

Indels:

Trctcacacaaccagctggcggtg 315

PheLeuThrGlyAsnGlnLeuAlaVal 9

US-10-774-176-5 (1-9) x ABK87174 (1-1263)

2001US-0302814P

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Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynucleotide or antibody.
                                                                             Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                     Human bladder cancer associated cDNA sequence SEQ ID NO:192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 296; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                    03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-035066EP.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                        03-JUL-2002; 2002WO-US021338
12-JUN-2003 (first entry)
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P-PSDB; ABR48236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mack DH, Aziz N;
                                                                                                                                                                    WO2003003906-A2.
                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                   03-JUL-2001;
                                                                                                                                                                                                              16-JAN-2003
This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protonon cells activated by the transactivator MYCN, where MYCN is a protonon cells activated by the transactivator MYCN, where MYCN is a protonon cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the US Patent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                 Human cDNA differentially expressed in MYCN activated cells SegID 105
                                                                                    88
                                                       human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                            25-PEB-2002; 2002US-00084817.
                                                                                                                                                                                                                                                                                                                    23-FEB-2001; 2001US-0270784P.
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NUCHTERN J G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-635698/60.
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                                                                                                                                                Homo sapiens.
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associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC5051 to ACC51059). ACC5051 to ACC51059 encode the human bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used for detecting a bladder cancer-associated sequence from the present invention have cytostatic activities, and can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in
The present invention describes a method for detecting a bladder cancer-
                                                                                                                                                                                                                                                                                                                                                    various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 TTCCTTACCGGCAACCAGCTGGCCGTG 399
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DB:
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ID ABX7
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AC ABX7
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DT 02-A
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Indels:

Best Local Similarity:

Query Match:

rrccrraccegeaccaecreecere 385 1 PheLeuThrGlyAsnGlnLeuAlaVal 9

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RESULT 11

86

ACC51052 standard; cDNA; 2053

ACC51052

ACC51052 ID ACC5 XX AC ACC5 XX

US-10-774-176-5 (1-9) x ADJ56299 (1-2020)

RESULT 13

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Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; procancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                     Detecting a lung cancer-associated transcript in a cell from a patient for tracating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
cancer-associated polynucleotide #196.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22, Page 335, 453pp; English.
                                                                                                                                                                                                10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-035066FP.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                      (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                18-APR-2002; 2002WO-US012476
                                                                                                                                                                                       2001US-0284770P
                                                                                                                                                                                                                                                                                                                    WPI; 2003-093161/08.
P-PSDB; ABU56603.
                                                                                                                                                                                                                                                                                              Murray R;
                                                                                                                  WO200286443-A2.
                                                                                                                                                                                      18-APR-2001;
                                                                                          Unidentified
                                                                                                                                         31-OCT-2002
                                                                                                                                                                                                                                                                                              Aziz N,
 Lung
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer—compound that modulates a lung cancer—associated for identifying a compound that modulates a lung cancer—associated for identifying a concer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell ung cancer or other behign or precancerous leasions, e.g. attendersis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences Invention

461 A; 602 C; 499 G; 491 T; 0 U; 0 Other; Sequence 2053 BP;

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2053
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          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                          1 PheLeuThrGlyAsnGlnLeuAlaVal 9
                                                                                    US-10-774-176-5 (1-9) x ABX76332 (1-2053)
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                              Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
                                                     Query Match:
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Trcttaccgcaaccagcrgccgrg 399

373

RESULT 14

AADS6200 standard; DNA; 2053

07-AUG-2003 (first entry)

AAD56200;

SXXXEX

1 PheLeuThrGlyAsnGlnLeuAlaVal

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US-10-774-176-5 (1-9) x AAD56197 (1-2053)

Best Local Similarity:

Query Match: DB:

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Gaps

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fargment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                  Human; p53 pathway; Leucine rich repeat capricious related protein; LRRCAPS; cancer; gene therapy; ds.
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              AAD56197 standard; DNA; 2053
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15-PEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Belvin M, Schleithoff L, P]
Prancis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                              21-OCT-2002; 2002WO-US033540
                                                                                (first entry)
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                                                                                                                    Human LRRCAPS DNA #11
                                                                                                                                                                                                                                                                                                                                                                                                                   (EXEL-) EXELIXIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                           Homo sapiens.
                                                                                  07-AUG-2003
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                                                AAD56197;
AAD56197
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vulnerary; gene therapy; vaccine; gene; ss.
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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 The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory;
                                                                                                                                                                                                                                                                                                                             ä
                               Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                           Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                           Plowman GD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 76-77; 99pp; English.
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                                                                                                                                                                                                                    22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                     21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                          Belvin M, Schleithoff L, P]
Francis-Lang H, Friedman L;
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Human LRRCAPS DNA #12
                                                                                                                                                                                                                                                                                          (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-421410/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                   WO2003035831-A2.
                                                                                     Homo sapiens.
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%XCCCCCCCX8X44444X8X8X8888X888X8X8X88X88X88X8

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The invention relates to nucleic acids and proteins (ADN)36683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a determining the presence or absence of a pathological cell in a content of the invention or by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention; antibodies with specifically bind a nucleic acid of the invention; use of such antibodies for drug targeting; confidence of the invention was of such antibodies for drug targeting; polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attendance action syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hevezi PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a nucleic acid sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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B, Zlotnik
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Wilson KE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginsburg WM,
R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2002; 2002US-0347349P.

08-FBB-2002; 2002US-0355250P.

13-FBB-2002; 2002US-0355714P.

20-FBB-2002; 2002US-035907P.

29-MAR-2002; 2002US-0368809P.

04-APR-2002; 2002US-0368809P.
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                                                                                                                                                                                                                                                                                                    21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0349374P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347211P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2002; 2002US-0372246P-05-JUN-2002; 2002US-0386614P-16-JUL-2002; 2002US-0396839P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-2002; 2002US-0397845P, 09-SEP-2002; 2002US-0409450P,
                                                                                                                                                                                                      13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                                                                                           2001US-0350666P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-468649/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADN38722
                                                             WO2003042661-A2
Homo sapiens.
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Mack DH, 1
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2053 9 0 0 0 0

Matches: Conservative: Mismatches: Indels:

9.93 44.00 100.0% 100.0%

Similarity:

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Gaps:

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ADL06473;

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The invention relates to novel polynuclectide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence
                                                                                                                                                                                                                                                                                                                                                                                          Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a
                                                                                                                                                   ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponds to one of the polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; breast cancer; prognosis; gene expression; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast cancer prognosis marker #1305.
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              ADN03961 standard; cDNA; 2053 BP.
                                                                                                                    Antipsoriatic cDNA sequence #180.
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                                                                                                                                                                                                                                                                                           25-SEP-2003; 2003WO-US030907.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR25444 standard; DNA; 2053
                                                                                01-JUL-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-305105/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity:
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Best Local Similari
                                                                                                                                                                                      Homo sapiens
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR25444;
                                                 ADN03961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                               Wu TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polymucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for represents or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TAT)
or
                                                                                                                                                                                                                                        Human; tumour-associated antigenic target; TAT; cell death; tumour;
                                                                                                                                                                                                    Human tumour-associated antigenic target (TAT) cDNA sequence #53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody that binds to a tumor-associated antigenic target peptide, useful for preparing a composition for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polakis P, Polson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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                     TTCCTTACCGGCAACCAGCTGGCCGTG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1, SEQ ID NO 53; 319pp; English
 PheLeuThrGlyAsnGlnLeuAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-2002; 2002US-0404809P.
21-AUG-2002; 2002US-0405645P.
23-SRP-2002; 2002US-0413192P.
15-OCT-2002; 2002US-0419008P.
15-NOV-2002; 2002US-0426847P.
02-JUL-2003; 2003US-0484959P.
                                                                                                    ADL06473 standard; cDNA; 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2003; 2003WO-US025892.
                                                                                                                                                                                                                                                        cancer; cytostatic; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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P-PSDB; ADL06552.
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Spencer SD, Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide, use
treating cancer.
                                                                                                                                                                                                                                                                                                                            WO2004016225-A2
                                                                                                                                                                                                                                                                                           Homo sapiens.
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WO2004065545-A2

TTCCTTACCGGCAACCAGCTGGCCGTG 399

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RESULT 17

Query Match:

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Wu TD,
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XBXBXBXBXBXBXBX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                      The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour-associated antigenic target (TAT) cDNA DNA103471, SEQ ID NO:2070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                   Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                           Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; cytostatic; gene; ss
                                                                  (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN38510 standard; cDNA; 2053 BP
                                            2003US-00342887.
                      15-JAN-2004; 2004WO-US001100.
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                                                                                                                             WPI; 2004-593473/57.
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                                                                                                      Van't Veer LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                            15-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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05-AUG-2004
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The invention relates to human tumour-associated antigenic target (TAT)

Coverexpressed in cancer tissues compared to normal tissues, and may thus
serve as effective targets for the diagnosis and treatment of cancer in
mammals. The invention also relates to nucleic acid and polypeptide
compared to the TAT nucleic acids and
polypeptides; expression vectors and host cells comprising a TAT nucleic
colypeptides; expression vectors and host cells comprising a TAT nucleic
acid; an antibody specific for a TAT polypeptide; a peptide or organic
molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
antibodies, antagonists, binding molecules and compositions are useful
for diagnosing or treating a cell proliferative disorder associated with
for diagnosing or treating a cell proliferative disorder associated with
for diagnosing or treating a cell proliferative disorder associated with
colorectal cancer, lung cancer, ovarian cancer, liver cancer, colorectal cancer, necessed TAT expression, particularly cancers of the central
colorectal cancer, melanoma and leukaemia. TAT nucleic acids may further be
used as hybridisation probes, in chromosome and gene mapping, in
chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; 88; multi-parameter high throughput screening; MPHTS; disease signature; neuropsychiatric; neurodegenerative; schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's; Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.
                                                                                                                                                                                                                                                New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2053 BP, 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA of an exemplary efficacy gene for BAD SeqID174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00000
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2070; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 TTCCTTACCGGCAACCAGCTGGCCGTG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-774-176-5 (1-9) x ACN38510 (1-2053)
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                                                                       Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                    prostate cancer or tumor.
(GETH ) GENENTECH INC.
                                                                                                                                              WPI; 2004-347921/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                   Zhang Z,
                                                                                                                                                                                P-PSDB; ABM80804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003096264-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2005
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This invention relates to a novel screening method identified as a multiparameter high throughput screening (MPHTS) assay. Specifically, it refers to an assay that utilises the disease signature of a plurality of specific genes associated with a bissase, and identifies differential expression between those cells taken from individuals differential expression between those cells taken from individuals of affected by that disease and those that are not affected. The present invention then describes the screening of candidate pharmaceutical compounds to identify those that have a potential therapeutic benefit for the treatment of neuropsychiatric and neurodespersative disorders including schizophrenia, bipolar affective disorder (BAD) and autism, as including schizophrenia, bipolar affective disorder (BAD) and autism, as the treatment of antidepressant. Furthermore, the screening method used in MPHTS will be automated, such that a large number of test compounds may be rapidly screened with a minimal amount of labour and effort. This polynucleotide is a human cDNA sequence of a gene that is differentially expressed in the presence of a therapeutic compound and compared that an exemplary efficacy gene for bipolar affective disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a compound that can treat disease or disorders, such as, neuropsychiatric disorder e.g., schizophrenia, or autism, comprises determining the expression of one or more efficacy genes in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klimczak LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hook D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; SEQ ID NO 174; 39pp; English
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given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altar CA, Brockman JA, Bvans D,
Palfreyman M, Rajan P;
                                                                                                                                                                                                                                                                                                                                                                                                        (PSYC-) PSYCHIATRIC GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contacted with the test compound
                                                                                                                                                                      25-8EP-2001; 2001US-0325150P-
14-WOV-2001; 2001US-0333047P-
18-JAN-2002; 2002US-034934P-
04-MAR-2002; 2002US-0361834P-
                                                                                   2001US-0299151P
2001US-0317828P
18-JUN-2002, 2002US-00175523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-118903/12.
                                                                                       18-JUN-2001,
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Drmanac RT, Liu C, 2001-639362/73

P-PSDB; ABG22988

(HYSE-) HYSEQ INC

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 30-MAR-2001; 2001WO-US008631

WO200175067-A2

11-OCT-2001

Claim 1; SEQ ID NO 22979; 103pp; English.

biodiversity.

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food cupplement. (II) and (II) are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colviptide and polymodicotide sequences have applications in adjoint of mutations diagnostics, forensics, gene mapping, identification of mutations capped amino acid sequences. Abs64197-AAS94564 represent novel human diagnostic coding sequences. Abs64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in

Sequence 2338 BP; 519 A; 677 C; 608 G; 534 T; 0 U; 0 Other;

2053 9 9 0 0 0 0 0

Length: Matches: Conservative: Mismatches:

9.93 44.00 100.0% 100.0%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Indels:

Gaps:

TTCCTTACCGGCAACCAGCTGGCGTG 399

373

ઠ 용 RESULT 21

AAS87175 standard; cDNA; 2338 BP

PheLeuThrGlyAsnGlnLeuAlaVal 9

J8-10-774-176-5 (1-9) x ADV35098 (1-2053)

electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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Human; full length cDNA; cDNA synthesis; oligo-capping; ss
            Length:
Matches:
Conservative:
Mismatches:
                                                                         Indel8:
                                                                                                                                                           630 TICCTTACCGGCAACCAGCTGGCCGTG 656
                                                                                                                                                                                                                                                                                                                   Human full-length cDNA, SEQ ID NO: 2864.
                                                                                     Gaps:
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                                                                                                                  US-10-774-176-5 (1-9) x AAS87175 (1-2338)
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                                                                                                                                                                                                                                                                                         (first entry)
             11.6
44.00
100.0%
100.0%
                                                       Best Local Similarity:
                                          Percent Similarity
Alignment Scores:
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                                                                                                                                                                                                                                                              AAK94253;
                                                                        Query Match:
                                                                                                                                                                                                    RESULT 22
                                                                                                                                                                                                                    AAK94253
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                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder; ss.
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DNA encoding novel human diagnostic protein #22979.

Homo sapiens

(first entry)

13-PEB-2002

AAS87177 XXX XXX AAC AAC XXX DT 133 XXX DDB DNI XXX HUM XXX HOW XX HOW XX HOW OS HOW

AAS87175;

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                     New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
                                                                                                                                                                                    Hayashi K, Ishii S, Kawai Y;
K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2359 BP; 498 A; 692 C; 634 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                    Isogai T,
na T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK94254 standard; cDNA; 2361 BP.
                                                                                                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                      11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                   07-JUL-2000; 2003EP-00025638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000EP-00114089
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Wakamatsu A, Sugiyama T,
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Best Local Similarity:
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                                                       08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful length clones were obtained by construction of full length cDNA. The full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length CDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                                                                                   Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID NO 2864; 1380pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                 Nishikawa T, Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL30831 standard; cDNA; 2359
                                                                                                                                                                                    11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765.
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                   Homo sapiens.
                                                                                                                                                                   08-JUL-1999;
                                                       EP1130094-A2
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Query Match:

ADL30831

8

BXBXXXXXXXXXX

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in CD-ROM format directly
                                                                                            830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmunod disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA encoding protein that promotes STAT6 activation #64.
                                                                                                                                                      claim 8; SEQ ID NO 2866; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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Matches:
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26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002US-0436467P.
15-MAY-2003; 2003JP-00137505.
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15-MAY-2003; 2003JP-00137505.
16-MAX-2003; 2003US-0470836P.
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                                                 WPI; 2001-524255/58.
P-PSDB; AAM93334.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves adminiatering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or antigen. The nucleic acid is useful for diagnosing a disease or activity of the compounds which inhibit or promete STAT6 activation. A transformant expressing the protein is useful for screening compounds which inhibit or promete STAT6 activation. A transformant of compounds which inhibit or promete STAT6 activation. A transformant composition, antibodies and antisense molecules are useful for the treating disease associated with STAT6 activation such as allowing a disease associated with STAT6 activation such as allowing the protein diseases and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osecearthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activation or inhibition of STAT6. The present sequence represents a compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for creating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for creating and preventing disease associated with excessive compounds for the protein which processive activation or inhibition of STAT6. The present sequence represents a continual continual manual processive activation.
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                                                                                                         wew signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. diabetes and cancer.
                    Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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                    Muramatsu S,
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                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 127; 1368pp; English.
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                    Honda G,
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                    Sugahara T, Matsuda A,
                                                              2004-122214/12
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Best Local Similarity:
                                                                                   P-PSDB, ADI26163
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RESULT 28
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                                                                                                                                                                                 This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                        New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ds, breast cancer; breast cancer-associated gene sequence; development; pharmacogenetics; biosensor development.
                                                                      cawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                        Sequence 2361 BP; 506 A; 684 C; 638 G; 533 T; 0 U; 0 Other;
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                                                                       Nishikawa T, Isogai T,
                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
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08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-001183865.
07-JUL-2000; 2000EP-00114089.
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09-APR-2001; 2001US-00829472.
09-APR-2001; 2001US-028269P.
04-MAY-2001; 2001US-0288590P.
29-MAY-2001; 2001US-0294443P.
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                                                                                                    WPI; 2004-204755/20.
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                                                                                 Wakamateu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a blological sample from the patient with a nucleotide that by a blological sample from the patient with a nucleotide that in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are concertanced of the invention can be used in diagnostic purposes and also as the arguer for acreening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are concer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-constituinty datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761.
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                                                                                                                                            Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polymucleotide that selectively hybridizes with breast
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                                                                                                                                                                                                                                                                                                         Claim 9; Page 372; 414pp; English
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
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Afar D;
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                                                      2002-583738/62
Gieh KC,
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                                                                                      N-PSDB; ABJ05564
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Mack DH,
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DB:
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WO2002102235-A2.

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 # identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, non-small cell for treating lung cancer, non-small cell for treating lung cancer, contact benign or precancerous leadings, e.g. attelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstital pulmonary disease, fibrosis, bronchiectasis. The genes, polynucleotides and polypeptides are useful contactasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                                                                                                                        Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22, Page 336, 453pp, English
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                                                                                                EOS BIOTECHNOLOGY INC
29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P.
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                                                                                                                                                                                                                        WPI; 2003-093161/08.
P-PSDB; ABU56604.
                                                                                                                                                               Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
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                                                                                                (EOSB-)
                                                                                                                                                               Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
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Location/Qualifiers 1. .927 /\*tag= a

Bapiens

Homo

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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
determining tumour prognosis, early detection of pre-cancerous lesions,
and as vaccines. This sequence corresponds to one of the nucleic acids
used for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; differential expression; cancer; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-774-176-5 (1-9) x ADB80503 (1-927)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 297; 332pp; English.
                                                                                                                              ; 2001US-0315287P.
; 2001US-0317544P.
; 2001US-0350666P.
; 2002US-0372246P.
                                                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
                                                                         18-JUN-2002; 2002WO-US019297
                                                                                                              2001US-0299234P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN38723 standard; cDNA; 927
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40.00
100.0$
90.9$
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                                                                                                                                                                                                                                                                                                       WPI; 2003-167431/16.
                                                                                                                                                                                                                                                                Mack DH, Gish KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                        P-PSDB; ADB80504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                  27-AUG-2001;
05-SEP-2001;
                                                                                                                                                                                        12-APR-2002;
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                                                                                                              L8-JUN-2001;
                                                                                                                                                                   13-NOV-2001;
                                    27-DEC-2002
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DB:
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289 TTCCTTACCGGCAACCAGCTGGCC 312
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2001US-0275578P.
2001US-0275579P.
2001US-0275601P.
2001US-0276000P.
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2001US-0274281P.
2001US-0274322P.
2001US-0274849P.
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2001US-0277833P.
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2001US-0279036P.
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2001US-0280802P.
                                                                                                                 ABV99349 standard; DNA; 1156
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2001US-0278894P
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                                                                                                                                                                                                                                                      Human NOV8a coding sequence.
                                                                                                                                                                                                       27-JAN-2003 (first entry)
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13-MAR-2001; 2
13-MAR-2001; 2
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08-MAR-2001;
09-MAR-2001;
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16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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08-MAR-2001;
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23-MAR-2001;
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28-MAR-2001;
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30-MAR-2001;
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02-APR-2001;
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                                                                                                                                                            ABV99349;
                                                                    RESULT 31
                                                                                              ABV99349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
corber diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising
nucleic acid of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
cantibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
antibodies, inflammatory diseases, and unchammate diseases, rethnal
neovascularistation syndromes, scarring and uterine fibroids. They may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hevezi PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a nucleic acid sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gish KC, Glynne R, He
Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 41; 1385pp; English
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Mack DH, Murray R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                               2001US-0332464P.
2001US-0334393P.
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2001US-0340376P.
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                                                                                                                                                            13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                         2001US-0350666P
                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0359077P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0370110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0386614P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0397845P
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P-PSDB; ADN38724.
                                                                    WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                    08-JAN-2002; 20-JAN-2002; 20-JAN-2002; 213-PEB-2002; 29-MAR-2002; 29-MAR-2002; 12-APR-2002; 2
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16-JUL-2002;
                          Homo sapiens
                                                                                                                                                                                                                               21-NOV-2001;
29-NOV-2001;
                                                                                                                                                                                                                                                                                                 14-DEC-2001;
                                                                                                                                                                                                                                                                            03-DEC-2001;
                                                                                                                                                                                                         13-NOV-2001;
                                                                                                               22-MAY-2003
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Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0280822P.
2001US-0280900P.
2001US-0281194P.
2001US-0283675P.
2001US-0287424P.
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18-JUN-2001; 2001US-0299027P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32-MAY-2001;
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US-10-774-176-5 (1-9) x ADN38723 (1-927)

927 0 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

31.8 40.00 100.0% 100.0% 90.9%

Local Similarity:

Query Match:

Percent Similarity:

gnment Scores:

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**Gaps**:

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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
       19-JUN-2001; 2001US-0299310P.
10-JUL-2001; 2001US-0399310P.
11-JUL-2001; 2001US-0391310P.
15-AUG-2001; 2001US-0312903P.
11-SEP-2001; 2001US-0318462P.
27-SEP-2001; 2001US-0325430P.
27-SEP-2001; 2001US-0325681P.
27-SEP-2001; 2001US-0325681P.
14-NOV-2001; 2001US-03330380P.
14-NOV-2001; 2001US-0332172P.
14-NOV-2001; 2001US-0332172P.
14-NOV-2001; 2001US-0333277P.
14-NOV-2001; 2001US-0333184P.
                                                                                                                                                       21-NOV-2001; 2001US-0332094P.
03-DEC-2001; 2001US-0337426P.
03-DEC-2001; 2001US-0338092P.
                                                                                                                                                                                    2001US-0337185P
                                                                                                                                                                                                       08-MAR-2002; 2002US-00093463
                                                                                                                                                                                                                          (CURA-) CURAGEN CORP
                                                                                                                                                                                    04-DEC-2001,
                                                                                                                                                                                                                                                                                              Zhong M;
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Casman SJ; SA, Vernet CAM; New NOVX polypeptides and polynuclectides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma. WPI; 2002-732824/79. P-PSDB; ABP70071.

Claim 16; Page 114-115; 619pp; English.

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome ssociated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic distribances associated with obesity, metabolic syndrome X or wasting ciscular sesociated with chronic diseases or various cancers. The NoVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell profiferation, haematopolesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods

Seguence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

1156	œ	0	0	0	0
Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
41.2	40.00	100.04	100.01	<b>3</b> 6.06	9
Alignment Scores: Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

U8-10-774-176-5 (1-9) x ABV99349 (1-1156)

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ds; gene; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
       229 TTCCTTACCGGCAACCAGCTGGCC 252
œ
                                                                         E. faecium DNA sequence SEQ ID 1806.
1 PheLeuThrGlyAsnGlnLeuAla
                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                    ם
                                                                                                                                            98US-00107532.
                                                                                                                                                       97US-0051571P.
98US-0085598P.
                                    ADC92179 standard; DNA; 972
                                                                                                                                                                                      Doucette-Stamm LA, Bush D;
                                                            01-JAN-2004 (first entry)
                                                                                                       Enterococcus faecium.
                                                                                                                                                                                                   WPI; 2003-799836/75
                                                                                                                                                                                                        P-PSDB; ADC95833
                                                                                                                   US6583275-B1
                                                                                                                                            30-JUN-1998;
                                                                                                                                                        02-JUL-1997;
                                                                                                                                                               14-MAY-1998;
                                                                                                                                24-JUN-2003
                                                ADC92179;
                        RESULT 32
            셤
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New isolated nucleic acid derived from Enterococcus faecium encoding a Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection

Example 1; SEQ ID NO 1806; 243pp; English.

The invention relates to an isolated nucleic acid derived from
Enterococcus faecium encoding an Enterococcus faecium polypeptide having
Composition of fully defined sequences given in the (or comprising 40
sequential nucleotides chosen from any of the nucleic acids, its
complement or sequences hybridising to it). Also included are a
complement vector comprising the nucleic acid operably linked to
transcription regulatory element, a cell comprising the vector and a
single-stranded probe comprising the nucleic acid. The nucleic acids are
chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
The nucleic acids is useful for diagnosting pathological conditions
resulting from E. faecium bacterial infection (e.g. urinary tract
infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
infection) and for screening drugs such as agonists and antagonists.
Concleic acid is useful for recombinant production of Candida albicans
derived peptides or antisense polypeptides. Pharmaccutical compositions
and vaccines containing the nucleic acid are useful for preventing or
treating Enterococcus faccine infections. The present sequence represents one if the disclosed B. faecium nucleic acids.

Sequence 972 BP; 234 A; 166 C; 217 G; 355 T; 0 U; 0 Other;

Alignment Scores:	a a	Length	972
	2		
Score:	38.00	Matches:	œ
Percent Similarity:	88.9%	Conservative:	0
Best Local Similarity:	88.94	Mismatches:	1
Query Match:	86.4%	Indels:	0
DB:	10	Gaps:	0

US-10-774-176-5 (1-9) x ADC92179 (1-972)

encoding protein that promotes STAT6 activation #63.

(first entry)

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Be; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthitis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
ADI26160 standard; cDNA; 2557 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002US-0436467P.
15-MAY-2003; 2003JP-00137505.
                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2003; 2003WO-JP007123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2003; 2003US-0470836P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugahara T, Matsuda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASAH ) ASAHI KASBI KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-122214/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ADI26161
                                                                                                                                                                                                                                                                                                                 WO2003104277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2002; 26-JUN-2002; 26-DEC-2002; 2
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                     22-APR-2004
                                                                                                                                                                                                                                                                                                                                                     18-DEC-2003
                                                                                                           Human cDNA
(TAA) The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding free antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                          Mouse, TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence encodes the mouse 5T4 tumour-associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        Mouse 5T4 tumour-associated antigen gene.
                                          841 TTTCTGACAGGAGACAGCTCGCAGTA 867
                 0
                 PheLeuThrGlyAsnGlnLeuAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                            AAA27059 standard; DNA; 1281 BP
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                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        WO200029428-A2
                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1998;
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                                                                                                                                                               AAA27059;
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Ishizawa K;

Muramatsu S,

o,

Honda

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for for treating disease associated with STAT6 activation and/or prevention for the treating disease associated with STAT6 activation and/or prevention for the treating disease associated with STAT6 activation and/or prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activity. The protein or nucleic acid is effectively useful for screenin compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation or inhibition of STAT6. The present sequence represhuman cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 A; 729 C; 696 G; 619
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Matches:
Claim 4; SEQ ID NO 125; 1368pp; English.
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38.00
88.9%
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Indel8:

Gaps:

289 TTCCTTACCGGCAACCAGATGACCGTG 315

RESULT 34 ADI26160

PheLeuThrGlyAsnGlnLeuAlaVal

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US-10-774-176-5 (1-9) x AAA27059 (1-1281)

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Length: Matches: Conservative: Mismatches:

132 38.00 88.9\$ 77.8\$

Best Local Similarity:

Query Match:

Percent Similarity:

for screening

Query Match: DB:

ADI26158

Homo

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mouse; murine; cancer; psoriasis; ulcerative colitis; inflammation; ischaemic heart disease; thrombosis; immune disorder; bacterial disorder; viral disorder; ds; gene.
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                    activity. The protein or nucleic acid is effectively useful for screenir compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mouse nucleic acid molecules and polypeptides, useful for treaticancer, psoriasis, ulcerative colitis, inflammation, ischemic heart disease or thrombosis.
viral hepatitis and AIDS. The protein has efficient promoting STAT6
                                                                                                                                Sequence 2557 BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;
                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                 Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                    PheleuThrGlyAsnGlnLeuAlaVal 9
                                                                                                                                                                                                                                                                                                                                                          US-10-774-176-5 (1-9) x ADI26158 (1-2557)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mouse gene sequence #612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD035939 standard; DNA; 2557
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2002US-0431606P.
2003US-0476621P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2003; 2003WO-US033948
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38.00
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77.8%
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05-DEC-2002;
09-JUN-2003;
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                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD035939;
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                                                                                                                                                                                                                                                                                               Query Match:
DB:
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                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 36
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888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or autoseptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for treating a disease associated with STAT6 activation such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosus; sepsis; asthma; allergic rhinitis;
Ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepais, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; gene; human; signal transducer and activator of transcription STATE; immunogen; STATE activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding protein that promotes STAT6 activation #62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muramatsu S, Ishizawa K;
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  Mismatches:
                      Indels:
Gaps:
                                                                                                                                                            Claim 4; SEQ ID NO 123; 1368pp; English
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                                                                                                                                  1 PheLeuThrGlyAsnGlnLeuAlaVal
                                                                                     x ADI26160 (1-2557)
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                                                                                                                                                                                                                                                                     ADI26158 standard; cDNA; 2557 BP
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26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002US-0436467P.
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16-MAY-2003; 2003US-0470836P.
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77.8%
86.4%
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  Local Similarity:
                                                                                         US-10-774-176-5 (1-9)
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Kamiya M;

Hayashizaki Y,

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RESULT 37

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBR2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                      Drosophila melanogaster genomic polynucleotide SEQ ID NO 24691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 24691; 21pp + Sequence Listing; English.
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Matches:
Conservative:
Mismatches:
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                        171 TTCATCACTGGTGACCAGCTTGCAGTA 145
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   1 PheLeuThrGlyAsnGlnLeuAlaVal
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                                                                                                              ABL24406 standard; DNA; 1553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P
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                                                                                                                                                                                   26-MAR-2002 (first entry)
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37.00
100.0%
77.8%
84.1%
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                                                                                                                                                                                                                                                                              pharmaceutical; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                 WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions.
                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
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                                                                                                                                                 ABL24406;
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ID ABZ3:
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AC ABZ3:
XX
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                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant expression vector; transcription regulatory element;
Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
                                   Sequence 2557 BP; 610 A; 794 C; 688 G; 465 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 81 A; 88 C; 101 G; 72 T; 0 U; 0 Other;
                                                                                                                                               -00
                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae polynucleotide segid 642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 642; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                            Trcttaccgcaaccagatgacctg 31
                                                                                                                                                                                                                                                      PheLeuThrGlyAsnGlnLeuAlaVal
                                                                                                                                                                                                                  US-10-774-176-5 (1-9) x ADO35939 (1-2557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP.
retrieved from the WIPO website
                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0117747P
                                                                                                                                                                                                                                                                                                                                                              ACH94847 standard; DNA; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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37.00
100.0%
77.8%
84.1%
                                                                                         296
38.00
88.9%
77.8%
86.4%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-895346/82.
                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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                                                                     ignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 342
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                    ACH94847;
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18

1553 7 2 0 0

ABZ32426

US-10-774-176-5 (1-9) x ACH94847 (1-342)

Query Match:

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Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                   Fungus, yeast, tetracyclin, promoter, GRACE strain, blosynthesis, signal transduction, DNA replication, cell division, growth; proliferation, Candida albicans, fungicide, antifungal, gene; ss.
                                                                                                                                                                                                        Ohlsen KL;
                  Candida albicans essential gene SEQ ID NO 6713.
                                                                                                                                                                                                        Bussey H,
                                                                                                                                                                                                        Boone C,
                                                                                                                                                29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                26-DEC-2001; 2001WO-US049486
30-JAN-2003 (first entry)
                                                                                                                                                                                      (ELIT-) BLITRA PHARM INC.
                                                                                                                                                                                                        Roemer T, Jiang B,
                                                                                                                                                                                                                           2002-566694/60.
                                                                                                                                                                                                                                    P-PSDB; ABP73876.
                                                                         Candida albicans
                                                                                          WO200253728-A2.
                                                                                                              11-JUL-2002.
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying constalled by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertions or replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, blosynthetic, transporter, transcriptional, cranslational, signal transduction, DNA replication and cell division activity to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential candida albicans gene used in the method of the invention. Note: The sequence data for this patent is not represented in the printed by a processing the present sequence information supplied to Derwent by a process. the European Patent Office

Claim 37, SEQ ID NO 6713; 167pp + Sequence Listing; English.

T; 0 U; 0 Other; Sequence 303 BP; 96 A; 65 C; 51 G; 91

Length: 303 Matches: 7	Conservative: 0	Indels: 0 Gaps: 0	
70 36.00			
Alignment Scores: Pred. No.: Score:	Percent Similarity:	uery Matcl B:	

PheLeuThrGlyAsnGlnLeu

US-10-774-176-5 (1-9) x ABZ32426 (1-303)

TTTTTAACTGGAAATCAACTG 65 85

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Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                        Treacy M;
                                                                                                                                                                                                        Merberg D,
                                                                                                                                                                                                        Racie LA,
                                                                                                                                                                                                        Lavallie ER,
               AAV90012 standard; cDNA; 332
                                                                                                                                                            98WO-US006955.
                                                                                                                                                                          97US-00838821.
                                            15-FEB-1999 (first entry)
                                                                                                                                                                                         (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                               Spaulding V, Agostino MJ;
                                                                                                                                                                                                         Jacobs K, Mccoy JM,
                                                                                                                                                                                                                              WPI; 1999-070077/06.
                                                            clone CW1414.
                                                                                                gene therapy; ss
                                                                                                                Homo sapiens.
                                                                                                                               WO9845436-A2.
                                                                                                                                                            10-APR-1998;
                                                                                                                                                                          10-APR-1997;
                                                                                                                                             15-0CT-1998.
                            AAV90012;
RESULT 40
AAV90012/c
                                                            EST
```

New polynuclectides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.

Claim 1; Page 403; 618pp; English.

The present sequence represents a human expressed sequence tag (EST). The polynuclectide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activity, had not supporting activity, immune stimulating or suppressing activity, had activity, chemotactic/chemokinetic activity, activity, chemotactic/chemokinetic activity, and ham activity, chemotactic/chemokinetic activity, intellammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy

Sequence 332 BP; 82 A; 68 C; 53 G; 125 T; 0 U; 4 Other;

	332						
	m	7	-	0	0	0	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
	77.9	36.00	100.0%	87.5	81.8%	7	
lignment Scores:	red. No.:	core:	ercent Similarity:	est Local Similarity:	mery Match:	. :a	

US-10-774-176-5 (1-9) x AAV90012 (1-332)

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ABA09091 standard; cDNA; 396 BP ABA09091 ID ABA(

RESULT 41

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Human; cytokine; cell prollferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemctaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; matastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; archritis; chronic inflammatory condition; proliferative retinopathy; archerosclerosis; oconary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasculoric; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. Human secreted protein homologue-encoding cDNA, SEQ ID NO:867. (first entry) 11-JAN-2002 ABA09091 

Homo sapiens.

WO200157188-A2

09-AUG-2001

05-PBB-2001; 2001WO-US003800.

03-PBB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.

HYSB-) HYSBQ INC

Liu C, Drmanac RT Tang YT,

WPI; 2001-457740/49. P-PSDB; ABB11847 nan proteins and DNA encoding sequences useful for preventing, treating ameliorating a medical condition in a mammalian subject e.g. arthritis Human proteins and and cancer

Claim 1; Page 765-766; 1963pp; English.

Immunomodulatory activity; tissue growth activity; thematopolesis regulatory activity; tissue growth activity; tissue drivity; immunomodulatory activity; activin- or inhibin-related activities; commonocatic or chemotractic or may be involved in oncogenesis, cancer cell proliferation or metastasis.

The invention are useful for preventing, treating or ameliocating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or archritis), proliferative retinopathy, atherosclerosis, coronary heart disease, attential ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and careful growth. Polypeptides involved with tissue regeneration and healing (e.g., of burns, incidions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; seem cell growth factor activity; Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures New nucleic acid that is a 5' expressed sequence tag (5' EST) for Claim 1; SEQ ID NO 704; 71pp + Sequence Listing; English. Sequence 396 BP; 98 A; 77 C; 96 G; 125 T; 0 U; 0 Other; 396 0 0 0 0 Conservative: Mismatches: Indels: Giordano J; Human secreted protein 5' BST, SEQ ID NO: 704. Length: Matches: 100 ATTACAGGGAACCAACTGGCTGTG 123 σ US-10-774-176-5 (1-9) x ABA09091 (1-396) Duclert A, 2 LeuThrGlyAsnGlnLeuAlaVal 멾 21-FEB-2000; 2000EP-00200610. AAC00706 standard; cDNA; 407 99US-0122487P 95.7 36.00 100.0% 06-OCT-2000 (first entry) 87.5**%** 81.8**%** Dumas Milne Edwards J, WPI: 2000-500381/45. Percent Similarity: Best Local Similarity: P-PSDB; AAG00700 (GEST ) GENSET 26-FEB-1999; EP1033401-A2 Alignment Scores: Homo sapiens 06-SEP-2000. AAC00706; Query Match: RESULT 42 8888888888888 CCCCCCCCCCX8X4444X8X1X4X4X4X4X6X8X8X8X8X8X8X ઠે

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the 6713 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense, ds, prokaryotic essential gene, cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                               0 U; 0 Other;
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Matches:
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                                                                                               Sequence 407 BP; 124 A; 99 C; 80 G; 104 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-774-176-5 (1-9) x AAC00706 (1-407)
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ACA48087/C

ACA48087,

ACA48087,

XX

ACA48087,

XX

19-JUN-2003 (first entry)

XX

WALisense, ds; prokaryotic essentidend design; gene.

XX

Antisense, 2002, 2002WO-US09107.

XX

21-WAR-2002; 2002WO-US09107.

XX

21-WAR-2001; 2001US-00948993.

PR

66-SEP-2001; 2001US-00948993.

PR

66-SEP-2001; 2001US-00948993.

PR

66-SEP-2002; 2002US-00362699P.

XX

XX

XX

ELIT-) ELITRA PHARM INC.

XX

WHI; 2003-029926/02.

DR

PPSDB; ABU44217.

XX

New antisense nucleic acids required for real isolate candidate molecules for real isolate candidate whose expression of the mucleic acid; (4) an antisense nucleic acid; (5) producing the confiscation; (7) identifying a confiscation; (7) identify
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identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of atrains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational for identifying proteins or screening homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prolation in cells other than S. aureus, S. typhimurium, C. prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clectronic format directly from WIPO at the printed of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J, Wehrman T, Wang Z, Ma Y;
Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide, useful in preparing a composition for diagnosing or treating inflammatory, neurodegenerative or stem cell disorders, e.g., aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory; haematopolesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1383 BP; 381 A; 240 C; 342 G; 420 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 TTCCTTACCGGTAATCACATGGCGATC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PheLeuThrGlyAsnGlnLeuAlaVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-774-176-5 (1-9) x ACA48087 (1-1383)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS11585 standard; DNA; 2273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-2004 (first entry)
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Best Local Similarity:
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14-AUG-2000; 2000US-0225757F;
14-AUG-2000; 2000US-0225757F;
14-AUG-2000; 2000US-0225759F;
18-AUG-2000; 2000US-0226681F;
22-AUG-2000; 2000US-0226681F;
22-AUG-2000; 2000US-0226868F;
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01-SEP-2000; 2000US-0229344F;
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06-SEP-2000; 20000S-0229509P.
06-SEP-2000; 20000S-023043PP.
06-SEP-2000; 20000S-023043PP.
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08-SEP-2000; 20000S-0231444P.
08-SEP-2000; 20000S-0231444P.
08-SEP-2000; 20000S-0231444P.
08-SEP-2000; 20000S-0231444P.
08-SEP-2000; 20000S-0231444P.
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2000US-0240960P.
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14-SEP-2000; 2000US-0232397P
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13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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25-SEP-2000;
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27-SEP-2000;
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08-NOV-2000;
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     The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the NIPO web-site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human reproductive system related antigen DNA SEQ ID NO: 8734.
                                                                                                                                   Sequence 2273 BP; 527 A; 612 C; 625 G; 509 T; 0 U; 0 Other;
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Matches:
Conservative:
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2000US-0190076P.
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36.00
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17-MAR-2000;

19-APR-2000;

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14-AUG-2000;

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04-FBB-2000;
24-FBB-2000;
02-MAR-2000;
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                                                                                                                                                                       Pred. No.:
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Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                                                                                                          Human testicular antigen encoding DNA fragment SEQ ID NO: 3263.
 ABL98611/c
ID ABL98611 standard; DNA; 3109 BP.
                                                                                                                                                                                                                                                                                                                                                   2000US-0180628P.
2000US-0184664P.
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2000US-0229287P.
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                                                                              21-JUN-2002 (first entry)
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17-MAR-2000;
18-APR-2000;
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22-AUG-2000;
22-AUG-2000;
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                                                 ABL98611;
                     Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 8734; 1297pp + Sequence Listing; English.
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Matches:
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08-NOV-2000; 2000US-0246528P.
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2000US-0232080P 2000US-0232081P

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RESULT 46

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2000US - 02399315P

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2000US - 0241286P

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27-SBP-2000;
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29-SBP-2000;
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17-NOV-2000;
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The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
                                                                                                                                                                                                                                                             Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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01-DEC-2000; 2000US-0250391P.

05-DEC-2000; 2000US-0251030P.

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06-DEC-2000; 2000US-0251479P.

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24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
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Ghassemian M, Briggs SP, Cooper B, Glazebrook J; Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;

BW,

Zhu T;

2004-090562/09.

WPI;

BRIGGS S P. COOPER B. GLAZEBROOK J. LANGE B M. GHASSEMIAN M.

(LANG/) (GHAS/)

(BRIG/) (VGOD) GOFF S A. KATAGIRI F.

(GLAZ/) (KATA/)

KREPS J. MOUGHAMER T. PROVART N. RICKE D. ZHU T.

(KRBP/) (MOUG/) (PROV/) (RICK/)

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New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 273; 117pp; English
                                                                                                                                                                                                                                                                                                     P-PSDB; ADI45343
                                                                                                                                                                                                                        Lange BM,
Goff SA,
The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test for selecting an agent that alters abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmocic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                          New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice, isoprenoid biosynthesis, ss; gene, plant, isopentenyl diphosphate, IPP, dimethylallyl alcohol; DMAPP, short-chain plastid prenyltransferase; glaberellin, carotenoid, abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
                                              Goff SA, Katagiri F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3180 BP; 1056 A; 596 C; 784 G; 744 T; 0 U; 0 Other;
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Conservative:
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                                          Kreps J, Briggs SP, Cooper B, Glazebrook J,
Moughamer I, Provart N, Ricke D, Zhu T,
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                (SYGN ) SYNGENTA PARTICIPATIONS AG
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The invention relates to a polymucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide encoding a polygeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isopremoids in a plant, an expression cassette comprising the polympetide involved in or associated with the biosynthesis of isopremoids in a plant, an expression cassette comprising the polympetides and polymcleotide, a host cell comprising the expression cassette. The polypeptides and polymucleotides include those associated consisted. The biosynthesis of short-chain plastid alcohol (DMAPP), the biosynthesis of short-chain plastid alcohol (DMAPP), the biosynthesis of short-chain plastid alcohol (DMAPP), the biosynthesis of short-chain plastid capturiansferases, the biosynthesis of short-chain plastid alcoholar and/or abscisic acids, the biosynthesis of tocopherols.

CC premyltransferases, the biosynthesis of short-chain plastid plastid capturing and/or abscisic acids, the biosynthesis of ubiquinone, biosynthesis of concerning the biosynthesis of concerning the biosynthesis of concerning the propartion and biosynthesis of concerning the polymolectides. The biosynthesis of conceptual or should be should be seen and second molecules are useful for producing transgenic plants, where the corresponding gene has been disrupted, e.g. to result in a conceptual plants may also have increased yields and/or produce a conceptual plants may also have increased yields and/or produce a conceptual plants may also have increased yields and/or produce a conceptual plants may also have increased yields and or produce a conceptual plants may also have increased descrease or an alteration in the function of the product and uncleic acid molecules are useful for targeted gene disruption, as well as markers and probes. Note: The sequence dene for this pattent did not form the corresponding of the printed gene disruption, but was obtained in electronic
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26-8EP-2001; 2001U8-0325277P. 04-APR-2002; 2002US-0370620P. 04-APR-2002; 2002US-0370743P. 26-SEP-2002; 2002US-00259194

JS2004010815-A1

15-JAN-2004.

Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;

26-DEC-2002; 2002WO-US041414. 26-DEC-2001; 2001US-00035832

WO2003057146-A2

17-JUL-2003.

Homo sapiens.

gene; ds.

(SAGR-) SAGRES DISCOVERY.

WPI; 2003-587068/55.

Morris DW;

Human TNFSF11 carcinoma associated gene, SEQ ID NO:1316.

06-NOV-2003 (first entry)

ADA02798;

1074 TTCTGCACAGGAAATGAACTTGCTGTG 1048

ADA02798 standard; DNA; 52754

1 PheLeuThrGlyAsnGlnLeuAlaVal

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recarion (PKR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed cannot be applied to the sequence of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stee expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in dispinance of stees of presence of data and products dependent on DNA and the produce other types of data and products dependent on DNA and the produce of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the contract of the contra
                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                         DNA encoding novel human diagnostic protein #20857.
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AAS85053/c
ID AAS85053 standard; cDNA; 5833 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                AAS85053;
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New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

Claim 1; SEQ ID NO 1316; 245pp; English.

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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a cinvention also encompasses expression vectors and host cells comprising a character or the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism or transported host norogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host corrinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or thissues CA nucleic acids, proteins and antibodies are also useful as therespeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this cancer in the printed specification, but was obtained the print of the printed sequence are decorated.
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34 77.3 119077 8 34 77.3 119077 8 34 77.3 11262168 8 34 77.3 1126233 14 34 77.3 122623 14 34 77.3 122623 14 34 77.3 122623 14 34 77.3 122624 8 34 77.3 122624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 1312624 8 34 77.3 131262 8 34 77.3 131262 8 34 77.3 131262 8 34 77.3 141309 6 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 141309 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8 34 77.3 1510812 8	
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PAT 10-DEC-2003
                                                                                                                                                                                                                                               Felis catus (cat)
Felis catus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
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Mammalia; Butheria; Laurasiatheria; Carnivora; Pissipedia; Pelidae;
Pelinae; Pelis.
                                                                                                                                                                                                                                                                                                           Carroll, M.M., Kingsman, S.M. and Redchenko, I.M.
MHC class I peptide epitopes from the human 5t4 tumor-associated
antigen
Patent: WO 03068816-A 1 21-AUG-2003;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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AX821533 GI:39724929
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                                                     Percent Similarity:
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AX821533
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Felis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
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Oxford Blomedica (UX) Limited (GB)
Location/Qualifiers
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AC117919
BX548071
AL670399
AC162417
AC099690
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AC110855
CR752646
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AC119297
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          AC096528
AC138863
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AC11219
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AC145052
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CR456625
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AC128319
AC130996
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AC015847
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AC122278
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AC123017
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RESULT 1
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PAT 15-SEP-2000
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                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
Bllard,F.M. and Myers,K.A.
Antibodies
Antibodies
Patent: WO 0136486-A 14 25-MAY-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                    Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOWEDICA LTD (GB)
Location/Qualifiers
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synthetic construct
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AX025011
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                                                             AX025011.1 GI:10184932
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DB:
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AX149553
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1 (bases 1 to 1263)
Carroll, M.w. and Myers, K.A.
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Location/Qualifiers
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PD 17-SEP-2002
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JP 2002530060-A/1.
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Homo sapiens
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Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer
Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
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I (bases I to 2053)

Myers, K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.
Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains leucine-rich repeats
J. Biol. Chem. 269 (12), 9319-9324 (1994)
                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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PB Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                   Sequence 17612 from Patent W002068579. CQ731678

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                                                              289 TTCCTCACGGGCAACCAGCTGGCGGTG 315
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5T4 gene; 5T4 oncofoetal antigen.
Homo sapiens (human)
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                                           1 PheLeuThrGlyAsnGlnLeuAlaVal
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            US-10-774-176-5 (1-9) x AX467371 (1-1263)
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Homo sapiens
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HS5T40A
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Canis sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                              Carroll, M.W. and Myers, K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: RP 1160213-A 1 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1263
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               289 TTCCTCACGGGCAACCAGCTGGCGGTG 315
                                                                                         AX316086 1263 bp
ax316086.1 GI:17899278
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Sequence 1 from Patent WO0238612.
AX467371
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AX316086
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PAT 17-MAR-2004
                                                  Homo sapiens (human)
JP 2002017375-A/2713
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                          10,

C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifier
                                                                                                                                                                                                                     CI2N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koga,H.

Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
1. 2359
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YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Sequence 2864 from Patent EP1396543.
CQ782724
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Location/Qualifiers
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Best Local Similarity:
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|db_xref="UniProt/TrEMBL:Q13641"
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LAVLPAGAFRRPPLALALNLSGSRLDGYPAGAFEHLPSSLQLDLSHPLADLISPF
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SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
TLASLGGLPHTRYPLDNNPWYCDCHMADWYFNLKSTRVVGGKORLTCAXPEKWRNT
LELNSADLLDCDPILPPSLGYSYYFLGIVLALIGAIFLLOMYKNTRAC
RDHGGYHYRYEIIADPRLTRUSSNSDV*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transmembrane peptide"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 2359)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                /tissue_type="placenta"
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373. .966
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Mismatches:
Indels:
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'db_xref="InterPro:IPR000483"
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BD127282.1 GI:3322227
JP 2002017375-A/2713.
Homo sapiens (human)
Homo sapiens
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Primer for synthesizing
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                                                                     'sex="female"
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Query Match: DB:

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PAT 18-SEP-2002
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JP 2002017375-A/2714
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc (12P21/02,C12Q1/68/C12P21/08,G06P17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers

T CDS (426). (1685).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Rutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.
l Chases I to 2361)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
                                                                                                                                                                                                                                        13 2361 bp DNA linear PAT l
for synthesizing full-length cDNA and use thereof.
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                                                               US-10-774-176-5 (1-9) x AK074786 (1-2359)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKU/4786 2359 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90305 fis, clone NT2RP2000694, highly similar to Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene. AK074786
  SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
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LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVIYLMRKGIKK"
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Ninomiya, K.
Ninomiya, K.
Unpublished
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                                 23.35
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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LELNSADLOCDPILPPELQTSYYPLGIVLALIGAIPLLVLYLNRKGIKKWMHNIRDAC
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                Chordata, Craniata, Vertebrata, Buteleostomi,
Buarchontoglires, Primates, Catarrhini,
                                                                                     Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Staté activetion gene
Patent: WO 30104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                                                                                                     Koga,H.
Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 2866 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Mammalia; Butheria;
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AFSGSNASVSAPSPIVELILNHIVPPEDERQNRSFEGMVVALLAGGALQGLRRLELA
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LELNSADLDCDPILPPSLQYSYVFLGIVLALIGAIFLLGAIFLLYLYLNRKGIRKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNISSNSDV"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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DNA Res. 12, 117-126 (2005)
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Oligo capping; fiæ (full insert sequence).
Homo sapiens (human)
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/organism="Homo sapiens"
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Web site: http://www.nisc.nth.gov/
Contact: nisc_mgc@nhgri.nth.gov
Akhter_N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesler,N., Ayele,K., Beckstrom-Sternberg,S.M., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighl,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskerl,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB168308 2714 bp mRNA linear PRI 18-JUN-2005 Macaca fascicularis testis cDNA clone: QtsA-11109, similar to human trophoblast glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 26 Row: m Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729717.

Location/Qualifiers
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SHPTYLPROVLAQLPSLEHLDLSNBLVSLTYVSRNLTHESLHLESBLHESDALKVTHNG
TLAELQGLPHIRVELDINNPWVCDGTBADMYTMLKETBVVQSYDRLTGAYPEKKRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRGIKKMFHNIRDAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
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LAVLPAGAFARRPPLAELAALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPP
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
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/product="5T4 oncofetal trophoblast glycoprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MGC:15317 INMAGE:4138906"
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/clone Tib="NIH MGC 17"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                               Gaithersburg, Maryland;
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/gene="TPBG"
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It (bases 1 to 2379)

Straubsberg, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G.,

Riausner, R.D., Collinns, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, P.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, W., Madan, A., Young, A.C., Shevchen, E.D.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

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Homo sapiens trophoblast glycoprotein, mRNA (cDNA clone MGC:15317
IMAGE:4138906), complete cds.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (03-SR2-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                               /cell_line="NT2"
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retinoic acid (RA) induction"
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On Aug 19, 2003 this sequence version replaced gi:22713382.
Contact: MGC help the sequence version replaced gi:22713382.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparary Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
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         clone="NT2RP2000903"
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BC037161.2 GI:33872201
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TITLE
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HSA012159 5551 bp DNA linear PRI 15-APR-2005
Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
AJ012159
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Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ012159.1 GI:3805946
5T4 gene; 5T4 oncofetal trophoblast glycoprotein. Homo sapiens (human)
Pono sapiens
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Mismatches:
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2698. .2703
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2716. .5400
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/gene="5T4"
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/gene="5T4"
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/gene="5T4"
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44.00
100.0%
100.0%
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Best Local Similarity:
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                                                                                                                                                                                                                   Alignment Scores:
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DB:
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ORGANISM
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HSA012159
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AUTHORS
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Hashimoto, K., Kusuda, J. and Sugano, S.

Hashimoto, K., Kusuda, J. and Sugano, S.

Direct Submission

Submitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku-ku, Tokyo, 162-8640, Japan (8-mail:khashi@mhi.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)

The International consortium for macaque cDNA sequencing and analysis consists of: Department of Virology and Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan; Division of Genetic Resources, National Institute of Infectious Diseases of Japan, Tokyo, Japan; National Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan; Department of Kolocy & Evolution, University of Chicago, Chicago, IL, USA; Center for Information Clone distribution: clone distribution information can be found at: http://www.nih.go.jp/yoken/genebank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              international consortium for macaque cDNA sequencing and analysis.

DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Custom primers were used for 5' and 3'-end sequencing. The full-insert sequencing was done by primer-walking method using ABI DNA sequencer.
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glycoprotein (TPBG), mRNA, RefSeq: NM_006670.3"
/codon_start=1
                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                 Osada, N., Hirata, M., Tanuma, R., Kusuda, J., Hida, M., Suzuki, Y., Sugano, S., Gojobori, T., Shen, J.C.-K., Wu, C. I. and Hashimoto, K. Substitution rate and structural divergence of S'UTR evolution: Comparative analysis between human and cynomolgus monkey CDNAs Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="macaque cDNA library QtsA"
/dev_stage="adult"
oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OnpA: parietal lobe Other: temporal lobe right OflA: frontal lobe left OmoA: medulla oblongata ObsA: brain stem Ocar: occipital lobe right OtaA: testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Macaca fascicularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /proteIn_id="BAE00432.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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                    SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                   REFERENCE
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  CEYWORDS
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APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
ALAVLPAGARRRPPLAKLAANLSGSRLDGWRAGPFBHLPSERQUDLSHPLADDLSPP
AFGSSNASYGAPSPLYELI LIMI VPPEDERQNRSFEGWVVAALLAGRALGGLRELELA
SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(10004. .10982)
| Jocus Laga=RR3-492P14.2-001"
| Jocus Laga=RR3-492P16.2-001"
| Jocus = Mmatch: proteins: P81877 Q99LX9 Q9BWW6 Q9CYZ8 Q9D6L4
Q9P038 Q9X4T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKORLTCAYPEKMRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIPLLVLYLNLKGIKKMMHNIRDAC
                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="RP3-492P14.1-001"
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/product="artophoblast glycoprotein"
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AL544610 AW471072 AW662538 BE260089 BF306457 BF306926
BF314984 BI196133 B1562387 BM069633 BM670613
match: CDANAs: AJ420536.1 Z29083.1"
|jgene="TPBG"
RP3-492P14 is from the library RPCI-3 constructed by the group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="RP3-492P14.1-001"
join(109639. .109916,110631. .116836)
/gene="TPBG"
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protein id="CA121546 1"
db xref="G156203539"
db xref="Genew:12004"
db xref="Genew:12004"
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complement(10004. 10982)
/locus_tag="RP3-492P14.2-001"
/pseudo
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109639. .116836
/gene="TPBG"
                                 Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                     Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="q13-15"
/clone="RP3-492P14"
/clone_lib="RPCI-3"
                                                                                                                                     --- Genome Center
                                                                                                                                                                                                                                                                 Contact: vega@sanger.ac.uk
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AL121977.11 G1:11863678
HYG; CpG island; TPBG.
Homo sapiens (human)
Ribeacce.
                                                                                                                                                                                       /db_xref="InterPro: IPROO1611"
/db_xref="InterPro: IPROO1611"
/db_xref="InterPro: IPRO01611"
/db_xref="InterPro: IPRO01891"
/db_xref="UniProc7"
/d
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
BMH: SMBL: SWH: SWISSPROT; Tr:, TREMBL: Wp:, WORNPEP: Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human achromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
      product="5T4 oncofetal trophoblast glycoprotein"
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9
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Matches:
Conservative:
Mismatches:
Indels:
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| db_xref="GAI:3805947" |
| db_xref="GAS.013641" |
| db_xref="Interpro:IPR000372" |
| db_xref="Interpro:IPR000483" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3719 TICCTTACCGGCAACCAGCTGGCCGTG 3745
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1 (bases 1 to 121909)
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3517. .4690
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/gene="5T4"
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Best Local Similarity:
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DB:
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DEFINITION
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Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 165928 bases at least Q40
Consensus quality: 165688 bases at least Q30
Consensus quality: 165175 bases at least Q20
Insert size: 167725; sum-of-contigs
Insert size: 177628; 3.4% error; agarose-fp
Quality coverage: 6.25% in Q20 bases; sum-of-contigs Quality
coverage: 6.02% in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20221: contig of 20921 bp in length 21021: gap of 100 bp 28602: contig of 7881 bp in length 28702: gap of 100 bp 37137: contig of 8435 bp in length 37237: gap of 100 bp 68400: contig of 31163 bp in length 68500: gap of 100 bp B9511: contig of 21111 bp in length 89511: gap of 100 bp 101523: contig of 11812 bp in length 101623: gap of 100 bp 107502: contig of 5879 bp in length 107502: contig of 100 bp 128891: contig of 1440 bp in length 143311: gap of 100 bp 128891: contig of 1440 bp in length 143311: gap of 100 bp 128891: contig of 1440 bp in length 143311: gap of 100 bp 151795: contig of 7964 bp in length 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151795: contig of 7964 bp in length 151895: gap of 100 bp 151895
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5 165244: gap of 100 bp
5 16825: Contig of 3581 bp in length.
Location/Qualifiers
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Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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CR854913_2 200001 310000
CR854913_3 300001 388345
Continuation (4 of 4) of CR854913 from base 300001 (CR854913 Danio rerio clone DKBY-18P1
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Danio rerio clone DKEY-42017, *** SRQUENCING IN PROGRESS ***, 12
unordered pieces.
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Submitted (12-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 15A, UK. B-mail enquiries:
zfish-help@eanger.ac.uk Clone requests: clonerequest@eanger.ac.uk
On May 13, 2005 this sequence version replaced g1:55058488.
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Center code: SC
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Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
Patent: WO 02059377-A 57 01-AUG-2002;
BOS Blotechnology, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Sequence 57 from Patent WO02059377.
AX829164.1 GI:39838931

    .927
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	110000 8 0 0 0	linear genomic DNA,
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APO08208 144 APO08	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB: US-10-774-176-5 (1-	Oy 1 PheLeuTh Db 37755 TTTTTAAC RESULT 26 APO05756 LOCUS APO05756 LOCUS APO05756 DEFINITION Oryza sati

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RAGGGAESAAPVPLHHRIRCHRSPPPPPPLSDPCGRWPPRLPTVGSATTRLTIVGSV
TAVASLLRPLPLPEPSTASGGRRGERRSGGEEEBAVVVALARRR"
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KGSPEEEEAHPPPATGNNALASNNNGCFQTRSPSTPVVGWPPVRTFRRNLATSSKASL
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QRDPLTAGAKDCQQEDVAISGLLDGTGEYTLVYEDYEGYKLVGDVPWGMFVSSVKRL
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21029. .21282,22175. .22283,22950. .23497))
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contains full-length cDNA(s): AK121870"
                                                                                                                                                                                                                                                                                                                                                                                                          non-coding transcript probably inactive due to no initiation codon in CDS"
                                                                                                                                                                                                           complement(join(<11805. .12148,12855. .>13042))
joan="OSJABB0035808.3"
/note="supported by fill-length cDNA(8): AKI11070"
complement(11805. .13042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by GlimmerM
this category is not included in IRGSP standard"
complement (27886. .28131)
                                                                                                                 this category is not included in IRGSP standard" complement(11805. .13042)/gene="OSJNBb0035N08.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this category is not included in IRGSP standard" complement(14428. .14868)
/gene="OSJNBb0035N08.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      included in IRGSP standard*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<14428. .>14868)
/gene="OSJNBb0035N08.5"
/note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                         note="contains full-length cDNA(s): AK111070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="putative aux/IAA protein"
protein id="BAD26156.1"
db_xref="GI:49388936"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="hypothetical protein"
'protein id="BAD26155.1"
'db_xref="G1:49388935"
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/gene="OSJNBb0035N08.8"
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/gene="OSJNBD0035N08.8"
/note="hypothetical ORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (13420. .13668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (13420. .13668)
/gene="OSJNBb0035N08.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical ORF
predicted by GlimmerM
                             'gene="OSJNBb0035N08.2"
'note="hypothetical ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5873. .16028
gene="OSJNBb0035N08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="OSJNBb0035N08.6"
                                                                                                                                                                                                                                                                                                                                         gene="OSJNBb0035N08.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted by GlimmerM this category in
                                                                                       predicted by GlimmerM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="OSJNBb0035N08
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misc feature
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Direct Submission

Direct Submission

Submitted (18-58P-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibazarai 305-8602, Japan

(B-mail: tasasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Pax:81-298-38-7468)

On Jun 28, 2004 this sequence version replaced gi:42627749.

Genes were predicted from the integrated results of the following: (http://www.rgftberry.com/), GeneMark.htmm

(http://www.tigr.org/tdb/glimmerm/glim_form.html), RiceHWM

(http://www.tigr.org/tdb/glimmerm/glim_form.html), RiceHWM

(http://www.tigr.org/tdb/glimmerm/glim_form.html), RiceHWM

(http://globin.cse.psu.edu/html/docs/sim#.html), RiceHWM

(http://globin.cse.psu.edu/html/docs/sim#.html), RiceHWM

(http://globin.cse.psu.edu/html/docs/sim#.html), gap.bary.atedictor

(http://globin.cse.psu.edu/html/docs/sim#.html), gap.bary.atedictor

(http://globin.cse.psu.edu/html/docs/sim#.html), gap.bary.atedictor

(http://www.tigr.org/software/glimmerm/), BilaSTN and blacondarabase.nr (ftp://ncbi.nlm.nlm.gov/blast/db) and the cone

genomic sequence database at RGP or DDBJ. Protein homologies of the coding

regions were searched against NCBI NonRedundant Protein database

with blaSTP. ESTS represent the identified CDNA sequences using

BlaSTN with the corresponding DDBJ accession no.

Rushar with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology level

such as same name, 'putative' and 'like protein' A gene

such as same name, 'putative' and 'like protein' A gene

such as same name, 'putative' and 'like protein' A gene

such as same name, 'putative' and 'like protein' A gene

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prodicted by a single gene prediction program is also classified as a

miscella
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/gene="complement (join(157. .256,518. .608,645. .687,1665. .1820))
/gene="complement (join(157. .256,518. .608,645. .687,1665. .1820))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The orientation of the sequence is from Milrev to -21Mil of the BAC clone. This sequence of OSJNBD0035N08 clone has an overlap with P0620H05 (DDBJ: AP005334) clone at 5' end and with OJ1711 D06 (DDBJ: AP004857) clone at 5' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                               Samaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OSJNBb0035N08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this category is not included in IRGSP standard" complement (6895. .7272)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki, T., Matsumoto, T. and Katayose, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                      Published Only in Database (2002) 2 (bases 1 to 136267) Sasaki,T., Matsumoto,T. and Katav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="hypothetical ORF
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/clone="OSJNBb0035N08"
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                             AP005756.3 GI:49388934
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The figure incommentation of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping and project (Bric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-007-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 53109, USA.

Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 3, 2001 this sequence version replaced gi:14389375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this
                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                               Goyea, E. and Abbott, A.
The sequence of Homo sapiens BAC clone RP11-792N18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                         1 (bases 1 to 60199)
Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: H_NH0792N18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://bacpac.med.buffalo.edu)
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                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 60199)
Waterston, R.H.
Direct Submission
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Waterston, R.
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     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                         Hominidae; Homo.
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                                                                                                                                                                                                                                                                             note="start and end point are not identified"
oin(31945. .31975,32081. .32221,32569. .32627,32831. .32890)
gene="OSJNBb0035N08.10"
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                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
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/translation="MACGLKKVSGDLRPLCSGSTAVDQRLCAEEDRPPALSLAPASSP
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complement (33602. .35288)
/gene="OSJNBb0035N08.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAD26158.1"
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ATKVEKSRKQMKERKNRAKKIRGVKKTRAGDAGKKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="supported by full-length cDNA(s): AKO58248"
complement(join(33810. .33842,33945. .34031,34799. .34969,
35069. .35194))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(33602. .33842,33945. .34031,34799. .34969,
35069. .35288))
                                                                                                                         category is not included in IRGSP standard"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="OSJNBb0035N08.12"
/note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="putative 40S ribosomal protein S24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="OSJNBb0035N08.11"
/note="contains RST(8): C99556(R20550)
contains full-length cDNA(8): AK058248"
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                                                                                                                                                                                                                                                                                                                                                         note="predicted by GeneMark.hmm etc."
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="BAD26159.1"
/db_xref="GI:49388939"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                     |oin(<31945. .31975,32081.
32831. .>32890)
/gene="OSJNBb0035N08.10"
                       complement (27886. .28131)
/gene="OSJNBb0035N08.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="OSJNBb0035N08.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35886. .36086
/gene="OSJNBb0035N08.12"
                                                                                                                                                                           gene="OSJNBb0035N08.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="OSJNBb0035N08.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113563 Trirraacregraaccaccracer 113586
                                                                       note="hypothetical ORF
gene="OSJNBb0035N08.9"
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                                                                                              predicted by GlimmerM
this category is not i
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                          misc_feature
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DB:
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ACCESSION
VERSION
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No..
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셤 ઠ

(NID:98607340) "

BE144616

BG176347 (NID:g12683154)"

L44570 (NID:g1050230)"

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209688 bp DNA linear HTG 01-JUL-2005 Bos taurus clone CH240-79C10, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST AI586327 (NID:94572224) v845c07.x1*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST AA081610 (NID:g1623668) zn18f02.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST N50278 (NID:g1191444) yy84h04.rl"
EST BG818090 (NID:g14165677)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST AL517220 (NID:g12780713)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST BE843212 (NID:g10275590) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST AU135771 (NID:g10996310)"
                                                             EST BG919089 (NID:g14299565)"
                                                                                                                              EST BG293731 (NID:g13053681)"
                                                                                                                                                                                                                                                                  EST BF136337 (NID:910975377)"
                                                                                                                                                                                                                                                                                                                                                                     EST BF740944 (NID:g12067620)"
                                                                                                                                                                                                                                                                                                                                                                                                                                     EST BF898703 (NID:g12290162)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST BF711979 (NID:g12011454)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST BG285102 (NID:913036703)"
                                                                                                                                                                                                                                                                                                                                                                                                      EST BG993923 (NID:g14397993)"
                                                                                               EST AW999985 (NID: 98260219) "
                                                                                                                                                                                                 EST AW390509 (NID:g6895168)"
                                                                                                                                                                                                                                 EST BE176840 (NID:98639569)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST AW526523 (NID:97168902) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST AW960351 (NID:98150035) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT60293.2 GI:68300973
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                  5221. .5867
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5242. .5716
/note="similar to
                                                                                                                                                                                                                                                                                                                  5406. .5515
/rpt_family="MIR"
5412. .5913
/note="similar to
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/note="similar to
5652. .5805
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note="similar to
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note="similar to
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5837. .5859
/note="similar to
                  1318. .4535
'note="similar to
1467. .5255
                                                                                                   t
                                                                                                                  1873. .5472
'note="similar to
                                                                                                                                                                                1931. .5551
'note="similar to
                                                                                                                                                                                                                                                                                                                                                                                     5442. .5859
/note="similar to
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note="similar to
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note="gimilar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="similar to
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note="similar to
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/note="similar to
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 note="similar to
                                                                                                                                                 1901. .5268
/note="similar to
                                                                                                                                                                                                                                                                                     360. .5859
'note="similar to
                                                                  note="similar to
                                                                                   745. .5242
note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.05e+03
39.00
100.0%
77.8%
88.6%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                     repeat_region
                  misc_feature
                                                 misc_feature
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DB:
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                The clone sequenced to the left is RPI1-634H22; the clone sequenced to the right is RP4-701016, 2000 bp overlap. Actual start of this clone is at base position 1 of RPI1-792N18; actual end is at base position 1.0f RPI1-792N18; actual end is at base position 137566 of RP4-701016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST A1586327 (NID:94572224) v845c07.x1"
                                                                                                                                                                                                                                                                                                                                                                                      EST AI586327 (NID:94572224) v845c07.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      969. .2492
note="similar to BST AI694560 (NID:g4971900) wd72g06.xl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST AA747684 (NID:92787642) nx85h05.81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NID:93423248) ow89c06.81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST A1433833 (NID:94291946) til7a07.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST A1289276 (NID: 93932540) qw22e04.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST AA827680 (NID:g2900121) od56a09.81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST BE630588 (NID:g9913276) uu37h03.x1*
                                                                                                                                                                                                                                                                                                                                                                                                                                        343. .1698
note="similar to EST T84576 (NID:g712928) yd50b08.rl"
                                                                                               Reads from AC083880 (H_NH0634H22) were used to finish AC083883 (H_NH0792N18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NID:g12374134)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NID:g10525460)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NID:911541508)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NID:g10275590)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST BG065876 (NID:g12548439)"
                                                                                                                                                                                                                                                                                                                                                                                                                       (NID:g11927405) *
                                                                                                                                                                                                                                                                                                                                                    note="similar to BST AW866995 (NID:g8001047)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757. .2478
note="similar to EST AW976081 (NID:g8167305)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NID:94608454)"
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                                                                                                                                                                                                                                                                                                                                                                                                                       note="similar to EST BF662271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST AI084825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BST BP956859
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                                                                                                                                                                1. .60199
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/mol type="genomic DNA"
/db_rref="taxon:9606"
/chromosome="7"
 VECTOR: PBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2361 .2498
/rpt_family="Alu"
/rpt_family="Alu"
/rpt_family="AT_rich"
2538 .2618
/rpt_family="L2"
3091 .3493
/note="similar to BST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937. .1959
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                                                                                                                                                                                                                                                                     clone="RP11-792N18"
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161. .455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2072. .2489
/note="similar to E
2088. .2584
/note="similar to B
                                                                                                                                        N18).
Location/Qualifiers
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note="similar to
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/note="similar to
4308. .5014
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note="similar to
                                                                                                                                                                                                                                                                                                                                                                                      note="similar to
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note="similar to
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note="similar to
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note="similar to
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note="Bimilar to
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                                                                                                                                                                                                                                                                                                                    rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               019. .4
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Baylor Plaza, Houston, TX 77030, USB.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas
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                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                             Pecora, Bovidae, Bovinae, Bos.
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assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 202990 bases at least Q40
Consensus quality: 204529 bases at least Q30
Consensus quality: 205759 bases at least Q20
Estimated insert size: 207978; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bom.tmc.edu
Contact: hgroject Information
Center project name: FFEX
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Howels, M., Hodgaen, A., Hogues, J., Howels, R., Howels, J., Hodgaen, R., Jolivet, A., Sarpathy, S., Kelly, S., Hulyk, S., Hulwe, J., Idhebird, D., Jackson, R., Jackson, E., Jackson, L., Jacob, L., Lebow, H., Levan, J., Lewis, L., Liu, Y., Liu, W., Liu, Y., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, M., Manndartne, M., Manndarte, S., Martin, R., Manjun, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Manjun, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Mangum, A., Mangum, P., Martin, R., Morris, S., McLeod, M. P., Morfis, S., McLeod, M. P., Morfis, S., Morris, S., Morris, S., Morris, S., Morris, S., Morris, S., Morris, S., Martin, R., Morris, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pauly, C., Pauly, M., Martin, R., Reves, K., Regier, M., Savery, G., Scherer, S., Soct, G., Shatsman, S., Shen, H., Shartelbeyn, A., Sadergren, B., Song, X.-Z., Soct, G., Shatsman, S., Shen, H., Savery, G., Scherer, S., Soct, G., Shatsman, S., Shen, H., Savery, G., Scherer, S., Ster, A., Tabor, P., Taylor, T., Thomas, M., Marren, M., Walker, B., Walter, M., Willson, M., Walter, R., Wooden, H., Walker, B., Walter, M., Wooder, M., Walter, M., Wooder, M., Walter, M., Marren, M., Wooder, M., Walter, M., Wolle, M., Morris
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May 10, 2003 this sequence version replaced gi:23664494.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc..cm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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Direct Submissaton
Submitted (11-UUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
Direct Submission
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Rattus norvegicus clone CH230-132K18, WORKING DRAFT SEQUENCE, 2
unordered pieces.
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                                                                                                                                                               /estimated length=unknown
148434. .148483
/estimated length=50
171936. .171985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /estimated length=unknown 205190. .205289 /estimated length=unknown 206748. .206847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   estimated length=unknown (01271. .201585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208506. .208605
/estimated_length=unknown
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/estimated length=50
186762. .186811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              estimated length=315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       estimated length=554 98624. .198723
                                                                                                                                                                                                                                                                                                                                                                                                            /estimated_length=50
196723. .197276
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Best Local Similarity:
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SOURCE
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                                                                    NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "vorking draft' sequence. It currently consists of 2 concigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Submitted (14-JUL-2002) Department Of Chemistry, And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Glires; Rodentia, Sciurognathi, Muroidea; Muridae, Murinae, Mus.
10, tases 1 to 228883)
10, T. and Roe, B.A.
Mus musculus Chromosome 10 BAC Clone rp23-3984
Unpublished
Consensus quality: 221525 bases at least Q20
Bstimated insert size: 229249; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC127173 228883 bp DNA linear ROD 30-JUI
Mus musculus strain C57BL/6J clone rp23-39k4 map 10, complete
                                                                                                                                                                                                                                                        1 220835: contig of 220835 bp in length 220836 220935: gap of unknown length 220936 222692: contig of 1757 bp in length. Location/Qualifiers 1. .222692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80400
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .219445)
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220836. .220935
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                                                                                                                                                                                                                                                                                                                                                                                                             clone="CH230-132K18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1783
/note="wgs contig"
1834. .3259
/note="wgs contig"
complement(218613.
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Do, T. and Roe, B.A.
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AC127173
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AUTHORS
TITLE
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SM Mus musculus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurcgnathi; Muridae; Mus.

1 (bases 1 to 230689)
Si Muzny, D., Adams, C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
Beraducci,A., Biswalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,
Checko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R.,
Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A.,
Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De
Anda;C., Delgado,O., Denson,S., Durn,A., Buchi,K.,
Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Bugene,C., Fa,M.,
Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fu,C., Ghose,S., Gill,R., Garcia,R., Garcia,R.,
Gaskin,C., Gench,S., Ghose,S., Gill,R., Garcalez,D.,
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Mus musculus 10 BAC RP23-451H6 (Roswell Park Cancer Institute
(C57BL/6J Female) Mouse BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
/note="This is one of two clones in the same well from
                                                                                                                                                                                                                                                                    Direct Submission
Submitted (30-JUL-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
3 (bases 1 to 228883)
Dio.T. and Roe, B.A.
Divert Submission
Submitted (24-APR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
4 (bases 1 to 228883)
Do, T. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                          OK 73019, USA
On Jul 30, 2003 this sequence version replaced gi:30089776.
                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR.
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Mismatches:
Indels:
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Matches:
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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function="clone overlap" 35. .397
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complement(13498. .13768)
rpt family="MLTIB"
3957. .13984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (16460. 16837)
/rpt_family="MTE-int"
7097. .17340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt family="BGLII"
8387. .2010.
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rpt family="MTB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(GA)n"
complement (4579. .4750)
/rpt_family="RMERI7C"
4751. .4841
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complement (5306. 5636)
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5635. 6661
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complement (6889. .7517)
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7518. .8950
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complement(1909. .2073)
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2637. .2725
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106. 4578
                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(CATATA)n"
complement(4368. .4405)
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11848. 12038
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complement(17960. 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="L1Md_F2"
662. .6757
rpt_family=" (GAAA) n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Lx"
9097, 9178
/rpt_family="B2_Mm2"
9557, 9773
/rpt_family="Lx8"
11284, 11359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="GA-rich" 3371. .13426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .16459
family="(TTTA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7. .13984
family="AT_rich"
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20213. .20323
              complement (1. .47110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="RLTR16"
1460. .11574
                                                                                                         rpt_family="(TA)n"
                                                                                                                                                                                                                                                                                                 rpt_family="B1F1"
048. .4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="Lx5"
                                                                                                                                                                                                                                                     rpt_family="B4A"
650. .2801
                                                                                                                                                                                                                                                                                                                                                rpt_family="B4A"
204. .4243
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Hall, B., Hamid, H., Hamilton, K., Harbes, B., Harris, R., Havlak, P., Hawkins, B., Havkins, B., Hackens, M., Hodgson, A., Hogues, M., Hollins, B., Hackens, M., Hodgson, A., Yackeon, A., Jackson, L., Jang, H., Johnson, B., Jackson, R., Jackson, L., Jang, H., Johnson, B., Johnson, R., Yackson, C., Lara, F., Leal, S., Liang, H., Johnson, B., Johnson, R., Kalis, C., Lara, F., Leal, S., Lee, K., Lee, S., Ledall, F. L., Lemon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y.-S., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuhewa, L., Lozado, R., Luk, T., Madu, R., Mahoney, C., Malloy, K., Mansouri, D., Martinez, E., Mclelland, H., McPherson, J., Mcraddao, C., Merzker, M., Martinez, E., Mullosavljevic, A., Minja, B., Morgan, M., Norwig-Eastaugh, E., Nott, A., Nwaokelemeh, O., Obregon, M., Ochi-Okorie, C., Odeh, E., Okwuonu, G., Okwuonu, K., Parker, D., Pasternak, S., Patel, B., Patel, W., Paul, H., Perser, M., Petrosan, O., Phan, T., Primus, B., Pu, L.-L., Puazo, M., Qin, X., Quinn, A., Quinoz, J., Rabata, D., Rachlin, B., Reigh, R., Ren, Y., Reuter, M., Richards, S., Santos, B., Savery, G., Scherer, S., Shen, H., Sanders, W., Santibanez, J., Santos, R., Savery, G., Scherer, S., Shen, H., Sanders, W., Trejos, Z., Usmani, K., Vargo, C., Varduzco, D., Villasana, D., Virk, D., Virk, D., Villasana, D., Virk, D., Wulliams, R., Wolley, K., Warlen, Y., Wulliams, C., Zhang, Z., Zhang, Y., Yur, Yur, Y., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-M37-2005) Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 28, 2005 this sequence version replaced gi:66275319.

Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemisteries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-APR-2005) Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 230689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-MAY-2005) Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 230689)
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Drafting Center Code: WIBR
Contact: hgsc.help@bcm.tmc.edu.
Location/Qualifiers
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/organism="Mus musculus"
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COMMENT

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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Havyay, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Henderson, N., Hernandez, J., Henderson, N., Hernandez, J., Henderson, N., Hollins, B., Howelle, S., Hiladun, S.L., Hodgson, A., Hogels, M., Howelle, S., Hiladun, S.L., Hodgson, M., Hodgson, R., Johnson, R., Liu, W., Kally, S., Khan, J., Lewis, L., Liu, T., London, P., Loorgacre, S., Lopez, J., Liu, M., Mahladtre, M., Mahladtre, S., Marchin, R., Martin, R., Martin, R., Martin, R., Mandou, M., Mandoud, R., Mandoud, R., Martin, R., Mandoud, M., Norris, R., Martin, R., Martin, R., Martin, R., Martin, R., Mandoud, M., Norris, R., Mandoud, M., Norris, R., Mandoud, M., Norris, S., Mandoud, M., Norris, R., Mandoud, M., Norris, R., Mandoud, M., Norris, R., Mandoud, M., Norris, R., Perez, L., Peran, R., Perez, L., Peran, R., Perez, L., Peran, R., Perez, L., Peran, R., Perez, R., Perez, L., Peran, R., Robort, C., Suderstank, S., Paul, H., Perez, A., Robe, M., Robe, R., Ruige, P., Rayes, C., Rodkey, T., Rodis, A., Rose, M., Rose, R., Ruige, P., Sanders, W., Savets, A., Rose, M., Rose, R., Ruiz, S., Usman, K., Strong, R., Sutten, C. D., Samed, A., Sodergren, B., Sout, G., Shatsman, S., Stein, Wang, C., Wallson, M., Walker, B., Wang, J., Walgh, R., Wallson, L., Walker, B., Wang, J., Walght, M., Walfer, R., Waller, R., Waller, R., Waller, R., Waller, R., Waller, D., Walder, R., Waller, R., Waller, M., Yakob, S., Yen, J., Yoon, U., Yoon, V., Walder, R., Walder, R
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Direct Submission

Direct Submission

Direct Submission

Submitted (13-May-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:3364780.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Worley, K.C.
Direct Submission
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Allen, C., Allen, H., Alebrooks, S., Amin, A., Angulano, D.,
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
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Eggan, A., Bscotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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Rattus norvegicus clone CH230-20206, *** SEQUENCING IN PROGRESS
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Rattus.
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Matches:
Conservative:
Mismatches:
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/rpt family="MLTIC"
complement (27422, .27562)
/rpt family="RSINB1"
27563, .27602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (24906, .24966)

rpt family="tRNA-Ala-GCA"
complement (25702, .25779)

rpt_family="MIR"
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2125. .22186
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4840.
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음 8

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Sciurognathi; Muroldea; Muridae; Murinae; Rattus.
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                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Estimated insert size: 232032; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                  11 227313: contig of 227313 bp in length
12 227413: gap of unknown length
14 228646: contig of 1133 bp in length
15 228646: gap of unknown length
165 230264: gap of unknown length
165 230264: gap of unknown length
165 231593: contig of 1518 bp in length
165 231593: contig of 1329 bp in length
164 231694: contig of 1255 bp in length
165 231694: contig of 1255 bp in length
166 231694: contig of 1795 bp in length
167 231694: contig of 1795 bp in length
168 231694: gap of unknown length
169 231694: contig of 1795 bp in length
160 2416161618
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Mismatches:
Indels:
Gaps:

    .234843
    organism="Rattus norvegicus"

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/estimated length=unknown
/estimated length=unknown
230165. .230264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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/clone="CH230-20206"
66562. .66637
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clone end:Sp6
site:EcoRI
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Schusopharn; Musicas; Muticas; Mutines; Martins.

1 (Deagnain; Musicas; Muticas; Mutines; Martins.)

2 Milary, D. Marie., Metker, Miles. J. Abramano, S., Addams, C., Alder J., Allan, J., Alpanoka, S., Amin, A., Angulano, D., Allan, J., Blair, J., Ched., J., Chaderon, B., Davil, M., Lord, J., Chaderon, S., Dunn, A., Dutbin, K., Duval, B., Baves, K., Brapa, M. L., Berotco, M., Bugene, C., Svans, C., Coyles, L., Poster, M., Perser, C.M., Garner, M., Harnis, S., Hander, B., Howells, S., Hander, B., Han
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Submitted (12-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TY 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21908887.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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Submitted (19-UIL-2002) Human Genome Sequencing Center, Department
Submitted (19-UIL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259795)
Rat Genome Sequencing Consortium.
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Best Local Similarity:
Query Match:
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Query Match:
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AUTHORS
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NOTE: This sequence may represent more than one_clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                         Center Clone name: CH210-46018
------- Summary Statistics
Assembly program: Phrap; version
Consensus quality: 234408 bases at least Q40
Consensus quality: 237198 bases at least Q30
Consensus quality: 237198 bases at least Q30
Consensus quality: 238865 bases at least Q20
Sstimated insert size: 255691, sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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4 256063: gap of unknown length
4 259795: contig of 3732 bp in length.
Location/Qualifiers
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Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bom.tmc.edu
Center project Information
Center project name: GYCL
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Matches:
Conservative:
Mismatches:
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complement (246071. .245516)
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clone_end:Sp6
site:EcoRl
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256064. .257208
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clone_end:Sp6"_
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/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="CH230-46018"
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Best Local Similarity:
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Pred. No.:
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Submitted (12-JUN-2002) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT amis-expression enhancer trap dissociation transposon, MT and effective suppressor mutator transposon. 3 denotes a sequence derived from the 3'end of the transposon BSRC GARNet, ATIS project
Transposon BBSRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
                                                                                                                                                                                                                                                                                    AL807132 365 bp DNA linear STS 11-JUN-2003 Arabidopsis thaliana transposon insertion STS SM_3.19725, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                         ALBO7132.1 GI:21622180
STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Akaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="Derived from superpool 18.11 NASC code N40810"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
Unpublished
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/variety="Columbia-0 NASC stock code N1092"
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Mismatches:
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/standard_name="SM_3.19725"
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/clone="AC011809"
                                                                         US-10-774-176-5 (1-9) x AC128267 (1-259795)
                                                                                                                                1 PheLeuThrGlyAsnGlnLeuAlaVal
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ORGANISM

SOURCE

AUTHORS TITLE

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PEATURES

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Score:

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PAT 15-SEP-2000
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                          Euteleostomi;
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5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: BF 1160323-A 205-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOWEDICA LTD (GB)
Location/Qualifiers
1. .1281
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/db_xref="taxon:10090"
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/mol_type="unassigned DNA"
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Sequence 2 from Patent EP1160323.
AX316087
AX316087.1 GI:17899279
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                                                                                                                            Sequence 2 from Patent WO0029428.
AX025012
 Gaps:
                                                   PheLeuThrGlyAsnGlnLeuAlaVal 9
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AX316087
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Clurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1281)
Carroll, M.W. and Myers, K.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UL-1999 GB 991739.4 PR
MILES WILLIAM CARROLL, KEVIN ALAN MYERS
CIZNIS/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065, C12N15/00,
                     ce 1. 1281 /organism='Mus musculus (mouse)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               linear
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JP 2002530060-A/2
17-SRP-2002
18-NOV-1999 JP 2000582415
18-NOV-1999 GB 9825303.2,27-JAN-1999 GB
UL-1999 GB 9917995.4
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PA
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Patent: JP 2002530060-A 2 17-SEP-2002;
OXFORD BIOMEDICA LTD
                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                                                                          /mol_type="genomic DNA"
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Mus musculus (house mouse)
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Polypeptide.
BD249732
BD249732.1 GI:33059502
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Key
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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Atlausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Altachul, S.F., Zeeberg, B., Wagner, L., Schamen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Mazny, D.M., Sodergren, B.J., Lulyk, Glbbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, B.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Generation and mouse cDNA sequences

Ly 77921 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022 1 2022
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Marky, MacMapaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Rattus.
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Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
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/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                            652 TTCCTCACTGGCAACCAGATGACCGTG 678
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                                   US-10-774-176-5 (1-9) x AF063939 (1-2333)
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Director MGC Project.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AF063939 2333 bp mRNA linear ROD 01-JAN-2000 Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA,
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APATI-ASGAQPPPARRCPAYGRCSRARTWYKVRNILLEVPDALPPYVRNIFTTGNQ
MTVL.PAGARRAPPALAULAVLANLSGNHILKBYQAAFBEILPGILRRLD.GHNPLTRYLSAP
TPAGSNVSVSTPSPLLELILNHIVPPEDQRQNGSFRGMVAFRGMVAAALRSGLALRGL
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KYLHNSTLEBRYGLAHVRYPLDNNPWYCDCYNDADMYSMLKETEVVPDKRLTCRPPEK
MRNRGLLDLTSSDLDCDATLPQSLTYSYVPLGIVLALIGAIFLUVLYLNRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPSLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Ninkina,N.N. and Buchman,V.L.
Structure and expression of the rat 5T4 gene
   71100
                               Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                     289 TTCCTTACCGGCAACCAGATGACCGTG 315
                                                                                                                            Сарв:
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Rattus norvegicus
                                                                                                                                                                                     US-10-774-176-5 (1-9) x AX316087 (1-1281)
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2315. .2320
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38.00
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            Percent Similarity:
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KEYWORDS
SOURCE
ORGANISM
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5'UTR

SOS

gene

Pred. No.:

Score:

ORIGIN

3'UTR

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USA

UNIA

UNIA

Contact: MGC help desk

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Whe sites http://www.nisc.nih.gov/

Contact: nisc. mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakealey, R.W., Bouffard, G., Breen, K., Brinchey, C.,

Blakealey, R.W., Bouffard, G., Breen, K., Brinchey, C.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masheillo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Tgouchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRMX Plate: 123 Row: p Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854.
Location/Qualifiers
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MTVLPAGAPARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
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YCHIRSTLERMQGLAHYKPFDNNPWNCOCYMADMYNMLKETEVVPDKARLTCAPPEK
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/note="COG4886; Region: COG4886, Leucine-rich repeat (LRR)
                                                                                                                                                                                                                                                    Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDMA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAAFLASGSAQPPPARRCPAACECSEAARTVKCVNRNILEVPADLPPYVRNLFIJGNO
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NIRDACRDHMGGYHYRYEINADPRLINLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSLPSSSTS
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
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/lab host="DH10B"
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Matches:
Conservative:
Mismatches:
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/gene="Tpbg"
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Myers, K.A.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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556. 1836
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Patent: WO 03104277-A 123 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
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          PAT 14-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /proteIn_id="CAF06466.1"
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                            Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene Patent: WO 03104277-A 125 18-DEC-2003; Asahi Kasei Kabushiki Kaisha (JP) Location/Qualifiers
          linear
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Mus musculus (house mouse)
Mus musculus
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Mismatches:
Indels:
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Mus musculus
                                                                                   AX961914.1 GI:40881324
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86.4%
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               AE001073 AE000782
AE001073.1 GI:26
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MRNRGLLDLINSSBLOCAVLPQSLQTSYVFLGIVIALIGAIFLLEVLYLNRKGIKKWMH

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Archaeoglobus fulgidus DSM 4304 section 34 of 172 of the complete
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               Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
Location/Qualifiers
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VVVEQNGERKELQCDTAVIAVGTKFNNGLYDELQGKVSELYKIGDCVKPRKALDATRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to SP:P32382 GB:X67220 PID:48123 percent identity: 43.26; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                  note="hypothetical protein; identified by GeneMark;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                              SVAYDHPELREEQVLEKVLKLLEDTT"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AF0455"
                                                                                                                                                                                                                     5883. .6800
/gene="AF0454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8851. .9306
/gene="AP0456"
                                                                                                                                                                                                                                                                  5883. .6800
/gene="AF0454"
                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1/transl_table=
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38.00
100.0%
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RVVELVEQLERGWVESEAIRDYLRREREERR "
                                                                                                                                                                                                                                                                                                                                         /trānslation="MKKGGDAVNKRRVMVVBDDSAVLETVQIMLGDKYBIIPATNGBB
AVKKYKMFKPDVVLMDVMMPVMDGVBATKBIKKIDPQAKIIGLTAYARKKGKBLLDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2754. .3743
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/note="sholiar to SP:P10955 GB:J03174 PID:152215 PID:49404
percent identity: 32.40; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="meavktglegeddlegeyrgolillagnpgsgkttfcakflye
garregenglyisigeskeepyeymkkigmdperlekkepktybmlaptsedalmol
sgeltkomalyisigeskeepyeymkkigmdperleanilmalktisrelksyvlateemp
igetrigogiebpyndoyivlalevpergemanytkirgkplichrokroldraynpergepp
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SAAANVA I NGENVTY I SPEBPRQQI BETLKFLGYGBVBGLEI ILSLNPPRI SLRALYDI
LSKTVLDHRTMLFI DGLNAI RREFGEAFHRVVRDVVFQMKKNGI TVVI SLI GGTI KET
LLSTI VDNVVBLRVVBKDGELRREI AVRKARMSRASNBVKRLVFDGKPAVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTMIMRSIIDSLEALFSSFPSSIAPNLYEVLNFHCKKHTGMNFA
RATLKNPKLTYEFLVKFFDSEMAVDVLDYLLSNPLKKYSIRAYGIIKSFKSGDNKKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to PID:1653695 percent identity: 29.42; dentified by sequence similarity; putative"
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| transl_table=11
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| fprotein id="AAB90789.1"
| db_xref="G1:2650181"
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/gene="AF0453"
/note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                       δ
                                                                                                                                        /note="similar to GB:M59781 SP:P24072 PID:142682 GB:AL009126 percent identity: 38.14; identified Beguence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /producE="signal-transducing histidine kinase"
/protein_id="AAB90782.1"
/db_xref="G1:2650174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="conserved hypothetical protein"
protein id="AAB90781.1"
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2754. .3743
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/transl_table=11
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/gene="AF0451"
3796. .4161
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/gene="AF0452"
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/gene="AF0452"
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/gene="AF0453"
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/gene="AF0449"
                                                                                                                  /gene="AF0449"
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transl_table=
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Genes with similarity to proteins in the databases are described
as 'putative', 'like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev
& A.Sanger Centre, http://gnomic.stanford.edu/-chris/GENSCANW.html), rexa (V.Solovyev
k A.Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Federapiel, M.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E., Chin, C., Chiou, J., Choi, B., Dunn, P., Gonzalez, A., Howng, B., Kim, C., Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Hukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., Thaveri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J., Theologis, A., and Davis, R.W.
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                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I chases I to 108767)
Federspiel, N. A., Palm, C. J., Conway, A. B., Conn, L., Hansen, N. F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetekaia, I., Kim, C., Lenz, C., Li, J., J., Liu, S., Halker, M., Yu, G., Ecker, J., Tortium, M., Vysotskaia, V. S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R. W.
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Submitted (15-OCT-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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5621. .5788,5881. .6111,6229. .6402)
/gene="F6A14.1"
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                                                                      Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
/chromosome="I"
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/gene="F6A14.1"
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       GI:6579253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 108767)
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                                                                                                             Arabidopsis thaliana
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                                                                                                          ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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TATALIA LI ONE "MONOACVRPOSKESKPSKPKKPNRDRKLINPPAGDFTRSPAPI
RVLKVDVIPMANGTOLSDKYLIGREGGREGTEGTHEALACKSISKRKLRTA
VDI BEDVRREVAIMSTLEHPHVUKLKASYEDNENVHLVMELCEGGELFDRI VVRGHYR
VDI BEDVRREVAIMSTLAKOVMUKASYEDNENVHLVMELCEGGELFDRI VVRGHYT
RRAAAAVARTTAEVVMCHSNGVWHDDLKPBRFLFANKKRNBPLKALDFGLEDRI VVRGHYT
RGVLDFKRDPBPTALBESKLVKODLDPDFTKRLTAGVVLAHPWIQNAKKAPNVPLGD
IVRSRLKGPSPWMRFKKKVLKUTAHTAEHLSIQEVRUITKMESLADDDKOGKITYPELKAG
IQKVGSQLGEPRIKMARVADVDGNGFLDVGBFVAVIIHLGKIRNDELKRAPPPPK
GGSTYIELDBELRRALADBLGEPDASVLSDIMREVDTDKOGRITYPELKAG
GGSTYIELDBELRRALADBLGEPDASVLSDIMREVDTDKOGRINYDEFVTMMKAGTDWR
KASRQYSRERFKSEINLAMCOGSLHLHDALTGQTVPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / LTAILS ALL OIS 1973 OF STRING AEDDESKI IYRGMKVMPP I GNETFEKLGIVGSS
SNLVIYLTTVPNMKSITAAKVVNIYGGTSNFGTI VAAFLCDSYFGRYKTLSFAMIACF
IGSVAMDLTAVIHPLHPAQCAKEIGSVCNGPEIGQIMFLAGAMVLLVIGAGGIR PENDE
PERDOPDPKTKEGKRGIESPFNWYPPTPFAQMVSLTLIVVVGSNVSWSIGLAIPAI
IMPLIGGIP FPAGSKYLVYKKAGGSP HISITRVIVVA KKRRIKEVORPNELYNTASDF
KNSKLGHTEQPRFLDKSAI GTQDDKLNKDGSPVDAWKLCSWQQVEEVKCVIRVLPVML
SAALFYLAY IQGTTYTI PGSLGSDRELGFGSPYD PAGSYTVENLAGHT FIP IVDRVL
VPFLRXYTAXIDGGITYTI FDGLGSDRELGFGSPST PAGSYTVENLAGHT FIP IVDRVL
AISSNGSGMIL PQLUAGIADALAGVGQMEFYYKQPPRNRSPAGSLYYCGIGLASYL
STFLLSAVHDTTEGFSGGSKILPEDLNKGRELEYFYFLVPRMRSPAGSLYYCGIGLASYL
STFLLSAVHDTTEGFSGGSKILPEDLNKGRELEYFYFLVAMMRSPAGSLYYCGIGLASYL
STFLLSAVHDTTEGFSGGSKILPEDLNKGRELEYFYFLVAMMRTIALAYPLLVSHWYRYK
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PPFSSGIVRLQVPIBQKIGALDWLHAQNELLPRSFPSRRSDSGRPDLLQDFSSDNGS
DHNPGVSQGIGGSAVFRDDWRSIRRFLSSKSPLIRAYGGLRFDFTGKIAVE
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DPIAWLARLGCTSGODAYGFCLGPPGAPAFIGMTPBRLFHRRHGVCSRALAATRREG
SKVRRENEIBRDLTTSPKDDLEFSIVRENIREKLTTTCDRVVVRPHKSVRKLARVQHLY
SQLAGQLKREDDBFRILTALHFTPAVGGCPVSEARLITKQIESFDKGMYAGPPIGFGG
GESEFSVGIRSALVEKGLALITALHFTPAVGGCPVSEARLITKQIESFDKGMYAGPPIGFGG
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/gene="F6A14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNEKSSIQGLSMGIEYKALSNPNEKLEIDHNQETWSLEISNNNKIRSQNSFGFKNDGD
DHEDEDEILPQNLVKKTRVSMNDGCQWRKYGQKIAKGNPCPRAYYRCIAASCPVRKQ
VQRCSEDMSIILSTYRGTHNHPLPWRSATAMASATSAAASMLLGGASSSSAAADLHGL
PRESIGNNITPRPKTHPLQAPSGSGHPFULDLTYSSSQQPFLSMLNRFSPSPSNVS
RSNSYPSTNIARSNWTJLAMWGGGRPSDQYRAAYGNINTHQQSPYHKIIQTRTAGS
SPDPPGRSSSSHSPQINLDHIGIKNIISHQGAPTAGS
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KGHHQDKGEDEDREKVNEREELVSLSLGRRLNSEVFSGSNKEEKNKDVERABGDRNYD
this BAC (gb|AC011809), 24 bp before the predicted start codon."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join (6629. .7529, 7607. .8160,8258. .8475,8980. .9070))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F6A14.2"
/note="Similar to peptide transport proteins"
                                                                                                                                                           product="calcium-dependent protein kinase
protein id="AAF27092.1"
/db_xref="G1:6730697"
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/codon start=1
/protein id="AAF27094.1"
/db_xref="GI:6730699"
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complement (10694. .14124)
/gene="F6A14.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /proteIn_id="AAR27095.1"
/db_xref="G1:6730700"
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/db_xref="G1:6730698"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                          Submitted (13-JUN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Eish-help@sanger.ac.uk Clone requests:
http://www.sanger.ac.uk/Projects/D rerio/fags.shtml#dataeight
On Jun 14, 2005 this sequence version replaced gi:67624883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Chosensus quality: 142933 bases at least Q40
Consensus quality: 143582 bases at least Q40
Consensus quality: 144106 bases at least Q30
Insert size: 145319; sum-of-contigs
Chast size: 155572; 28% error; agarose-fp
Quality coverage: 7.39x in Q20 bases; sum-of-contigs Quality
coverage: 7.05x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently a consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54092: Contig of 36735 bp in length 54192: gap of 100 bp 62657: contig of 8465 bp in length 62757: gap of 100 bp 82728: contig of 19971 bp in length 82828: gap of 100 bp 6417: contig of 13589 bp in length 86517: gap of 100 bp 105685: contig of 13168 bp in length 105785: gap of 100 bp 121122: contig of 13168 bp in length 131122: contig of 1318 bp in length 1310003: contig of 8781 bp in length 130103: contig of 8781 bp in length 130103: contig of 8781 bp in length 130103: gap of 100 bp 146219: contig of 16116 bp in length
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gap of 100 bp
contig of 12691 bp in length
gap of 100 bp
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1. 4466
1. .4466
Fragment chain:1"
4567. .17257
fragment chain:1"
4567. .17257
fragment chain:1"
17358. .54092
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .146219
/organism="Danio rerio"
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/db_xref="taxon:7955"
/chromosome="16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                ---- Genome Center
   Danio rerio (zebrafish)
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17357:
54092:
54192:
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17258
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54093
54193
62658
62758
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105686
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121223
130004
130104
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SOURCE
ORGANISM
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                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(26772. .27077,27487. .27567,27648. .28677,28771. .28802)
/gene="PGA14.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA linear HTG 14-JUN-2005 Danio rerio chromosome 16 clone CH211-119N15, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.
CR762469 GR762469.4 GI:67763654
                                                                                                                                                                                                                                                                                                                       /translation="MTLLRAISNAVANODKVDSQSDYPIPLSHDGIFANLKPKLENPN
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EKVGISERAESENVLGDQAGSEIQILVEKNGFLMGRDVSGLVLKGCIGLEMWELVBILSI
SNKLVDHSSYSYLVASNLVSKRSDLLCVVIKERASDLGATELLSILKYFLCPSKEAIST
MAKKREEWESQAM.AIEKVSKTELSKKSKVAEEASILLMVAHDGFSTSELCLHTLAS
RNVDEVMFASAVSKLNGNEMGSFIRYLSKWMKKYEMFPQAGFCPKAASKLGLKCNW
PELTDITKCLGLLIDENPSTLVLYSDLHEELKSIARVADGLASESKLSCFVANVVESL
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/db_xref="GI:6730702"
/db_xref="GI:67307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKPVPQPKKASLRKSQKKPASNPQIVEAEPARPKKSVRKVPSSNLDNSSVAQTSSELE
KPRRSFRKVSTSQSVEPLPSMNNPQVDLEKVYRGLRKVHNPVVENSIQPQLVPQIAVE
KPRGSLEESVARPDEERKEDEVAETVOQPERELIQTHTPLGTNESLDSTLVNQIEESEE
NVMAEKEEDVRGERTPKQNHKENSAGKEDQFSGKGKASSVTATQTAEFQESGNGNQTSS
PGIPSYMQATKBARKALRLQGSSSPRQLGTTEKASRRYSLPSSGNSAKITSHSPKTRV
SNSSGKSGNKTEKTLLSSREGNGKATPVEWKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(35250. .35476,36230. .36440,36528. .36662,36742. .36803,36897. .37110,37199. .37384,37491. .37583,37674. .38073,38169. .38296,38844. .38987,39095. .39217,39414. .39513,39610. .39646,39743. .39839,39921. .40037,40123. .40177,40266. .40561))
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/db_xref="GI:6730704"
/translation="MDCIKSIGRSAFVAIAPESPFIAAGTWAGAVDLSFSSANLEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to WEB1/SEC31-like protein transport protein; Similar to WEB1/SEC31 protein transport protein"
                                                                                                                                                           /note="Unknown protein; Location of ESTs TASG082,
gb|z18037 and 158G12T7, gb|AA720219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Unknown protein; Location of BST G12B1T7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108767
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                       /proteIn_id="AAR27096.1"
/db_xref="G1:6730701"
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   IMGGDLKIDHNVTRNEAEKSP"
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                       23743. .24942
/gene="F6A14.6"
23743. .24942
                                                                                                                             /gene="F6A14.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F6A14.8"
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/gene="F6A14.7"
                                                                                                                                                                                                                                  codon start=1
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38.00
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* B20 14217: contig of 13398 bp in length 14318 16197: contig of 13398 bp in length 16198 16297: gap of unknown length 16198 16297: gap of unknown length 16198 16297: gap of unknown length 16298 188432: contig of 13728 bp in length 18533 32260: contig of 13728 bp in length 18533 32260: contig of 44384 bp in length 16745: contig of 44384 bp in length 16745 109615: contig of 44384 bp in length 16745 109615: contig of 44284 bp in length 16745 109715: gap of unknown length 169716: lescontig of 44286 bp in length 169716: lescontig of 64286 bp in length 169918 lescontig of 64286 bp in length 169918 lescontig of 64286 bp in le
Submitted (22-MAR-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 22, 2003 this sequence version replaced gi:28460769.
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| organism="Bos taurus" |
| fmol Lype="genomic DNA" |
| db xref="caxon:9913" |
| clone="RP42-262C3" |
| clone lib="RP42" |
| clone RP42-108E2 (center project name ddr) |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing ventury plaemid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 15386 bases at least Q40 Consensus quality: 153884 bases at least Q20 Consensus quality: 154212 bases at least Q20 Insert size: 138000; agarose-fp Insert size: 154301; sum-of-contigs Quality coverage: 9.57x in Q20 bases; sum-of-contigs Quality coverage: 8.56x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                               1. .719
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 262C03
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E (Dasea 1 to 155001)
S Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Bachjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carlaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, B., Lardo, P., Lee-Lin, S.-O., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, R.H., Masiello, C., Maskeri, B., McDowell, J., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, P.J., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC140093 155001 bp DNA linear HTG 22-MAR-2003
Bos taurus clone RP42-262C3, WORKING DRAFT SEQUENCE, 8 ordered
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Submitted (21-FBB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gatthersburg, MD 20877, USA
3 (bases 1 to 155001)
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Conservative:
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105786. 121122
/note="assembly fragment: 00217
fragment chain: 2"
121223. 130003
fragment chain: 2"
121223. 146219
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fragment_chain:1"
54193. .62657
                                                                                                                 note="assembly_fragment:00126
ragment_chain:1"
                                                                                                                                                                                                                                   note="assembly_fragment:00611
ragment_chain:2"
12829. .86417
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fragment_chain:3"
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HTG; HTGS PHASE2; HTGS DRAFT.
BOB taurus (cow)
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CSTBL/6d mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                      Submitted (21-JUN-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MMD 63108, USA.
On May 4, 2005 this sequence version replaced gi:61656412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //note="Sequence derived from PCR product of genomic DNA" 31565. .31779
                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted
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                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
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Location/Qualifiers
Location/Qualifiers
/organism="Mus musculus"
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Matches:
  Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 167046) Wilson, R. K. Direct Submission
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/db_xref="taxon:10090"
/chromosome="9"
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16685._.16712
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Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Uppublished (2001)
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Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
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Indels:
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720. .819
/estimated length=unknown
820. .14217
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note="assembly_fragment"
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                                                                                'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                     18533. .32260
/note="assembly_fragment"
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clone_end:SP6
vector_side:right"
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AC158516.2 GI:63025421
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Wilson, R.K.
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38.00
100.0%
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Direct Submission
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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                               http://genome.wustl.edu
                            MAPPING INFORMATION:
                                                                                                                                 SOURCE INFORMATION:
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                                                                                                                                                                                                                   ROD 21-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (19-ABX-2005) Genome Sequencing Center, 4444 Forest Park
Burkway, St. Louis, MO 63108, USA
(bases 1 to 168567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Direct Submission

Obbinited (01-UDV 2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

(bases 1 to 168567)
                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Buharchontoglires; Glires; Rodentia; Bciurognathi; Muridae; Mus.

1 (Dases 1 to 168567)
Tomlinson, C., Lewis, S., Cotton, M., Bielicki, L. and Levy, A.
The sequence of Mus musculus BAC clone RP24-155K11
Unpublished (2001)
                                                                                                                                                                                                                     AC160108 168567 bp DNA linear ROD 21-JUN-2
Mus musculus BAC clone RP24-155K11 from chromosome 13, complete
            400
          Mismatches:
Indels:
Gaps:
                                                                                                                                   110550 TTCCTTACCGGCAACCAGATGACCGTG 110524
                                                                                                              PheleuThrGlyAsnGlnLeuAlaVal 9
                                                                              US-10-774-176-5 (1-9) x AC158516 (1-167046)
                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                     ACI60108 AC118718
ACI60108.2 GI:66841676
          77.8$
86.4$
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                                                                                                                                                                                                                                                                                                                                          Mus musculus
Best Local Similarity:
Query Match:
DB:
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                   AC160108/c
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The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male GSTBL/6J mouse splean and/or brain genomic DNA. The Clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                              / Jobos. 19903
/ Inote="Unresolved simple sequence repeat."
/ Inote="Sequence derived from one plasmid subclone."
55407. .55625
/ Inote="Sequence derived from PCR product of project DNA"
75668. .56851
/ Inote="Sequence derived from PCR product of project DNA"
71549. .71707
/ Inote="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149542. 149670
/note="Sequence derived from PCR product of project DNA"
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/note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168567
7
                                                                                                     This sequence is the entire insert of the clone.
Location/Qualifiers
1. .168567
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Matches:
Conservative:
Mismatches:
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/note="Unresolved simple
                                                                                                                                                                     'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                           /mol_type="genomic DNA'
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                    /clone="RP24-155K11"
/clone_lib="RPCI-24"
19608. .19903
                                                                                                                                                                                                                                    chromosome="13"
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Search completed: April 25, 2006, 20:29:24 Job time : 3108.7 secs

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e. phred quality
>=30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone, fosmid clone or direct clone walk sequence.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to obtain the consensus sequence. The
assembly was confirmed by restriction digest.
This finishing standard has slightly changed from the previous
Human standard. Specifically, standards for regions of low sequence
complexity (such as dinuclectide repeats and small unit tandem
repeats) have been relaxed. These regions are very prevalent in the
michael sequence and the return on extended finishing efforts is

Web site: http://genome.wustl.edu Contact: submissions@watson.wustl.edu

Center project name: M\_BB0155K11

Drafting center: WIBR

NOTICE:

If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

OM protein

Run on:

Title: Perfect sc Sequence:

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AAF89736 Nuclectid
AAR87174 CDNA enco
AAA27059 Mouse 5T4
AAG56199 Human LRR
AAJ56299 Human CDN
ACC51052 Human Dla
ACC51052 Human LRR
AAG56197 Human LRR
AAG56197 Human LRR
AAG56197 Human LRR
AAG56197 Human LRR
AAG10361 Antipsori
AAC2544 Breast ca
ACC38510 Tumour-as
ACC35098 Human CDN
AAC35098 Human CDN
AAG4253 Human ful
AAG4253 Human ful
AAG4254 Human ful
AAG4254 Human ful
AAG426162 Human CDN
AAG6162 Human CDN
AAG6166 Human CDN
Abt 07721 Breast ca
Abx76333 Lung canc
Adb80503 Ovarian c
Adn38723 Cancer/an
Add56198 Human LRR
Abv99349 Human NOV
Abk87175 CDNA enco
Adb97513 Feline 5T
Adb9752 DNA encod
Aaa27058 Human 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adt15316 Plant cDN
Abl06214 Drosophil
Abl33308 Human imm
                                                                                                                                                                                                                                                                                                                                                                                                                          Aax20580 Polynucle
Adh84583 Enterococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abl06215 Drosophil
Aac46422 Arabidops
Aac36467 Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , gene therapy, DKFZp566I133 activity inhibitor; differential expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breast cancer differentially expressed gene product #47
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                                                AADS6198
ABV99349
ABV87175
ADB97513
ADB97452
AAAZ7058
AAAZ7058
AAR89736
AAAZ7059
AAAZ7059
                                                                                                                                                                         ADJ56299
ABX76332
ABX76332
AAD56197
AAD56200
ADJ38721
ADJ06473
ADM03961
ADM25444
ACM38510
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AAK94254
AD126162
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ADL26160
AD126158
AAX20580
ADH64583
ABM06215
AAC36467
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ABL06214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2003; 2003WO-US000657
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   2557
2557
204
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  cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer;
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   ADK11641;
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB spool/US10714176/runat_26052006_091441_24976/app_query.fasta_11-0=0=\delta bss/ABSSWEB spool/US10714176/runat_26052006_091441_24976/app_query.fasta_10=0=\delta compared by the com
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Adul1677 Solid tum
Aaa27060 Canine 5T
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249.339 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                        ; Search time 377.5 Seconds
                version 5.1.8
- 2006 Biocceleration Ltd
                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
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ADU11677
AAA27060
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Ygapext
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                GenCore (c) 1993
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Ygapop 10.0 , Y
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Database

Result Š.

Minimum DB Maximum DB

Searched:

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The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKRZp5661133 activity. The methods are useful for treating cancer, e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention.
                                          Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for inhibition of DKFZp5661133 activity.
                                                                                                                                          Claim 30; SEQ ID NO 47; 257pp; English
RXFFFX8X000000X8
```

Sequence 246 BP; 77 A; 49 C; 59 G; 61 T; 0 U; 0 Other; Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 92.3 41.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: .. 02

σ 1 AlailePheLeuLeuValLeuTyrLeu

US-10-774-176-24 (1-9) x ADK11641 (1-246)

ADU11677 standard; DNA; 475 BP 4DU11677; ADU11677 셤 ò

Solid tumour prognosis gene seqid 2116. 27-JAN-2005 (first entry)

cytostatic; gene therapy; expression profile; solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds.

Unidentified

#02004097052-A2

11-NOV-2004.

29-APR-2004; 2004WO-US013587

29-APR-2003; 2003US-0466067P. 23-JAN-2004; 2004US-0538246P.

(AMHP ) WYETH

(STRA/) STRAHS A.

Trepicchio WL, Burczynski ME, Twine NC, Slonim DK; Immerman F, Dorner AJ; WPI; 2004-804779/79. Strahs A,

A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene. Disclosure; Page; 111pp; English. The invention describes a method comprising comparing an expression profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially

unaupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the apopulation of patients who have the solid tumour, and where the case of patients has a first clinical outcome, and cutcome. Also described are: a system comprising (i) a memory or a cutcome. Also described are: a system comprising (i) a memory or a cutcome. Also described are: a system comprising (i) a memory or a cutcome. Also described are: a system comprising (i) a memory or a cutcome in a peripheral blood sample of a patient who has a solid tumour, (ii) at least another storage medium including data that control of the gene in a peripheral blood sample of a patient who has a solid tumour capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the cyprogram capable of comparing the expression profile, and (iv) a processor capable of executing the cyprogram where expression levels of the gene in peripheral blood monouclear cells of patients who have the solid tumour correlate with clinical outcomes of the patients who have the solid tumour prognosis genes, where each of the patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as solid tumour. Trognosing and treating cutcome, and the second class of patients has a second class of cutcome, and the second class of patients as solid tumours. This sequence the first class of patients has a second class of cutcome, and the second class of patients as solid tumours. This sequence the first class of patients has a second class of the method, system, and array are useful for prognosing and treating cutcome, and the second class of patients as solid tumours. The sequence data for this patent did not form part of the invention. Note: The sequence this patent did not form patient of the printed specification, but was obtained in electronic format expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an 

Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other;

Matches: Conservative: Mismatches: Indel8: 41.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-10-774-176-24 (1-9) x ADU11677 (1-475)

381 GCTATTTTCCTCCTGGTTTTGTATTTG 407 σ 1 AlailePheLeuLeuValLeuTyrLeu

RESULT 3 AAA27060

g

AAA27060;

ВР

AAA27060 standard; DNA; 901

(first entry) 22-AUG-2000 Canine 5T4 tumour-associated antigen gene.

Canine, TAA, tumour-associated antigen, anti-tumour, cytostatic, immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer, 

Canis sp.

1. .858 /\*tag= a /product= "5T4 antigen" Location/Qualifiers misc feature

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99GB-00017995.
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Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.

WPI; 2000-387735/33. P-PSDB; AAY94351 The present sequence encodes the canine 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in

Disclosure; Page 78-79; 79pp; English

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carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the human or murine 574 gene sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
                                                                                                                                                                     C; 212 G; 153 T; 0 U; 112 Other;
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Mismatches:
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Matches:
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2001US-00829472.
2001US-0282698P.
2001US-0288590P.
2001US-0294443P.
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cc in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are compounded of the invention can be used in diagnostic purposes and also as cargets for screening for therapeutic compounds that modulate breast concer (e.g. hormones or antibodies). Identification of genes that are cover or under expressed in breast cancer can additionally provide high-constroin, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0761 crepresent the 69 breast cancer-associated gene sequences of the invention XX Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                       927
                                       Length:
Matches:
Conservative:
Mismatches:
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10-MAY-2001; 2001US-039245P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-03360666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-033246P.
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                                                                                  Best Local Similarity:
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 # identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated for identifying a compound that modulates a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous leadions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity preumonitis, interstitial pulmonary fibrosis astema and for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences

ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
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05-SEP-2001; 2001US-0317544P.
13-NOV-2001; 2001US-0350666P.
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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                   The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynuclectide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for the detection method of the invention.
                                                                                                                                           Claim 10; Page 297; 332pp; English.
P-PSDB; ADB80504
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

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927
                    Conservative:
Mismatches:
             Matches:
       Length:
                                  Indels:
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Alignment Scores:
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US-10-774-176-24 (1-9) x ADB80503 (1-927)

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760 GCTATTTTCCTCCTGGTTTTGTATTTG 786
1 AlallePheLeuLeuValLeuTyrLeu 9
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ADN38723 standard; cDNA; 927 ADN38723; ADN38723 THE SET OF THE SET OF

17-JUN-2004 (first entry)

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41

fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss. Human; differential expression; cancer; angiogenic disorder;

Homo sapiens.

WO2003042661-A2

22-MAY-2003.

13-NOV-2002; 2002WO-US036810

13-NOV-2001; 2001US-0350666P. 21-NOV-2001; 2001US-0332464P. 29-NOV-2001; 2001US-033539P. 03-DEC-2001; 2001US-0335394P. 14-DEC-2001; 2001US-0340376P. 09-JAN-2002; 2002US-0347211P. 10-JAN-2002; 2002US-0347349P. 08-FEB-2002; 2002US-0355250P.

2002US-0359077P. 2002US-035809P. 2002US-0372246P. 2002US-0372246P. 2002US-0396614P. 2002US-0396775P. 09-SEP-2002; 2002US-0409450P. 13-FEB-2002; 2 20-FEB-2002; 2 29-MAR-2002; 2 04-APR-2002; 2 05-JUN-2002; 22-JUL-2002; 22-JUL-2002; 

(EOSB-) EOS BIOTECHNOLOGY INC

Glynne R, Hevezi PA; 3, Zlotnik A; Gish KC, Gl Wilson KE, Ginsburg WM, R, Watson SR, Murray R, Afar D, Mack DH,

WPI; 2003-468649/44.

P-PSDB; ADN38724

Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting useful for diagnosing, prognosing or to a nucleic acid in a biological sample.

Claim 8; SEQ ID NO 41; 1385pp; English

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention. The invention is antibodies which specifically bind a polypeptide of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; colypeptides and mucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present invention relates to nucleic acids and proteins (ADN38683-ADN40064) sequence represents a nucleic acid sequence of the invention

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

927 Conservative: Mismatches: Length: Matches: Indels: 41.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred. No.:

US-10-774-176-24 (1-9) x ADN38723 (1-927)

GCTATITICCICCIGGITITICIALITIC 786 σ 1 AlailePheLeuLeuValLeuTyrLeu

AAD56198 RESULT

AAD56198 standard; DNA; 973 SXXXXXXXXXXXX

AAD56198;

(first entry) 07-AUG-2003

Human LRRCAPS related DNA #5.

Human; p53 pathway; Leucine rich repeat capricious related protein; LRRCAPS; cancer; gene therapy; ds.

Homo sapiens

us-10-774-176-24.p2n.rng

Belvin M,

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2001US-0274101P.
2001US-0274134P.
2001US-0274322P.
2001US-0274432P.
2001US-0274449P.
2001US-0275235P.
2001US-0275235P.
2001US-0275239P.
2001US-02756776P.
2001US-0276776P.
2001US-0276776P.
2001US-0276776P.
2001US-0277321P.
2001US-02773321P.
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2001US-0279036P.
2001US-0279344P.
2001US-0279995P.
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2001US-0281194P.
2001US-0283675P.
2001US-0287424P.
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2001US-0309198P.
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2001US-0318770P.
2001US-0325430P.
                                                                            08-MAR-2002; 2002WO-US007288
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2001US-0330380P.
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2001US-0332172P.
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13-MAR-2001,
14-MAR-2001,
16-MAR-2001,
19-MAR-2001,
20-MAR-2001,
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26-MAR-2001; 2
27-MAR-2001;
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31-OCT-2001;
14-NOV-2001;
14-NOV-2001;
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09-MAR-2001;
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02-APR-2001;
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                                             19-SEP-2002
The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the rest agent as a candidate p53 pathway modulating agent. The method is useful for identifing a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosupressive; osteopathic; antiparkinsonian; cancer; antiinfertility; carebroprotective; gene therapy; NOVX; NOV; Ertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; heematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                                                                                                                                                                                                                                                                              Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                     Li D;
                                                                                                                                                                                                     Plowman GD, Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                            Example 5; Page 74-75; 99pp; English.
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                                                                        21-OCT-2002; 2002WO-US033540.
                                                                                                    22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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                                                                                                                                                                                                  Schleithoff L,
ng H, Friedman
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            WO2003035831-A2
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Pred. No.:
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                                          01-MAY-2003
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001US-0337426P.

2002US-00093463

08-MAR-2002;

(CURA-) CURAGEN CORP.

sapiens

Homo

ABV99349;

775

à 合 RESULT 9 ABV99349

Query Match: DB:

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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99555 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes,
                                                                                                                                                                                                                                                                                    cancer,
                                                                                                 Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                  New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cance Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 114-115; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic or diagnostic methods
                                                                                                                                                                                                                                                                                                                                   disorders, and asthma.
                                                                                                                                                                             WPI; 2002-732824/79
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

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1156
9
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       Length:
Matches:
Conservative:
                                Mismatches:
Indels:
                                                 Gaps:
               41.00
100.0%
100.0%
100.0%
                                  Best Local Similarity:
                        Percent Similarity:
Alignment Scores:
Pred. No.:
                                          Query Match:
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991 GCTATTTTCCTCCTGGTTTTGTATTTG 1017

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ABK87175; RESULT 10 

(first entry) 07-OCT-2002

gb. Felis

Key

Location/Qualifiers 1. .1260 /\*tag= a

σ US-10-774-176-24 (1-9) x ABV99349 (1-1156) 1 AlallePheLeuLeuValLeuTyrLeu

ABK87175 standard; cDNA; 1260 BP

ADB97513 standard; DNA; 1260

RESULT 11 ADB97513 04-DEC-2003 (first entry)

ADB97513;

Feline; cat; oncofoetal leucine-rich glycoprotein; 574; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss. cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.

Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds. Feline 5T4 antigen DNA. Unidentified 

The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the professed leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell confideration, infections, and inflammantory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extractes of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The solution process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for the present sequence encodes feline 574 protein Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat. Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other; 1260 9 0 0 0 Matches: Conservative: Mismatches: Length: Indels: Gaps: /product= "5T4 protein" 1 AlaIlePheLeuLeuValLeuTyrLeu 9 US-10-774-176-24 (1-9) x ABK87175 (1-1260) Claim 4; Page 68; 68pp; English. OXFO-) OXFORD BIOMEDICA UK LTD. Carroll M; 13-NOV-2000; 2000WO-GB004317. 13-NOV-2001; 2001WO-GB005004 41.00 100.0% 100.0% 100.0% WPI; 2002-557449/59. P-PSDB; AAU98694. Drury N, Best Local Similarity: WO200238612-A2 Percent Similarity: Alignment Scores: 16-MAY-2002 Myers K, Query Match: .. 02 Score: ð DNA encoding feline 5T4 protein.

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The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 5T4 antigen. The invention further provides a polypelicope string comprising the 5T4 epitope; a uncleic acid sequence encoding the 5T4 epitope atring of the 5T4 epitope atring of the 5T4 epitope atring of the 5T4 epitope of the 5T4 epitope, a vector system capable of delivering the 5T4 epitope nucleic acid to a cell, a cell pulsed with the 5T4 epitope, a polypelitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease of a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising the presence of the 5T4 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 5T4 epitope in conjunction with an MHC class I molecule. The 5T4 epitope has cytostatic acid; and the vector system or cell is useful in the prevention and/or treatment of a disease, partendarly cancer. The detection method is useful for diagnosing or monitoring the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or preventing a disease. This polymucletide sequence represents the feline of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              New major histocompatibility complex class I peptide epitopes from human 5T4 tumor-associated antigen, useful for preventing and/or treating a
                                                               /product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                         Redchenko I;
Location/Qualifiers
1. .1260
/*tag= a
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                                                                                                                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, particularly cancer.
                                                                                                                                                                                            13-FEB-2003; 2003WO-GB000670.
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  Key
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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Length:
Matches:
Conservative:
Mismatches:
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Alignment Scores:
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US-10-774-176-24 (1-9) x ADB97513 (1-1260)

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1099 GCCATTTTCTTACTGGTTTTGTACTTG 1125
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ADB97452 standard; DNA; 1260 BP

ADB97452

(first entry) 04-DEC-2003

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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                            gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Major Histocompatibility Complex class II peptide epitope of 574, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TAA; tumour-associated antigen; anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                               /product= "Feline 5T4 antigen protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-663795/62
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                           WO2003068815-A2
                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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SOC CCC CCC CCC X S X L L L L L X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X 
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(TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen itself can be used to elicit an immune
                                                                                                                                                                                                                                                                                                                                     Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence encodes the human 5T4 tumour-associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 78; 79pp; English
                                                                                                                                                                                                                                   (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                98GB-00025303.
                                                                                                                                                                                  99GB-00001739.
                                                                                                                                 99WO-GB003859
                                                                                                                                                                                                                                                                                                                                   Tumor associated antigen,
                                                                                                                                                                                                                                                                    Carroll MW, Myers KA;
                                                                                                                                                                                                                                                                                                     WPI; 2000-387735/33.
                                                              WO200029428-A2.
                               Homo sapiens.
                                                                                                                                 18-NOV-1999;
                                                                                                                                                                  18-NOV-1998;
                                                                                                                                                                                                  30-JUL-1999;
                                                                                                                                                                                    27-JAN-1999
                                                                                                25-MAY-2000
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Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other; 1263 9 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 41.00 100.0% 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-774-176-24 (1-9) x AAA27058 (1-1263)

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AAF89736 standard; DNA; 1263 (first entry) 23-JUL-2001 AAF89736; 

Nucleotide sequence of canine 5T4 protein.

Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.

Location/Qualifiers gb Canie

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Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                   Carroll MW, Ellard FM;
                                                                                                                                    Kingsman A, Kingsman SM, Bebbington CR,
                                                                                                                                                                                                                            Disclosure, Fig 26, 118pp, English.
        /product= "5T4"
                                                                                                                  (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                      15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                             13-NOV-2000; 2000WO-GB004317
/*tag= a
                                                                                                                                                              WPI; 2001-343805/36.
                                                                                                                                                                       P-PSDB; AAB83839
                          WO200136486-A2
                                                                              .8-NOV-1999;
                                           25-MAY-2001
                                                                                                                                             Myers KA;
```

The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for invivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune disease, cancers, central nervous system disorders including Parkinson's disease, paridonneal diseases, cardioulmonary diseases, aradiovascular disease, gastrointestinal disorders inflections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce ScFv of the invention

Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other; 1263 9 0 0 0 Conservative: Mismatches: Matches: Length: 41.00 100.0% 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: No.: Score:

(1-1263)US-10-774-176-24 (1-9) x AAF89736

1 AlailePheLeuLeuValLeuTyrLeu 9

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Indels:

Query Match

Gaps:

1102 GCCATCTTCCTACTGGTTTTGTATTTG 1128 RESULT 15 ABK87174 

cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.

Canine; dog; oncofoetal leucine-rich glycoprotein; 574; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; 88. ABK87174 standard; cDNA; 1263 07-OCT-2002 (first entry) ABK87174; Canis

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in sequinicant proportion of tumours. The Squences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine protein are useful for isolating foetal cells from maternal blood. The
                                                                                                                                                                                                                                                                                                                                                                          Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus (es) The present sequence encodes canine 514 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
              Location/Qualifiers
1. .1263
/*tag= a
/product= "5T4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 67; 68pp; English.
                                                                                                                                                                                                                                                  (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                      Carroll M;
                                                                                                                                                                             13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                              13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                      WPI; 2002-557449/59.
P-PSDB; AAU98693.
                                                                                                                                                                                                                                                                                      Drury N,
                                                                                                       WO200238612-A2
                                                                                                                                          16-MAY-2002
                                                                                                                                                                                                                                                                                      Myers K,
                Key
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-774-176-24 (1-9) x ABK87174 (1-1263)

100.00

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

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Search completed: May 27, 2006, 10:38:36 Job time: 379.5 secs

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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AX829164 Sequence
AX467373 Sequence
AX821533 Sequence
AX821548 Sequence
AX821548 Sequence
BD249731 Polypepti
AX025011 Sequence
AX14695 Sequence
AX14696 Sequence
AX14696 Sequence
AX1608 Sequence
AX31608 Sequence
AX011678 Sequence
AX016339 Rattus no
BD127282 Primer fo
CQ782724 Sequence
AX074786 Homo sapien
AX061916 Sequence
AX074790 Homo sapien
BC082726 Sequence
AX074790 Homo sapien
AX061915 Sequence
AX074791 Homo sapien
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AX961914 Sequence
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AX061915 Homo sapien
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AX061914 Sequence
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AX1619
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737.A 32642 12-SEP-2002;
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Sequence 32642 from Patent W002070737.
CQ687716.1 GI:42218962
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Matches:
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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HSA012159
MMU012160
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AC128294
AC156733
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AP004082_
HSJ492P14
                                             DD161112
AX467373
AX821533
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BD249731
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CQ731678
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HSST40A
AF063939
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CQ782724
AK074786
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CQ782726
AK074790
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BC058198
AX961912
AX961914
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AX149553
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Pred. No.:
   source
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VERSION
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AUTHORS
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JOURNAL
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CQ687716
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SOURCE
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-MODELeframe+_p2n.model_-DEV=xlh
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-G_abss/ABSSWEB_grool/US10774176/runat_26052006_091443_24987/app_query.fasta_1
-DB=cenEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINWATGH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-OUTINT=DED -SOORTHE SCORES=ESC -HTR MAXE=10 -THR MINEO -ALIGN=15 -MODE=LOCALI
-OUTINT=ptc -NORM=ext -HEAPSIZE=500 -HINLEN=0 -MXXLEN=2000000000 -HOST=abss04
-USER=US10774176_@CGN 1 1 7524_@runat_26052006_091443_24987 -NCFU=6 -ICPU=3
-WARN TIMEDUT=30 -THREADS=1 -XGAPEN=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPEXT=7
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CQ920916 Sequence
BD249733 Polypepti
                                                                                                                        (without alignments)
257.039 Million cell updates/sec
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                                                                                                           May 27, 2006, 09:51:03 ; Search time 3358.6 Seconds
                 GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                  6366136 seqs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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9b_pat:*
9b_p1:**
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9b_sy:**
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Result Ņ. 4141

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PAT 15-SEP-2000
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
MILES WILLIAM CARROLL,KEVIN ALAN MYERS
C12N15/09,A61K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,
C07K19/00,
C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll, M.W. and Myers, K.A.
Polypeptide
Patent: WO 0029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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Location/Qualifiers
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Sequence 3 from Patent WO0029428.
AX025013 GI:10184934
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/organism="Canis sp."
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TITLE
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AX025013
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Methods for prognosis and treatment of solid tumors
Patent: WO.097052-A 2116 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
Location/Qualifiers
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Polypeptide
Patent: JP 2002530060-A 3 17-SEP-2002;
OXFORD BIOMEDICA LTD
OX Canis Sp. (dog)
PN JP 2002530060-A/3
PD 17-SEP-2002
PF 18-NOV-1999 GB 9825303.2,27-JAN-1999 GB 30-JUL-1999 GB 9917995.4
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JP 2002530060-A/3.
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Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigens, and Methods of Use.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Padigaru,M., Shenoy,S.G., Pochart,P.F., Kekuda,R., Gusev,V.Y.,
Zhong,M., Jr.R.J.T., Casman,S.J., Li,L., Miller,C.E.,
Patturajan,M., Anderson,D.W., Malyankar,U.M., Voss,E.Z.,
Spaderna,S.K., Gorman,L., Spytek,K.A., Liu,X., Burgess,C.E.,
Bena,C.E.A., Gerlach,V., Smithson,G., Mezes,P.D., Rastelli,L.,
Boldog,F.L., Guo,X., Vernet,C.A.M., Gangolli,E.A., Tchernev,V.T.
and Zerhusen,B.D.
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60/288066,30-APR-2001

60/288075,04-APR-2001

60/28802,02-APR-2001

60/288528,15-MAY-2001

60/291240,16-MAY-2001

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60/274281,08-MAR-2001

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                Conservative:
Mismatches:
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60/277327,20-MAR-2001
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60/275578, 20-MAR-2001
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60/279036,28-MAR-2001
60/299303,10-JUL-2001
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60/277833,23-MAR-2001
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08-MAR-2002 JP 2002571827
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JP 2005508604-A/23
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Homo sapiens (human)
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PD 07-AFR-2
PF 19-JUN-2
PR 19-JUN-3
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13-MAX-2001 U
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DD161112
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KEYWORDS
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
Patent: WO 02059377-4 57 01-AUG-2002;
BOS Biotechnology, Inc. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                        Carroll, M.W. and Myers, K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 3 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 57 from Patent W002059377.
AX829164
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AX316088
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AX829164
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PAT 10-DEC-2003

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felis catus (cat)
Felis catus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lauraslatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
                                                                                                                                                                                                                                                                                                                                                Carroll, M.M., Kingsman, S.M. and Redchenko, I.M. MHC class I peptide epitopes from the human 5t4 tumor-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll,M.O., Harrop,R.O. and Kingsman,S.O.
MHC class II peptide epitope of 5t4 antigen
Patent: WO 03068815-A 1 21-Aug-2003;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1260
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Matches:
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                                                                                                              1099 GCCATTTTCTTACTGGTTTTGTACTTG 1125
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AX821533
AX821533.1 GI:39724929
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Sequence 1 from Patent WO03068815.
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AX821548.1 GI:39724930
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Best Local Similarity:
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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                                                                                                                                  vladimir y gusev, mei zhong, raymond j taupier jr, stacie j PI
                                                                                                                                                                                                                                                         glennda smithson, peter d mezes, luca rastelli, ferenc l boldog
                                                                                                                                                                                                                                                                          xiaojia guo,
corine a m vernet,esha a gangolli,velizar t tchernev,bryan d
zerhusen
                                                                                                          PI muralidhara padigaru, suresh g shenoy, pascale f-g pochart, remesh kekuda,
                                                                                                                                                   casman,li li,
PI charles e miller, meera patturajan, david w anderson, uriel
                                                                                                                                                                                                edward z voss, steven k spaderna, linda gorman, kimberly PI
                                                                                                                                                                                                                              xiaohong liu, catherine e burgess, carol e a pena, valerie
 60/332172, PR
60/335301, PR
60/325430, PR
60/318770, PR
10/093463, PR
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60/333184,31-OCT-2001 US
60/325681,12-SEP-2001 US
60/318462,03-CAN-2002 US
60/337185,08-MAR-2002 US
60/3312903
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Matches:
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    .1156
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    .1260
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Location/Qualifiers
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Sequence 3 from Patent WO0238612.
AX467373
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14-NOV-2001 US
18-CCT-2001 US
27-5EP-2001 US
04-DEC-2001 US
16-AUG-2001 US
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Felis sp.
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PI xiae
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PI zerr
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FH Key
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PI xi
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PAT 10-DEC-2003

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PAT 14-DEC-2001
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Homo sapiens (human)
Memo sapiens
Eukaryota, ms. Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W., Ellard, F.M. and Myers, K.A.
                                                                                              Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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Matches:
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Gaps:
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Patent: WO 0136486-A 14 25-MAY-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 14 from Patent W00136486.
AX149553
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AX316086
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AX149553
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MILES WILLIAM CARROLL, KEVIN ALAN MYERS
CI2N15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065,
C07K19/00,
C12N15/00
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1. .1263
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Indels:
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Matches:
Conservative:
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Indels:
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1 (bases 1 to 1263)

Carroll, M.W. and Myers, K.A.
Polypeptide
Patent: JP 2002530060-A 1 17-SEP-2002;

OXFORD BIOMEDICA LTD
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    .1263
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                                                                                    Gaps:
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PN JP 2002530060-A/1
PP 17-SEP-2002
PF 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9825303.2,
30-JUL-1999 GB 9917995.4
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PC C12N15/09, A61K39/00, A61K48/(PC C72N15/00)
PC C12N15/00
PC C12N15/00
PC POlypeptide Location/Que
FT SOURCE (organism='FT)
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JP 2002530060-A/1.
Homo sapiens (human)
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              27.7
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BD249731
                                   Percent Similarity:
Best Local Similarity:
Query Match:
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  Alignment Scores:
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Search completed: May 27, 2006, 19:35:25 Job time : 3359.6 secs

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PAT 16-JUL-2002
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Canis sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalyia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               Carroll,M.W. and Myers,K.A.

St4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. .1263
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/mol_type="unassigned DNA"
/db_xref="taxon:9616"

    1263
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 1 from Patent W00238612.
AX467371 GI:21900602
Sequence 1 from Patent EP1160323. AX316086
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                        AX316086.1 GI:17899278
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Homo sapiens
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AX467371
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3 Cancer/an Human LRR Human NOV

Canine 5T Breast ca

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Abk87175 cDNA enco
Adb75513 Feline 5T
Adb7512 DNA encod
Aaa27058 Human 5T4
Abk87174 cDNA enco
Abk87174 cDNA enco
Abk87174 cDNA enco
Ad55629 Human LRR
Ad56299 Human LRR
Ad56299 Human LRR
Ad56299 Human LRR
Ad76332 Lung canc
Aad56197 Human LRR
Ad13613 Human LRR
Ad13613 Human LRR
Ad13613 Tunipsori
Ad25619 Human CDN
Ad25619 Human CDN
Ad13631 Full leng
Ad87175 DNA encod
Aak84253 Human ful
Ad130831 Full leng
Ad130831 Full leng
Ad130831 Full leng
Ad26162 Human cDN
Ad126168 Human cDN
Ad261289 Human cDN
Ad126168 Human cDN
                               Abx76333 Lung canc
Adb80503 Ovarian c
Adn38723 Cancer/an
Aad56198 Human LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse spliced transcript detection oligonucleotide SEQ ID NO:29022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
                                                                           Abv99349 B
Abk87175
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AAD56299
AAC561952
AAD56197
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AAD56197
AAD56197
AAD13611
AAD13611
AAX89175
AAX89175
AAX894253
AAX894253
AAX894254
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ADX945773
                              ABX76333
ADB80503
ADB80503
ADB80203
AAD56198
ABW99349
ABW87175
ADB97513
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AAA27058
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AAAB9736
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02-MAY-2001; 2001US-0287724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN56274 standard; DNA; 65
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WO200210449-A2.
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 ABN56274;
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 Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Abss/ABSSWEB spool/US10774/16/runat_26052006_091441_24976/app_query.fasta_1
-Q=/Abss/ABSSWEB spool/US10774/16/runat_26052006_091441_24976/app_query.fasta_1
-DB=N Geneesq_-OFWT=fastap_-SUFFIX=p2n.rng_-NINMATCH=0.1_-LOOPCL=0_-LOOPEXT=0
-UNITS=bits_-START=1_-END=-1_-MATRIX=blosum62_-FRANS=human40.cdi_-LIST=45
-UNITS=bits_-START=1_-END=-1_-MATRIX=blosum62_-FRANS=human40.cdi_-LIST=45
-UNITS=bits_-START=1_-END=-1_-MATRIX=blosum62_-FRANS=human40.cdi_-LIST=45
-UNITS=bits_-START=1_-END=-1_-HR AX=100_-THR MINO_-MAXIEN=2000000000 -HOST=abss02h
-USRR=US10774176_GCGN_1_1_238_Grunat_26052006_09141_24976_-NCPU=6_-ICPU=3
-NO MAAP_NGS_CORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG_-DEV_TIMEOUT=120
-WARN_TIMEOUT=30_-THRRADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6_-FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abn56274 Mouse spl
Acd97670 Human col
Aas87174 DNA encod
                                                                                       (without alignments)
249.339 Million cell updates/sec
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                            ; Search time 377.5 Seconds
           version 5.1.8
- 2006 Biocceleration Ltd.
                                                      nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                    5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
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ACD97670
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                                                                           May 27, 2006, 09:34:35
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
           GenCore (c) 1993
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geneseqn2003ds:*
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geneseqn1980s:*
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                                                                                                                                            SLQTSYVFL 9
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Potal number of

Searched:

score:

Title: Perfect sc Sequence:

OM protein

Run on:

Scoring table:

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transcription units that populate a genome. The library comprises several cligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcription unit of the genome, which encodes one or more messenger RNAs splice variants. The coligonuclectide libraries are useful for detecting mRNAs from a cligonuclectide libraries are useful for detecting mRNAs from a cligonuclectide libraries are useful for detecting mRNAs from a cligonuclecting to expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcriptom of a transcriptome of a particular disorder. ABN27253 to ABNS9589 represent oligonucleotide sequences from
                                                                                                                     ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                              New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                    The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65 BP; 9 A; 21 C; 12 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Example 1; SEQ ID NO 29022; 47pp; English
                        WPI; 2002-257383/30
                                                                                                                                                                        specific genes.
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960000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 0.822 43.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: OB:

1 SerLeuGlnThrSerTyrValPheLeu US-10-774-176-23 (1-9) x ABN56274 (1-65)

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ACD97670 standard; cDNA; 108 BP. RESULT 2 ACD97670 

23-SEP-2003 (first entry)

Human colon cancer cell expressed cDNA #6082.

Open reading frame detection; genome sequencing; colon cancer; breast cancer; bopulation genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; gene; ss.

Homo sapiens.

86

60 recerecasacererrarererrecre

AAS87174 standard; cDNA; 453

RESULT 3 AAS87174

JS2002155438-A1

24-OCT-2002

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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism the genome of organism, comprising contacting mRNA from cell of organism contacting manality in a single oligomucleotide primer (I) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting cDNA, sequence from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, conclection acid molecule from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, contact or agenome of an organism. Aman for sequencing all or part of a genome of an organism. Sequencing a contig, contact or or breast cancer cell. The method is useful for analyses of colon cancer or breast cancer cell. The method is useful for analyses of large or small populations. further, it can be used to study living.

CC populations of subjects and can be used to carry out genetic analyses of copulations or population more or less likely to be afflicted with diseases such as cancer, to determine antibiotic resistance or nontolesting out in all animals, plants, birds, fish, etc. Using this method, the study of whether the conditions are likely to be passed to offegring the study of whether the conditions are likely to be passed to offegring the study of whether the conditions are likely to be passed to offegring the area of agriculture, for example the genomes of food crops can be studied to determine if resistance genes are present, defects in plant condition of the pathogens which may require different approaches to the pathogens which may require different approaches to the subtode analysis which may require different approaches to the subtode analysis which may require all the pathogens which analyses of the pathogens which m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                                                          Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108 BP; 18 A; 33 C; 22 G; 35 T; 0 U; 0 Other,
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                                                                                                                                                                                        Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Page 866; 959pp; English
99US-00406117.
                                                98US-00196716
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(BREN/) BRENTANI R R.
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27-SEP-1999;
                                              20-NOV-1998;
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n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder; ss.
                     DNA encoding novel human diagnostic protein #22978.
                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                            Tang YT;
                                                                                    30-MAR-2001; 2001WO-US008631
          13-FEB-2002 (first entry)
                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                       2001-639362/73
                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                       WPI; 2001-639362/
P-PSDB; ABG22987.
                                                             WO200175067-A2
                                                   Homo sapiens
AAS87174
                                       food
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 22978; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) is useful in gene therapy techniques to restore normal activity of (II) to to treat disease states involving oxpressed supplement. (II) and its binding patreners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in the produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and cannot sequences a have the printed specification, but was obtained in the printed specification and specificat ftp.wipo.int/pub/published\_pct\_sequences

Sequence 453 BP; 108 A; 111 C; 113 G; 121 T; 0 U; 0 Other;

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Mismatches:
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Matches:
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                                 Best Local Similarity:
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Alignment Scores:
Pred. No.:
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US-10-774-176-23 (1-9) x AAS87174 (1-453)

238 recerecaacererrarererreere 264 SerLeuGlnThrSerTyrValPheLeu

RESULT 4

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Trepicchio WL, Burczynski ME, Twine NC, Slonim DK;
                                          cytostatic, gene therapy, expression profile, solid tumour, peripheral blood mononuclear cell, PBMC; prognosis, ds.
                                Solid tumour prognosis gene seqid 2116.
BP.
                                                                                            29-APR-2004; 2004WO-US013587
                                                                                                      29-APR-2003; 2003US-0466067P.
23-JAN-2004; 2004US-0538246P.
ADU11677 standard; DNA; 475
                     (first entry)
                                                                                                                                             Immerman F, Dorner AJ;
                                                                                                                                                       WPI; 2004-804779/79.
                                                                                                                      (AMHP ) WYETH.
(STRA/) STRAHS A.
                                                                      WO2004097052-A2
                                                           Unidentified
                     27-JAN-2005
                                                                                 11-NOV-2004.
                                                                                                                                       Strahs A,
          ADU11677;
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The invention describes a method comprising comparing an expression profile of at least one gene in a peripheral blood sample of a patient to the patient has a solid tumour, and each of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients, where cot patients as compared to PBMCs of a second class of patients, where both the first and second classes is a subcluster formed by an each of the first and second classes is a subcluster formed by an early of the first class of patients has a first clinical outcome, adoutcome, also patients who have the solid tumour, and where the majority of the second class of patients has a second clinical outcome, also described are: a system comprising (i) a memory or a cutcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at cast one gene in a peripheral blood sample of a patient who has a solid tumour, (i) at least enother storage medium including data that represent at least one reference expression profile of the gene, (iii) a processor capable of executing the expression profile of the gene, (iii) a processor capable of executing the comparing the expression profile of the patients who have the solid tumour correlate with commonuclear cells of patients who have the solid tumour correlate with the program, where each of the patients and second classes of patients as econd classes of patients as econd classes of patients as econd classes of patients has a first clinical outcome, and where the first class of patients has a second classe of patients are nearly as energy of concern and array are area as econd classes of patients has a first clinical manner and where the first class of patients has a first clinical manner and each an

A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.

Disclosure; Page; 111pp; English.

The method, system, and array are useful for prognosing and treating solid tumours. This sequence represents a solid tumour prognosis gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other;

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carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastesis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunorherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the human or murine 574 gene sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
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corresponding amino acids"
714. .723
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497. .511
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be part of the coding sequence and does not
corresponding amino acids"
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/*tag= a
/product= "5T4 antigen"
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C. THE FETT THE FETT

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Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polymucleotide that selectively hybridizes with breast
                                            cancer; breast cancer-associated gene sequence;
                                                      development; pharmacogenetics; biosensor development
                           Breast cancer-associated gene sequence 29.
                                                                                                                                                                                                                                                                                                                                Claim 9; Page 372; 414pp; English.
                                                                                                                                                         2001US-0265928P.
2001US-00829472.
2001US-0282698P.
2001US-0288590P.
                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                  2001US-0263965P
                                                                                                                               24-JAN-2002; 2002WO-US002242
                                                                                                                                                                                               2001US-0294443P
                                                                                                                                                                                                                                   Mack DH, Gish KC, Afar D;
         14-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                             cancer nucleic acids
                                                                                                                                                                                                                                                       2002-583738/62
                                                                                                                                                                                                                                                                N-PSDB; ABJ05564.
                                            Gene; ds; breast
                                                                                           40200259377-A2
                                                                                                                                                                            09-APR-2001;
04-MAY-2001;
                                                                                                                                                                                                29-MAY-2001;
                                                                                                                                                           02-FEB-2001;
                                                                                                                                                                     09-APR-2001;
                                                                       Unidentified
                                                                                                                                                  24-JAN-2001;
                                                                                                             01-AUG-2002
                                                       drug
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis of breast cancer cells detecting genes that are up or down-regulated in breast cancer cells defecting genes that are method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-sensitivity datasets which can be used in the areas of - ABT07761 the invention diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07693 - ABT07761 represent the 69 breast cancer-associated gene sequences of the inventi Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

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Best Local Similarity:
Alignment Scores:
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US-10-774-176-23 (1-9) x ABT07721 (1-927)

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ABX76333 standard; DNA; 927 ABX76333 ID ABX7 XX RESULT

ВЪ

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antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                   polynucleotide; gene; ds; cytostatic; emphysema;
                       Lung cancer-associated polynucleotide #197.
           (first entry)
                                   cancer-associated
           02-APR-2003
ABX76333;
                                   Lung
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WO200286443-A2.

31-OCT-2002

18-APR-2002; 2002WO-US012476

18-APR-2001;

10-MAY-2001; 2001US-0290492P. 09-NOV-2001; 2001US-0339245P. 13-NOV-2001; 2001US-0350666P. 29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P. EOS BIOTECHNOLOGY INC. (EOSB-)

Aziz N, Murray R;

WPI; 2003-093161/08. P-PSDB; ABU56604.

Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

Claim 22; Page 336; 453pp; English

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in a sequence that is at least 80 % identical to a gene that exhibits in creased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell ung cancer or other benign or precancerous lesions, e.g. atleetasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences and as targets for screening for therapeutic compounds that modulate lung cancer-associated polynucleotides of the nvention

BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other; Sequence 927

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     Length:
Matches:
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Mismatches:
Indels:
      16.5
43.00
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                             Similarity:
                     Percent Similarity:
Alignment Scores
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                             Best Local
        Pred. No.:
              Score:
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x ABX76333 (1-927) US-10-774-176-23 (1-9) σ

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1 SerLeuGlnThrSerTyrValPheLeu
                US-10-774-176-23 (1-9) x ADB80503 (1-927)
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Mack DH,
                                                                                                                                                                                      ADN38723;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
monitoring response to therapy, selecting patients for post-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                                                                                                        cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
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                                                                                                                                                                                                      Ovarian cancer-associated transcript #34.
                 TCCCTGCAAACCTCTTATGTCTTCCTG 735
SerLeuGlnThrSerTyrValPheLeu 9
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                    ВР
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27-AUG-2001, 2001US-031528PP.
05-SEP-2001, 2001US-03544P.
13-NOV-2001, 2001US-035066EP.
12-APR-2002, 2002US-0372246P.
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                                                                                                    ADB80503 standard; DNA; 927
                                                                                                                                                                      04-DEC-2003 (first entry)
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927 0 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

16.5 43.00 100.0% 100.0% 100.0%

Similarity:

Query Match: DB: Best Local

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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a
                                                                                                                               fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
                                                                                                                                                                             detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; valnerary; gene therapy; vaccine; gene; ss.
                                                                                       Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
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                                                                                                                    Human; differential expression; cancer; angiogenic disorder;
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E, Zlotnik A;
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Wilson KE,
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ВР
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Murray R, Watson SR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0356714P.
20-FEB-2002; 2002US-0359077P.
ADN38723 standard; cDNA; 927
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2001US-0334393P.
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                                                          17-JUN-2004 (first entry)
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polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides and nucleic acids. The nucleic acids, polypeptides antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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acid of the invention; antibodies which specifically bind a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p53 pathway; Leucine rich repeat capricious related protein;
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                                                                                                                                                                                               Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; gene therapy; ds.
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01-MAR-2002; 2002US-0361196P.
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Francis-Lang H, Friedman L;
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43.00
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nucleic
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Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosupressive; osteopathic; antiparkinsonian; cancer; antinfertility; cerebroprotective; gene therapy; NOWX; NOW; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haemacopoietic disorder; cardiovascular disorder; bronchial asthma, dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                       Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Conservative:
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2001US-0275235P.
2001US-0275578P.
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2001US-0275601P.
2001US-0276000P.
2001US-0276776P.
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2001US-0277321P.
2001US-0277327P.
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2001US-0280233P
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2001US-0274281P
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13-MAR-2001;
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                                                                  Alignment Scores:
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2001US-0280900P.
2001US-0281194P.
2001US-0287424P.
2001US-0288424P.
2001US-028842P.
2001US-0288328P.
2001US-0291190P.
2001US-0291099P.
2001US-029140P.
2001US-029140P.
                                                               2001US-0294889P.
2001US-0294899P.
2001US-0299027P.
2001US-0299303P.
                                                                                                                              2001US-0335301P.
2001US-0332172P.
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                                                                                                                                                                                             CURA-) CURAGEN CORP.
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P-PSDB; ABP70071.
                    13-APR-2001;
                                 03-MAY-2001;
                                            15-MAY-2001;
                                                     16-MAY-2001;
30-MAY-2001;
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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli BA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.

Claim 16; Page 114-115; 619pp; English

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a edicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or disgnosing diseases unch as metabolic disorders, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, heematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g.

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neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods
                                                                                                                                                                                                                                                                                                                         Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                                                                                                      cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                   Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;
                                                                                 1156
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Mismatches:
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Matches:
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                                                                                                                                                          US-10-774-176-23 (1-9) x ABV99349 (1-1156)
                                                                                                                                                                             1 SerLeuGlnThrSerTyrValPheLeu
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1. .1260
                                                                                                                                                                                                                                         ABK87175 standard; cDNA; 1260 BP
                                                                                 21.1
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                            Felis sp.
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Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat. P-PSDB; AAU98694.

(OXFO-) OXFORD BIOMEDICA UK LTD.

13-NOV-2001; 2001WO-GB005004. 13-NOV-2000; 2000WO-GB004317. Carroll M;

WPI; 2002-557449/59. Myers K, Drury N,

Claim 4; Page 68; 68pp; English.

The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also

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be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 5T4 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 5T4 protein are useful for isolating foetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus The present sequence encodes feline 5T4 protein
      888888888
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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Length:
Matches:
Conservative:
Mismatches:
                                                 Indels:
                                                         Gaps:
         23.3
43.00
100.0%
100.0%
                                      Best Local Similarity:
                             Percent Similarity:
Alignment Scores:
                                                Query Match:
DB:
           Pred. No.:
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US-10-774-176-23 (1-9) x ABK87175 (1-1260)

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BP

ADB97513 standard; DNA; 1260 ADB97513; 

04-DEC-2003 (first entry) Feline 5T4 antigen DNA Major Histocompatibility Complex cláss I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.

Unidentified

location/Qualifiers ๙ 1. .1260 /\*tag= a Key

/product= "Feline 5T4 antigen protein"

WO2003068816-A1

21-AUG-2003

13-FEB-2003; 2003WO-GB000670

13-FEB-2002; 2002GB-00003419.

(OXFO-) OXFORD BIOMEDICA UK LTD

Redchenko I; Kingsman S, Carroll M,

WPI; 2003-637141/60. P-PSDB; ADB97520.

class I peptide epitopes from human for preventing and/or treating a New major histocompatibility complex ST4 tumor-associated antigen, useful disease, particularly cancer.

Disclosure; Page 67; 73pp; English.

The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 5T4 antigen. The invention further provides a polyepitope string comprising the 5T4 epitope, a nucleic acid sequence encoding the 5T4 epitope or a polyepitope string of the 5T4 epitope, a vector system capable of delivering the 5T4 epitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope, a polyepitope of the

Disclosure; Page 49; 63pp; English

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comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 514 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 514 epitope and of the or clone capable of mucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 574 epitope in conjunction with an MHC class of mucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 574 epitope in conjunction with an MHC class of mucleic acid in the 574 epitope has cytostatic activity. The vaccine comprising the 574 epitope has cytostatic activity. The vaccine comprising the 574 epitope or its encoding nucleic acid and the vaccine system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for detecting the progression of a cancerous disease, and for detecting the presence of the 574 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or consecuted preventing a disease. This polymucleotide sequence represents the feline or clone treating and coding DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or
                                                                                                                                                                                                                                                                                                                     Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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/*tag= a
/product= "Feline 5T4 antigen protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding feline 5T4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB97452 standard; DNA; 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
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No..
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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide connucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.
$888888888888888$$
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                               Gaps:
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                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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US-10-774-176-23 (1-9) x ADB97452 (1-1260)

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1048 TCCCTGCAGACTTCTTATGTCTTTCTA 1074
 1 SerLeuGlnThrSerTyrValPheLeu 9
ð
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AAA27058 standard; DNA; 1263 BP AAA27058; RESULT 15 AAA27058

Human 5T4 tumour-associated antigen gene 22-AUG-2000 (first entry) 

Human; TAA; tumour-associated antigen; anti-tumour; cytostatic; immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer; Human; TAA;

Homo sapiens

WO200029428-A2.

25-MAY-2000

98GB-00025303. 99WO-GB003859 18-NOV-1999; 18-NOV-1998;

99GB-00001739. 27-JAN-1999; 30-JUL-1999;

(OXFO-) OXFORD BIOMEDICA UK LTD

Carroll MW, Myers KA;

WPI; 2000-387735/33.

Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.

Example 2; Page 78; 79pp; English

(TAAÎ. The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult issues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the The present sequence encodes the human 5T4 tumour-associated antigen

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present sequence. The 5T4 antigen was shown to be effective at eliciting an immunocherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                             Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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Mismatches:
Indels:
Gaps:
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Search completed: May 27, 2006, 10:38:33 Job time : 379.5 secs

1051 TCCCTGCAAACCTCTTATGTCTTCCTG 1077

1 SerLeuGlnThrSerTyrValPheLeu

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Sequence:

Title: Perfect

Run on:

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BD249732 Polypepti
AX055012 Sequence
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CR855786 Xenopus t
AF065393 Rattus no
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome Patent: WO 0210449-A 29022 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 bp DN Sequence 29022 from Patent WO0210449. CQ559387.1 GI:41525814
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AX467373
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Alignment Scores:
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-D=G=CenEmbl -QFWT=fastap_SUFFIX=p2n.rge_-MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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CQ687716 Sequence
CQ920916 Sequence
                                                                             (without alignments)
257.039 Million cell updates/sec
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                                                                   May 27, 2006, 09:51:03 ; Search time 3358.6 Seconds
          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Jatabase :

Result No.

us-10-774-176-23.p2n.rge

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PAT 17-JUL-2003
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                         linear
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JP 2002530060-A/3.
Canis sp.
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AUTHORS
TITLE
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                    Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Strahs, A., Immerman, F. and Dorner, A.J.

Methods for prognosis and treatment of solid tumors

Patent: WO 2004/097052-A 2116 11-NOV-2004;

Wyeth (US); Burczynski, Michael E. (US)

Location/Qualifiers

1. 475

/organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                       Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 32642 12-SEP-2002;
Chondrogene Inc. (CA)
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                                                                                                                                                       Sequence 32642 from Patent WO02070737.
CQ687716
CQ687716.1 GI:42218962

    .290
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CQ920916
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CQ687716
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Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigens, and Methods of Use.
DD161112.
DD161112.1 G1:83967439
JP 2005508604-A/23.
Homo sapiens (human)
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                                                                                                                                                                                                               PAT 12-DEC-2003
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Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
Patent: WO 0205937-A 57 01-AUG-2002;
EOS Biotechnology, Inc. (US)
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 57 from Patent WO02059377.
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AX829164.1 GI:39838931
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Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Polypeptide
Patent: WO 0029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB) , MYERS KEVIN ALAN (GB) , OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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Patent: EP 1160323-A 3 0-DEC-2001;
Oxford biomedica (WK) Limited (GB)
Location/Qualifiers
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    /organism="Canis sp."
    /mol_type="unassigned DNA"
    /db_xref="taxon:9616"

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                              US-10-774-176-23 (1-9) x BD249733 (1-901)
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AX025013
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0238612-A 3 16-MAY-2002;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers

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AX467373
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Encoding The Antigens, and Methods of Use

Muralidhara Padigaru, Sureeh Shenoy, Remesh Kekuda, Vladimir Gusev,
Pascale Pochart, Mei Zhong, Luca Rastelli, Peter Mezes, Glennda
Smithson, Xiaojia Guo, Valearie Gerlach, Stacie Casman, Ferenc
Boldog, Li Li, Bryan Zerhusen, Valizar Tchernev, Esha Gangolli, Corine
Vernet, Carol Pena, Catherine Burgess, Xiaohong Liu, Kimberly
Spytek, Linda Gorman, Steven Spaderna, Edward Voss, Uriel
Malyankar, David Anderson, Meera Patturajan, Charles Miller, Raymond J
Taupier Jr
OS Homo sapiens
PN JP 2005508604-A/23
PP 08-MAR-2005
PR 06-MAR-2001 US 60/294899, PR
31-MAY-2001 US 60/29489, 31-MAY-2001 US 60/29499, PR
30-MAY-2001 US 60/294489, 00-MAR-2001 US 60/29489, PR
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corine a m vernet,esha a gangolli,velizar t tchernev,bryan d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vladimir y gusev, mei zhong, raymond j taupier jr, stacie j
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60/294889, 31 MAY-2001 US
60/288666, 30-MAY-2001 US
60/2886675, 04-APR-2001 US
60/288628, 15-MAY-2001 US
60/288628, 15-MAY-2001 US
60/291240, 15-MAY-2001 US
60/27523, 08-MAR-2001 US
60/274194, 02-APR-2001 US
60/27431, 08-MAR-2001 US
60/274327, 20-MAR-2001 US
60/277327, 20-MAR-2001 US
60/277921, 21-MAR-2001 US
60/277921, 21-MAR-2001 US
60/277931, 21-MAR-2001 US
60/2799303, 11-MAR-2001 US
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31-MAR-2001 US
02-MAY-2001 US
03-MAY-2001 US
03-MAY-2001 US
03-MAY-2001 US
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31-MOV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
1.1263
1.1263
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43.00
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AX025011
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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 17-JUL-2003
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1263)
Carroll,M.W. and Myers,K.A.
                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                              Carroll,M.O., Harrop,R.O. and Kingsman,S.O. MHC class II peptide epitope of 5t4 antigen Patent: WO 03068815-A 1 21-AUG-2003; Oxford Biomedica (UK) Limited (GB) Location/Qualifiers
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Matches:
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Patent: JP 2002530060-A 1 17-SEP-2002;
OXFORD BIOMEDICA LTD
OX Homo sapiens (human)
PN JP 2002530060-A/1
PD 17-SEP-2002

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Gaps:
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Sequence 1 from Patent WO03068B15.
AX821548
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JP 2002530060-A/1.
Homo sapiens (human)
Homo sapiens
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Polypeptide.
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AX821548
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PAT 15-SEP-2000

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Search completed: May 27, 2006, 19:35:23 Job time : 3359.6 secs
   PAT 08-JUN-2001
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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St4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                             Xingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W.,
Ellard, F.M. and Myers, K.A.
Antibodies
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synthetic construct
other sequences; artificial sequences.
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AX316086.1 GI:17899278
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AX316086
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1051 recerdenancererrandrecree 1077

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Add97513 Feline 57
Add97452 DNA encod
Add5661 Novel can
Abb60734 Human can
Abb60734 Human can
Abb7633 Lung canc
Abb80503 Ovarian c
Add86198 Human LRR
Adv3949 Human LRR
Adv3949 Human LRR
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Adv3611 Pupoctic
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Adv3615 Human mus
Adv36162 Human mus
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Adv36169 Human mus
Adv48968 Plant ful
Adv48968 Plant ful
Adv48968 Plant ful
Adv48968 Plant ful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse 5T4 tumour-associated antigen gene.
       ADB97513
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ADQ56661
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ADI26162
ADL30833
                                                                                                                                                                                                                                                                                                                             ADJ27669
AAX41515
                                                                                  AAD56198
ABV99349
AAA27058
AAF89736
ABK87174
AAD56199
                                                                                                                                                                                                                                                                                                            AAL34954
ABX57942
                                                                                                                                                                                                                 ADN03961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAA27059 standard; DNA; 1281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-00025303.
99GB-00001739.
99GB-00017995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
WO200029428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2000.
AAA27059;
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 0 0 0 0 0 0
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-MODEL=frame+_p2n.model -DEV=xlh
-G=Abss/ABSWRBB spool/US10774176/runat_26052006_091441_24976/app_query.fasta_1
-G=Abss/ABSSWRB spool/US10774176/runat_26052006_091441_24976/app_query.fasta_1
-DB=N Geneseq -QFWT=fastap -SUFFIX=p2n.rng -MINMÄTCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORN=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02h
-USER=USI0774176_@CGN_1 1_2389_@runat_26052006_091441_24976 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBILOCE=100 -LOONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adi26160 Human cDN
Adi26158 Human cDN
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                                                                   (without alignments)
249.339 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                           May 27, 2006, 09:34:35 ; Search time 377.5 Seconds
                                                                                                                                                                                                 10489840
        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                          nucleic search, using frame plus p2n model
                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
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ADI26160
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Maximum DB seq length: 2000000000
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Database

Score

Result . 8 4 4 6 4 6 4 6 6 6

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Searched:

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Sequence:

protein -

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Scoring table:

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The TAA : The TAA ST4 is a glycoptocen which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastrasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been inculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                   Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                   The present sequence encodes the mouse 5T4 tumour-associated antigen
                                                                                                                                                                                                3xample 2; Page 78; 79pp; English.
                                                                       4PI; 2000-387735/33.
                       Carroll MW,
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Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;

1281 9 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 100.04 31 46.00 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: .. 0

US-10-774-176-22 (1-9) x AAA27059 (1-1281)

682 rircririccigecressarriacia 708 1 PheLeuPheLeuProArgAspLeuLeu 9 셤

ADI26160 standard; cDNA; 2557 RESULT

BP.

ADI26160;

(first entry) 22-APR-2004 Human cDNA encoding protein that promotes STAT6 activation #63.

STAT6; immunogen; STAT6 activation; allergy; inflammation; stat6; immunogen; STAT6 activation; allergy; inflammation; ancer; autoimmune disease; diabetee; hyperlipidaemia; infection; cancer; Thl hyperactive disease; xheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

Homo sapiens

WO2003104277-A2

18-DEC-2003

05-JUN-2003; 2003WO-JP007123

05-JUN-2002;

2002US-0385912P. 2002UP-00377326. 2002US-0436467P. 2003UP-00137505. 06-JUN-2002; 26-DEC-2002; 27-DEC-2002; 15-MAY-2003; 16-MAY-2003; 

ă (ASAH ) ASAHI KASEI

```
The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression a activity of the expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening composition. Compositions, antibodies and antisense molecules are useful cort the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, objective diseases associated with STAT6 activation and/or prevention of thyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of thyperlipidaemia, infections diseases and cancers. Compositions are useful for treating diseases. Compositions are also useful in rheumatoid arthritis, osteoarthitis, softenic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 cativation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                          l transducer and activator of transcription 6 activation
purified protein, for diagnosing and treating disease
i with activation/inhibition of transcription factor e.g.
  Muramatsu S, Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2557 BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;
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Mismatches:
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Matches:
                                                                                                                                                                                                                           Claim 4; SEQ ID NO 125; 1368pp; English
Honda G,
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46.00
100.0%
100.0%
  Matsuda A,
                                                                                                            New signal transducer
                                                                                                                                                                               diabetes and cancer.
                                           WPI; 2004-122214/12
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                                                                   P-PSDB; ADI26161.
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Sugahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                          associated
                                                                                                                                      promoting
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1237 TTTCTTTTCTGCCTCGGGACTTACTA 1263 x ADI26160 (1-2557) 1 PheLeuPheLeuProArgAspLeuLeu ADI26158 standard; cDNA; 2557 BP 22-APR-2004 (first entry) US-10-774-176-22 (1-9) ADI26158; ò g

STATÉ; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS. gene; human; signal transducer and activator of transcription Human cDNA encoding protein that promotes STAT6 activation #62. 

9

WO2003104277-A2

18-DEC-2003.

```
The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or itse spitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation such as composition. Compositions, antibodies and antisense molecules are useful for expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for treating diseases, inflammation, autoimmune diseases diabetes, allergic diseases, inflammation, autoimmune diseases diabetes, byperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arbitis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6. The prosein sequence represents a ccivaty. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive human rows are not inhibition of STAT6. The present sequence represents a professive when a professive and prover and the present sequence represents a professive when a professive and prover and the present sequence represents a professive and prover and a professive and prover and a professive and prover a prover and a professive and prover a professive and prover a professive and prover a professive and prover and a professive and prover and a professive and a professive and a professive and a prof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal transducer and activator of transcription 6 activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purified protein, for diagnosing and treating disease with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activation or inhibition of STAT6. The present Bequeics retronhuman cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                  Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                  Muramatsu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 123; 1368pp; English.
                                                                                                                                                                                                                                                                                                                                                  Honda G,
                                                                                                             06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002US-0337326.
27-DEC-2002; 2002US-0436467P.
15-MAY-2003; 2003US-037509.
16-MAY-2003; 2003US-0470836P.
                           05-JUN-2003; 2003WO-JP007123
                                                                                                                                                                                                                                                                                                                                                  Sugahara T, Matsuda A,
                                                                                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KK
                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 2004-122214/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ADI26159
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                                                                                     05-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoting
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BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;

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2557
9
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0
0
       Length:
Matches:
Conservative:
Mismatches:
                                        Indels:
       67.9
46.00
100.0%
100.0%
                                Best Local Similarity:
                        Percent Similarity:
Alignment Scores:
Pred. No.:
                                         Query Match:
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US-10-774-176-22 (1-9) x ADI26158 (1-2557)

## 1237 TTTCTTTCCTGCCTCGGGACTTACTA 1263 PheLeuPheLeuProArgAspLeuLeu

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ABK87175 standard; cDNA; 1260 BP ABK87175
ID ABK8
XX
AC ABK8
XX
XX
DT 07-C
XX
XX
XX
XX
XX
XX
XX
XX
XX

cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4. 07-OCT-2002 (first entry)

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Feline; cat; oncofoetal leucine-rich glycoprotein; 574; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
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Felis sp.

Location/Qualifiers 1. .1260 /\*tag= a

/product= "5T4 protein"

WO200238612-A2

16-MAY-2002

13-NOV-2001; 2001WO-GB005004

13-NOV-2000; 2000WO-GB004317.

(OXFO-) OXFORD BIOMEDICA UK LTD.

Carroll M; Drury N, Myers K,

WPI; 2002-557449/59 P-PSDB; AAU98694

encoding the and/or Novel canine or feline 5T4 polypeptide and polynucleotides polypeptide, useful in preparation of vaccine for treating preventing cancer in a subject, preferably a dog or cat.

Claim 4; Page 68; 68pp; English

The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 5T4, and the concofoetal leucine-rich glycoproteins known as 5T4, and the concofoetal leucine-rich glycoproteins known as 5T4, and the polymucleotide sequences encoding them. The 5T4 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutrical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, considerably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals resequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific concentrated and localisation of 5T4 in extracts of plasma, urine, consument and localisation of 5T4 in extracts of plasma, urine, consument and localisation for isolating focus calls from maternal blood. The contein are useful for isolating focus calls from maternal blood. The content are useful for isolating focus calls from maternal blood. isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es) The present sequence encodes feline 5T4 protein

Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

Length:
Matches:
Conservative:
Mismatches: Indels: 43.00 100.0% 88.9% 93.5% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-10-774-176-22 (1-9) x ABK87175 (1-1260)

RESULT 5 ADB97513

ADB97513 standard; DNA; 1260

ADB97513

661 TTCCTCTTGCCTCGGGACGTACTG 687

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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope string the 5T4 epitope; a uncleic acid sequence encoding the 5T4 epitope or a polyepitope; a uncleic acid ceptope; a vector system capable of delivering the 5T4 epitope nucleic epitope; a vector system capable of delivering the 5T4 epitope nucleic comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising the above; a method for treating and/or preventing a disease comprising the presence of the 5T4 epitope and/its encoding nucleic acid; a method comprising the 5T4 epitope and/its encoding nucleic acid; a method comprising the 5T4 epitope has cytostatic acid; it has specifically recognising the 5T4 epitope in conjunction with an MHC class comprising the 5T4 epitope has cytostatic acid; it has vaccine system or cell is useful in the prevention and/or treatment of a disease, comprising the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone created and the manifacture of a medicament for treating and/or cone con the antifacture of a medicament for treating and/or cone con the cone con the contract of the first encoding acid in the felline con contracting and sease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New major histocompatibility complex class I peptide epitopes from human 5T4 tumor-associated antigen, useful for preventing and/or treating a disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing a disease. This polynucleotide sequence represents the feline 574 antigen coding DNA of the invention.
                                                                                  Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                     /product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redchenko I;
                                                                                                                                                                                                                          Location/Qualifiers
1. .1260
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 67; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002; 2002GB-00003419.
                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2003; 2003WO-GB000670.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll M, Kingsman S,
                                           Feline ST4 antigen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-637141/60.
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                                                                                                                                                                                                                                                                                                                                      WO2003068816-A1
                                                                                                                                                                              Unidentified
04-DEC-2003
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Length: Matches: Conservative: Mismatches: Indels: 43.00 100.0% 88.9% 93.5% Percent Similarity: Alignment Scores: Pred. No.: Score:

US-10-774-176-22 (1-9) x ADB97513 (1-1260)

Best Local Similarity: Query Match: DB:

Gaps:

PheLeuPheLeuProArgAspLeuLeu 9

ADQ56661 RESULT

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The invention relates to a Major Histocompatibility Complex (MHC) class clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the prosession of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA
                                                                                                                                               gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                    /product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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Mismatches:
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                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 49; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kingsman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for the feline 5T4 protein
                                                                                                                 DNA encoding feline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002; 2002GB-00003420.
                          ADB97452 standard; DNA; 1260
                                                                                                                                                                                                                                                                                                                                                               13-FEB-2003; 2003WO-GB000618.
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93.5%
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P-PSDB; ADB97455.
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                                                                                                                                                                                            Unidentified
                                                                                     04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                 21-AUG-2003.
                                                         ADB97452;
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               ADB97452
RESULT
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Gaps:

Query Match:

ВР

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Novel canine microarray-related DNA sequence SeqID7963
                                                                          05-MAY-2003; 2003WO-US013853.
                                                                                  33-MAY-2002; 2002US-0377240P
ADQ56661 standard; DNA; 655
               (first entry)
                                                                                         (GENE-) GENE LOGIC INC. (PFIZ ) PFIZER PROD INC.
                                                                                                      Diggans JC, Porter M,
                                                                                                             WPI; 2004-561890/54.
                                                  Canis familiaris
                                                          402004063324-A2
                                                                                                                                living organism
               21-OCT-2004
                                                                  29-JUL-2004
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This invention is related to a novel isolated canine nucleic acid
sequences and the construction of canine microarrays containing a
significant portion of the canine genome. The isolated canine nucleic
acid sequences of the invention may be useful for assessing the
coxicity assays. The invention is therefore useful for assessing the
impact, including toxicity, of a compound, pharmaceutical agent or
environmental pollutant on a call or living organism. The methods are
useful for detecting genes that are up- or down-regulated in canines in
disease state. The sequences are useful as diagnostic agents or markers
to detect a callular response in a sample individually or as part of a
gene expression profile. It is also useful as a target for agents that
condulate gene expression or activity. The database is useful for
modulate gene expression or activity. The database is useful for
producing electronic Northerns that allow the user to determine the cell
type or tissue in which a given gene is expressed and to allow

containation of the abundance or expression level of a given gene in a
particular tissue or cell. The methods are useful for determining the
confermination of that a compound or test agent will induce various specific
likelihood that a compound or test agent will induce various specific
confisease, protein adduct formation or hebattis), those of the kidney,
chart, brain or testes, or other pathologies associated with at least one
cof the toxins. The methods are also useful for predicting or elucidating
the potential cellular pathways influenced, induced or modulated by the
compared to the profile induced by a known toxin. The present sequence is
compared to the profile induced by a known toxin. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a o
canine microarray; drug screening; toxicity assay;
environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 174 A; 89 C; 131 G; 253 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of a canine microarray of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 7963; 41pp; English.
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Conservative: Mismatches: Length: Matches:

41.00 88.9% 88.9%

Best Local Similarity:

Percent Similarity:

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The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypucleotide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reinhard C, Randazzo F;
                                                                                                                                                                                                                                                                                                                                                        gene mapping; tissue profiling; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sudduth-Klinger J, Reinharu J, ... Sudduth-Klinger J, Rot D, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 701; 883pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 544 BP; 189 A; 115 C; 126 G; 114 T; 0 U; 0 Other;
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8 0 0 0 0
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                                                                                                                                                                                                                                                                                                                           Human cancer related polynucleotide SEQ ID NO 701.
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Matches:
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Mismatches:
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US-10-774-176-22 (1-9) x ADQ56661 (1-655)
                                                                                                                                                                                                                                                                                                                                                                           Human; cytostatic; gene expression;
gene therapy; cancer; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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                                                                                                                                                                                    BP
                                                                                                                                                                                    ABN60734 standard; cDNA; 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2000; 2000US-0226326P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and inhibiting tumor growth.
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100.08
87.08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-241905/29
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2002
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                                                                                                                                                                                                                                    ABN60734;
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Query Match:
                                                                                                                                                                 ABN60734/c
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dene sednence;

Gene, ds; breast cancer; breast cancer-associated gene sec drug development; pharmacogenetics; biosensor development

Breast cancer-associated gene sequence 29

14-NOV-2002 (first entry)

ABT07721;

ABT07721 standard; DNA; 927 BP

RESULT 10

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The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which are differentially expressed in colon cancer cells. The invention also cardetess to vectors and host cells comprising a differentially expressed polynucleotide of the invention; a method for detecting a cancercus cell by detection of a gene product of the polynucleotides; a method for inhibiting a gene product of the polynucleotides; a method of treating an individual with cancer by administration of a medulator of a gene product of the polynucleotides; and an isolated antibody that specifically binds to a polyneptide encoded by one of the 9672 polynucleotides. The polynucleotides, polypeptide on a tibodies, and methods are useful for the detection of cancerous cells; for the diagnosis, prognosis and management of cancer, for the identification of agents that modulate the phenotype of cancerous cells; for the identification of cancer, especially colon cancer and metastacized colon cancer, but also breast or pancratic cancer. The polynucleotides are also useful as a source of probes or primers for use in diagnostic methods. The differentially expressed polynucleotides or their encoded protein can be accounted by the present and properties or expressed in colon cancer. The polynucleotides or represents a specifically claimed polynucleotide which is differentially expressed to modulate primary immune responses for the prevention or treatment of cancer. The present sequence represents a specifically claimed polynucleotide which is differentially context on the sequence data for this patent did on the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotides, which are differentially expressed in colon cancer cell, useful for treating cancer, e.g. colon cancer, breast
                                                                                                                                                                                                         Differential expression, diagnosis, therapy, drug screening, cancer, neoplasm, colon tumor, breast tumor, pancreas tumor, cytostatic, vaccine,
                                                                                                                                                            Human colon cancer differentially expressed polynucleotide, SEQ ID:5088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 563 BP; 192 A; 119 C; 135 G; 117 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escobedo J, Garcia PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 5088; 97pp; English.
                     ACL58953 standard; cDNA; 563 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer, or pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-2004; 2004WO-US015421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2003; 2003US-0475872P
                                                                                                               24-MAR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Randazzo F, Moler E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-075421/08
                                                                                                                                                                                                                                                                                                                                                #02005000087-A2
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                             36-JAN-2005
                                                                    ACL58953;
ACL58953/c
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24-JAN-2001; 2001US-0263965P.
02-FEB-2001; 2001US-0265928P.
09-APR-2001; 2001US-028269P.
09-APR-2001; 2001US-0282698P.
04-MAY-2001; 2001US-0288590P.
29-MAY-2001; 2001US-0294443P.

24-JAN-2002; 2002WO-US002242

WO200259377-A2 Unidentified.

01-AUG-2002

(EOSB-) EOS BIOTECHNOLOGY INC

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Afar

Gish KC,

Mack DH,

563 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

40.00 100.08 100.08 87.08

Percent Similarity: Best Local Similarity:

Query Match:

US-10-774-176-22 (1-9) x ACL58953 (1-563)

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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a blological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosts or preast cancer calls. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
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N-PSDB; ABJ05564.
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Best Local Similarity:
Query Match:
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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                        Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      Lung cancer-associated polynucleotide #197.
                                    US-10-774-176-22 (1-9) x ABT07721 (1-927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Page 336; 453pp; English.
                                                                                                                                                      ABX76333 standard; DNA; 927 BP
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09-NOV-2001, 2001US-0339245P.
13-NOV-2001, 2001US-033666F9.
29-NOV-2001, 2001US-03737370P.
12-APR-2002, 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002; 2002WO-US012476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0284770P
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-093161/08.
P-PSDB; ABU56604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aziz N, Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO200286443-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                  02-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002
                                                                                                                                                                                            ABX76333;
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The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polymucleotide that selectively
biological sample from the patient with a polymucleotide that selectively
chybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
chicken and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
concers, monitoring and early detecting patients for post-operative
committeering tumour prognosis, early detection of pre-cancerous lesions,
and as vaccines. This sequence corresponds to one of the nucleic acids
used for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                   cytostatic; gene therapy, vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
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                                                                                                                                      1 PheleuPheleuProArgAspleuLeu 9
                                                                                                       x ABX76333 (1-927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2001; 2001US-0299234P.
27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-0317544P.
13-NOV-2001; 2001US-0350666P.
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P-PSDB; ADB80504.
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                                               Best Local Similarity:
                                                                                                          US-10-774-176-22 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2002102235-A2
                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                            Query Match:
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Homo sapiens.
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Pred. No.:
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                                                                                                                                                                                                                                                           Query Match:
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                 Human; differential expression; cancer; anglogenic disorder; fibroctic disorder; psortiasis; isofonemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; defection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                 Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
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Wilson KE, Zlotnik A;
       Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                   US-10-774-176-22 (1-9) x ADB80503 (1-927)
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Murray R, Watson SR,
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2002US-0359077P.
2002US-0368809P.
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2002US-0347211P.
2002US-0347349P.
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2001US-0334393P.
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2002US-0372246P.
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2002US-0396839P.
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                                                                                                                                                                          ADN38723 standard; cDNA; 927
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                                                              Best Local Similarity:
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                                                     Percent Similarity:
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29-NOV-2001;
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Mack DH,
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                                                                                                                                                                                            ADN38723;
                                                                      Query Match:
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; or polypeptides and methods are useful for diagnosing, prognosing and treating antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a nucleic acid sequence of the invention.
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Mismatches:
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Claim 8; SEQ ID NO 41; 1385pp; English.
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human LRRCAPS related DNA #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-421410/39.
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Best Local Similarity:
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antinfertility; carebroprotective; gene therapy; NOVX; NOV; Fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; anglogenesis; ds.
                                                                                                                                                                                                 Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Example 5; Page 74-75; 99pp; English
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2001US-0275579P.
2001US-0275601P.
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2001US-0277321P.
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09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
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16-MAR-2001;
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2001US - 0278152P

2001US - 02788194P

2001US - 0279999F

2001US - 0279999F

2001US - 02799995P

2001US - 02799995P

2001US - 0280802P

2001US - 0280802P

2001US - 0280802P

2001US - 0280806P

2001US - 0281194P

2001US - 0281644P

2001US - 0281648P

2001US - 0291190P

2001US - 0291190P
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2001US - 0325681P
2001US - 0335301P
2001US - 0332172P
2001US - 0332271P
2001US - 0332271P
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2001US-033272P.
2001US-0332094P.
2001US-0337426P.
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2001US-0318770P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
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02-APR-2001;
04-APR-2001;
13-APR-2001;
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16-MAY-2001; 2
16-MAY-2001; 2
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31-MAY-2001; 2
31-MAY-2001; 2
18-JUN-2001; 2
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19-JUN-2001;
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31-OCT-2001;
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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Benean CEA, Burgess CE, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF; Zhong M;

WPI; 2002-732824/79. P-PSDB; ABP70071.

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.

Claim 16; Page 114-115; 619pp; English.

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99555 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder.

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The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obsestly, infectious disease, anorexia, cancerassociated cachexia, cancer, neurodegenerative disease, Alzheimer's disease, Parkinson's disease, immune disorders, heematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, ALDS, dyslipidemia, metabolic disturbances associated with obestly, metabolic syndrome X or wasting disorders associated with obselvy, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of therapeutic or diagnostic methods
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

Alignment scores: Pred. No.: Score:	423 40.00	Length: Matches:	1156
ercent Similarity:	100.04	Conservative:	7
est Local Similarity:	77.8	Mismatches:	0
Query Match:	87.0	Indels:	0
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US-10-774-176-22 (1-9) x ABV99349 (1-1156)	x ABV99349	(1-1156)	

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AC10235 Genomic s
AC10233 Sequence
AX821533 Sequence
AX821533 Sequence
AX821533 Sequence
AC06701 Rattus no
BC08701 Rattus no
AC10675 Homo sapi
AC132494 Rattus no
BV033626 S212P6412
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AC132494 Homo sapi
AC133494 Oryza sat
AC03244 Homo sapi
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AC144738 Oryza sat
AC142599 Homo sapi
AC140459 Mus muscu
AC150611 Callithri
AC150298 Callithri
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Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafiham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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BX932209
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AP008211_044
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BD249732 Polypepti
AX025012 Sequence
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257.039 Million cell updates/sec
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                                                                                                                             ; Search time 3358.6 Seconds
                      GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                             using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Database

VRT 02-FEB-2004

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Score

Result 80. 4 4 6 4 6 4 6

PAT 15-SEP-2000

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                             Polypeptide
Patent: WO 0029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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Mismatches:
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Sequence 2 from Patent EP1160323.
AX316087
AX316087.1 GI:17899279
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Sequence 2 from Patent W00029428.
AX025012
AX025012.1 GI:10184933
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EcoRI-NotI cut cDNA was then ligated into the vector. Vector:
pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia
coli DH10B.
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Carroll, M.W. and Myers, K.A.
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MILES WILLIAM CARROLL, KEVIN ALAN MYERS
C12X15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065, C12X15/00,

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JP 2002530060-A/2.
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Mus musculus
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PAT 14-DEC-2001

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating dectal Garzinoma. 5 month old virgin mouse." /clone_lib="NOI_CGAP_Mam6" /lab_host="DH10B"
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
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/db xref="CDD:COG4886"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Vector: pCMV-SPORT6"
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/protein id="AAH58198.1"
/db_xref="G1:34849574"
/db_xref="GeneID:21983"
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                                                                                                                                                                                                                                    /mol_type="mRNA"/strain="FVB/N"
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                             BC058198 21-OCT-2003
Mus musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145
IMAGE:5353871), complete cds.
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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  Conservative:
Mismatches:
Indels:
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PAT 14-JAN-2004

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PADFLASGSAQPPPAERCPAACECSEAARTVKCVNRNLLEVPADLPPYVRNLFLTGNQ
MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
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                         Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Murinae; Mus.
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Patent: WO 03104277-A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
                                                                                                                                           Sugahara, T., Matsuda, A., Honda, G., Muramatsu, S. and Ishizawa, K.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Patent: WO 03104277-A 123 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
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Sequence 125 from Patent WOO3104277.
AX961914
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/db_xref="taxon:10090"
5567. 1836
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/mol_typea"unassigned DNA"
/db_xref="taxon:10090"
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    /organism="Mus musculus"

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/db_xref="GI:40881325"
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                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                    TITLE
JOURNAL
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TRLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KYLHNSTLERWGGLAYKVFLDNNPWYCDCYNADMYAWLKETRVVPDKRRLTCRFPEK
MRNGLLDLNSSDLDCDAVLPGSLQTSYVFLG1LVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYRINADPRLYNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus 5T4 oncofetal trophoblast glycoprotein gene. AJ012160
vfagsnasvsapspleelilnhivppedorongsfegmvafegmvaalrsglalrgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 gene; 574 oncofetal trophoblast glycoprotein.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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product="5T4 oncofetal trophoblast glycoprotein"
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Conservative:
Mismatches:
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                                                                                                                                                                            Length:
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/organism="Mus musculus"
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clone_lib="Lambda Dash"
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/strain="129/Sv"
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/bound_moiety="Sp1"
3114. .3119 ...en1
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/bound_moiety="Sp1"
3124. .5779
/gene="5T4"
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AJ012160.1 GI:3805948
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/gene="5T4"
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/gene="5T4"
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3152. .3450
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3451. .5779
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/coduci="sealca"
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ataxia 1, autosomal dominant, ataxin 1)"
/produci="spinocerebellar ataxin 1)"
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VTSSPQFAAVPHTFVTTALPKSENFNPEALVTQAAYPAMVQAQIHLPVVQSVASPAAA
PPTLPPYFMKGSIIQLANGELKKVEDLKTEDFIQSAEISNDLKIDSSTVERIEDSHSP
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I SLTILKNLKNGSVKKGQPVDPASVLLKHSKADGLAGSRHRYAEQENG INGGSAQMLSE
NGELKFPEKMGLPAAPFLTKI EPSKPAATRKRRWSAPESRKLEKSEDEPPLTLPKPSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all
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/note="match: ESTs: AA779236 AA909468 AI052569 AI052586
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AL031120.1:17022. .152296,
complement(AL034375.23:32790. .86336),71405. .100765)
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complement (ALO34375.23:33172 . .33322),
complement (ALO34375.23:32790 . .32959),71405 . .73481,
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/note="match: proteins: P54253 P54254 Q63540"
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complement (AL137003.12:79221. .79259),
complement (AL137003.12:78411. .78525),
AL031120.1:17022. .17147, AL031120.1:89016.
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join(71565. .73481,93016. .93546)
/gene="SCA1"
    see
                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
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/db_xref="RZPD:RPCIP704D16467"
/db_xref="taxon:9606"
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/locus tag="RP3-467D16.1-001"
Pieter de Jong. For further details s
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
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/clone="RP3-467D16"
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                                                                                                                                         -- Genome Center
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                                                                                                                                                                                                                                                                                                                              Contact: vega@sanger.ac.uk
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                                                                                                                                                                                                                                    Center code: SC
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On Jan 25, 1998 this sequence version replaced gi:2632073.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw.; SWISSRROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/hrk6
RP3-467D16 is from the library RPCI-3 constructed by the group of
                                                                       /db_xref="InterPro::PR003591"
/db_xref="Md1:1341264"
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/tb_xref="UnilProtKBTR"
/t
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MRNRGLLDLNSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
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olivopontocerebellar; oxidoreductase; SCA1; spinocerebellar.
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Human DNA sequence from clone RP3-467D16 on chromosome 6p22.3-24.1

Contains the 5' end of the SCAl gene for spinocerebellar ataxia 1

(olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) with a poly-glutamine (CAG repeat) polymorphism and the 3' part of the GMPR gene for GMP reductase, Guanosine 5'-monophosphate
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="5T4 oncofetal trophoblast glycoprotein"
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Matches:
Conservative:
Mismatches:
Indels:
                                 xref="InterPro:IPR001611"
xref="InterPro:IPR003591"
xref="InterPro:IPR000483"
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1 (bases 1 to 143583)
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3866. .5056
/gene="5T4"
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5759. .5764
/gene="5T4"
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Homo sapiens
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Best Local Similarity:
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DB:
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HS467D16/c
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Direct Summission

Submitted (15-JUL-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dasses I to 14875).

Hawkins, T.L., Reeve, M. P., Birren, B.W., Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P., Barna, N., Chang, A., Christoffersen, A., Cooke, P., Daly, M.J., Devan, K., Devar, K., Forrest, C., Gage, D., Geraigery, K., Guitau, G., Hagos, B., Huang, J., Nacotot, L., Kirby, A., Lane, M., MacKenzie, J., Marquis, N., McDermott, J., Molla, M., Moloney, N., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A., Peterson, K., Rollins, G., Spencer, J., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L., Traish, A., Wilmer, F., Zemtseva, I. and Zody, M. Direct Submission

Submitted (31-JUL-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 31, 1997 this sequence version replaced gi:2286044.

The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Research Genetics/Cal Tech CITB978SK-B (plates 1-1949) \pi
                                       "I (bases I to 148750)

"Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W.,

Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P.,

Barna, M., Chang, A., Cooke, P., Daly, M.J., Devon, K., Dewar, K.,

Forrest, C., Gage, D., Geraigery, K., Guitau, G., Hagos, B., Huang, J.,

McDermott, J., Lane, M., Mcdoney, M., Marchan, A.,

Majlor, J., O'Connor, T., Olotu, A., Peterson, K., Rollins, G.,

Spencer, J., Stliwell, J., Stone, C., Strickland, C., Sydney, K.,

Traish, A., Wilmer, F., Zemtseva, I. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997) thttp://ftp.genome.washington.edu/RM/RepeatMasker.html. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(CA)n"
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/rpt_family="AluJb"
complement (7564, .7655)
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/rpt family="WER20"
complement (12108. 12218)
/rpt_family=" (TA) n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (1035. .1336)
/rpt family="Alusx"
complement (1714. .1779)
/rpt family="LINE2"
1797. .1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt. family="POLY_A"
8511 . 8869
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complement (9175. 9377)
/rpt. family="Aludy"
complement (10633. .10720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt family="AT rich"
complement (5988. .604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="(CATA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="FRAM"
complement(3652. .
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGGCTCPGDVAKAFGAGADFVMLGGNFSGHTECAGEVFERNGRKLKLFYGMSSTTAMN
KHAGGVAEYRASEGKTVEVPYKGDVENTILDILGGLRSTCTYVGAAKLKELSRRATFI
RVTQQHNTVFS"
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complement(1140400. .114082),complement(109254. .109413),

complement(104689. .104869))
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 148750)
Hawkins, T.L., Reeve, M.P., Birren, B.W., Fasman, K.H. and Lander, E.S.
AI882230 AU186122 AW045102 AW260712 AW612517 BB648048
BB666403 BB846770 BE087001 BE485829 BF571391 BF670717
BF697040 BF699359 BF699442 BG253572 BG537309 BI036991
                                                                        match: cDNAs: BC010948 BC010948.1 X79204 X79204.1
X91619.1"
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                     /gene="GMPR"
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                                                                                                                                                            gene="GMPR"
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AC002326/c
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VERSION
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13614. 14244
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Complement (19523. . 19825)
/ Typt family="AluSx"

Complement (19986. . 20036)
/ Typ family="(AluSx"

Complement (21348. . 21649)
/ Typt family="(AluSy"
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30397. .30442
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complement (30765. .30814)
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complement (16287. .16333)

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/rpt_family="AT_rich"

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17180 . 17442
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1743. 17481
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complement(17737. 17877)
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                                                                                                                                                    /rpt family="MER7B"
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4969. .15308
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complement (28223. .28436)
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ement(2010)
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/rpt_family="AluSq"
19192. .19370
/rpt_family="MER5B"
                                                                                                                                                                                                                                                                                                    . .15730
family="MER63B"
                                                                                                                                                                                                                       rpt family="MER7B"
5312. .15411
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           rpt_family="MIR" 3172. .13433
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ROD 21-JUN-2005
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
I (bases I to 167046).
Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
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Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
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Matches:
Conservative:
Mismatches:
Indels:
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/rpt family="(CAAA)n"
complement (37750. .38052)
/rpt family="Aludb"
complement (38309. .38411)
/rpt family="(GAAAA)n"
/rpt family="(GAAAA)n"
/rpt family="Aludo"
/rpt_family="(GAAA)n"
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complement(31291. .31811)
/rpt_family="LIPB3"
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                                                                                           /rpt_family="AluJb"
3227_...32384
/rpt_family="MIR"
complement (33427...3368)
/rpt_family="MLT1A2"
complement (36830...37191)
/rpt_family="THE1C"
complement (37777...37748)
                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
complement(40008..40033)
/rpt_family="AT_rich"
complement(42494..42754)
/rpt_family="AluSx"
complement(43281..43318)
/rpt_family="(CA)n"
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complement (43880. .44181)
/rpt_family="Alusx"
44713. .44831
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46081. .46372
/rpt_family="AluY"
complement(47354. .47468)
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45202. .45504
/rpt_family="AluSx"
45540. .45609
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AC158516 AC117768
AC158516.2 GI:63025421
HTG.
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39356. .39391
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Pred. No.:
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PAT 10-DEC-2003
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
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                                                               'note="Sequence derived from one plasmid subclone."
                     /note="Unresolved simple sequence repeat."
142336. .142347
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Polypeptide
Polypeptide
Patent: WO 0238612-A 3 16-MAY-2002;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9687"
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Sequence 1 from Patent WO03068816.
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AX467373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality ==10; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest. This finishing standard has alightly changed from the previous thuman standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CSTBL/6J mouse spleen and/or brain genomic Dw. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                            Parkway, St. Louis, MO 63108, USA 3 (bancer, 4444 Forest Park 3 (bases 1 to 167046)
                                                                                                                                                                                                                                                                                                                                                Louis,
                                                                                                                                                                                                  Submitted (04-MAY-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (best 1 to 167046)
Wilson,R.K.
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/note="Sequence derived from PCR product of genomic DNA"
31565..31779
/note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                   Submitted (21-JUN-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MMO 63108, USA.
On May 4, 2005 this sequence version replaced gi:61656412.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: M_BB0511A23
Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1.167046
| organism="Mus musculus"
| mol type="genomic DNA"
| db xref="taxon:10090"
| chromosome="9"
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16685. .16712
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                1 to 167046)
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                   Direct Submission
                                        Wilson, R.K.
                                                                                                                                                       Wilson, R.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF063939 aRNA linear ROD 01-
Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA,
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Matches:
Conservative:
Mismatches:
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Patent: WO 03068816-A 1 21-AUG-2003;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers

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AX821548
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                                                                                                                                                                       Direct Submission
Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 2333)
Ninkina, N.N. and Buchman, V.L.
Structure and expression of the rat 5T4 gene Unpublished
2 (bases 1 to 2333)
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Breast ca

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Abk87175 CDNA enco
Adb97513 Feline 5T
Adb97513 Feline 5T
Adb97425 DNA encod
Aa27059 Human 5T4
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Ad56199 Human LRR
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Ad18721 Cancer/an
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Ad894254 Human CDN
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Aas87174 DNA encod
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Adb80503 Ovarian c
Adn38723 Cancer/an
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Abk87175, cDNA, enco
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            ABX76333
ADB80503
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ABK87175
ADB97513
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ADI26158
ADI26158
ADF02237
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ABN60925
ADO35702
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 Hansen R;
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Adu11677 Solid tum
Aaa27060 Canine 5T
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249.339 Million cell updates/sec
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                                                                                     ; Search time 377.5 Seconds
              GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                             nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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geneseqn2003ds:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKRZp5661133 activity. The methods are useful for treating cancer, e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method comprising comparing an expression positie of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially
                     Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; gene therapy; expression profile; solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                                                  Sequence 246 BP; 77 A; 49 C; 59 G; 61 T; 0 U; 0 Other;
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                                                                 Claim 30; SEQ ID NO 47; 257pp; English
                                                                                                                                                                                                                                                                                                   1 AlaLeuIleGlyAlaIlePheLeuLeu
                                           inhibition of DKFZp566I133 activity.
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                                                                                                                                                                                                                                                                                                                                                                    ADU11677 standard; DNA; 475 BP
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23-JAN-2004; 2004US-0538246P.
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Immerman F, Dorner AJ;
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(STRA/) STRAHS A.
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unaupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the apopulation of patients who have the solid tumour, and where the case of patients has a first clinical outcome, and the first class of patients has a second clinical outcome, and the majority of the second class of patients has a second clinical outcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at tumour, (ii) at least once reference expression profile of the gene, (iii) a program capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the captession profile, and (iv) a processor capable of executing the expression profile, and (iv) a processor capable of executing the captession profile, and (iv) a processor capable of executing the expression levels of the gene in peripheral blood monourclear cells of patients who have the solid tumour correlate with clinical outcomes of the patients and ancleic acid or protein array comprising concentrated probes for solid tumour prognosis genes where each of the patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as solid tumours. This sequence tepresents a solid tumours prognosis gene of the method, system, and array are useful for prognosing and treating cutcome, and the second class of patients as a second classes of the invention. Note: The sequence tepresents a solid tumours: This sequence represents a solid tumours. This sequence represents a solid tumours prognosis; gene of the invention. Note: The sequence data for this patent did not form at the invention. Note: The sequence data for this patent did not form at the invention will be second class of patients has a second class of the printed specification, but was obtained in electronic format
expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine; TAA; tumour-associated antigen; anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
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/product= "5T4 antigen"
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response useful in vaccinating against and in treating tumors
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99GB-00017995.
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The present sequence encodes the canine 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in

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tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the human or murine 5T4 gene sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown
carcinomas but has a highly restricted expression pattern in normal adult
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09-APR-2001; 2001US-00829472.
09-APR-2001; 2001US-02869BP.
04-MAY-2001; 2001US-028459P.
29-MAY-2001; 2001US-0294443P.
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in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07693 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
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; 2001US-0290492P.
; 2001US-0339245P.
; 2001US-0350666P.
; 2001US-0334370P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2002; 2002WO-US012476
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Best Local Similarity:
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P-PSDB; ABU56604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
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DB:
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in creased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful contracting lung cancer, such as small cell lung cancer, non-small cell contracting lung cancer, cher benign or precancerous leations, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences the statest sequences compounds that modulate lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy, vaccine, ovarian cancer; diagnosis, post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                          U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          927
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Matches:
Conservative:
Mismatches:
Indels:
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27-ANG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-031544P.
13-NOV-2001; 2001US-0350666F.
12-APR-2002; 2002US-0372246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB80503;
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DB:
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Homo sapiens
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The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, electing mide of therapy, detection of pre-cancerous lesions, determining tumour prognosis, early detection of pre-cancerous lesions,
                       Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease;
                                                                                                                                                                                                                                                as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retinal neovascularistaton syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differential expression; cancer; angiogenic disorder;
                                                                                                                                                                                                                                                                                     Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Mismatches:
Indels:
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                                                                         Claim 10; Page 297; 332pp; English.
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20010S-03323493P.
20010S-0343394P.
20010S-0340376P.
20020S-0347311P.
2002US-0347349P.
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 P-PSDB; ADB80504
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10-JAN-2002;
08-FEB-2002;
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03-DEC-2001;
14-DEC-2001;
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Pred. No.:
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                            Hevezi PA;
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                                                                                                                                                                                                                                                                                                                                         Glynne R, Her
E, Zlotnik A;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                        Wilson KE,
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                                                                                                                                                                                                                                                                                                                                            Gish KC,
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                                                                                                                                                                                                                                                                                                                                         Ginsburg WM,
R, Watson SR,
29-MAR-2002; 2002US-0368809F.
04-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0370110P.
05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-039785P.
09-SEP-2002; 2002US-039485P.
                                                                                                                                                                                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                               Aziz N,
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Mack DH,
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us-10-774-176-21.p2n.rng

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2001US-0274101P.
2001US-0274194P.
2001US-0274281P.
2001US-0274322P.
2001US-0274849P.
2001US-0275235P.
2001US-0275578P.
2001US-0275578P.
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2001US-0277321P.
2001US-0277338P.
2001US-027731P.
2001US-027781P.
2001US-0278152P.
2001US-0278852P.
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2001US-0279344P.
2001US-027995P.
2001US-0280233P.
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2001US-0280802P.
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20010S-0283675P
20010S-0288064P
20010S-0288342P
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20010S-029109P
20010S-029109P
20010S-029488P
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2001US-0276994P.
2001US-0277239P.
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2001US-0318462P.
2001US-0318770P.
2001US-0325430P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0325681P.
2001US-0330380P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0335301P.
2001US-0332172P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0332271P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0333184P.
2001US-0333272P.
                                                               08-MAR-2002; 2002WO-US007288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-0337426P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP
              WO200272771-A2
                                                                                                                                                                13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
                                                                                                                                                                                                                   16-MAR-2001;
19-MAR-2001;
20-MAR-2001;
20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001;
28-MAR-2001;
30-MAR-2001;
30-MAR-2001;
02-APR-2001;
02-APR-2001;
02-APR-2001;
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26-MAR-2001;
27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2001;
14-NOV-2001;
                                                                                                                                       09-MAR-2001;
12-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2001;
                                                                                                                                                                                                                                                                                                         22-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-2001;
                                      19-SEP-2002
 The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antinfertility; carebroprotective; gene therapy; NOVX; NOV; Ertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma, dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                                                                                                                                                                                                                             Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                  ä
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                                                                                                                                                                 Plowman GD, Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763 GCCCTGATAGGCGCTATTTTCCTCCTG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaLeuileGlyAlailePheLeuLeu 9
                                                                                                                                                                                                                                                                                 Example 5; Page 74-75; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-774-176-21 (1-9) x AAD56198 (1-973)
                                                                                     22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                             21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV99349 standard; DNA; 1156
                                                                                                                                                                Belvin M, Schleithoff L, P
Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOV8a coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.9
40.00
100.0%
100.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-2003 (first entry
                                                                                                                                        (EXEL-) EXELIXIS INC
                                                                                                                                                                                                       WPI; 2003-421410/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
             WO2003035831-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                      01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV99349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
ò
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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases uch as metabolic disorders, diabetes, obesity, infectious diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases and aschma, AIDS, dyslipidemia, metabolic disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with obesity, metabolic syndrome X or wasting disorders associated with obesity, metabolic syndrome X or wasting coling sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods
Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                                  New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 114-115; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                               disorders, and asthma.
                                                                                                                                                                                            WPI; 2002-732824/79.
                                                                                                                                                                                                                        P-PSDB; ABP70071
                                                                                                                                            zhong M;
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other; Length: Matches: Conservative: Mismatches: Indels: 91.1 40.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.

Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal call; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.

Felis sp

Location/Qualifiers 1. .1260 /\*tag= a

979 GCCCTGATAGGCGCTATTTTCCTCTG 1005 1 AlaLeuIleGlyAlallePheLeuLeu 9 US-10-774-176-21 (1-9) x ABV99349 (1-1156)

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ABK87175 standard; cDNA; 1260 BP (first entry) 07-OCT-2002 ABK87175; RESULT 10 ABK87175 

The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell compositions in animals, proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracte plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for teeting foetal abnormalities, or to determine the sex of the foetus(es).

The present sequence encodes feline 574 protein Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat. Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other; Matches: Conservative: Mismatches: Indels: Length: /product= "5T4 protein" US-10-774-176-21 (1-9) x ABK87175 (1-1260) Claim 4; Page 68; 68pp; English. (OXFO-) OXFORD BIOMEDICA UK LTD Carroll M; 13-NOV-2000; 2000WO-GB004317. 13-NOV-2001; 2001WO-GB005004 40.00 100.0% 100.0% WPI; 2002-557449/59 P-PSDB; AAU98694. Drury N, Best Local Similarity: Percent Similarity: WO200238612-A2 Alignment Scores: Pred. No.: 16-MAY-2002 Myers K, Query Match: Score: 

ADB97513 standard; DNA; 1260 04-DEC-2003 (first entry) ADB97513; RESULT 11 ADB97513 

Feline 5T4 antigen DNA.

Major Histocompatibility Complex class I peptide epitope; MHC, 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.

Unidentified

gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.

DNA encoding feline 5T4 protein.

/product= "Feline 5T4 antigen protein"

WO2003068815-A2

21-AUG-2003

Location/Qualifiers 1. .1260 /\*tag= a

Unidentified

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major histocompatibility complex class I peptide epitopes from human tumor-associated antigen, useful for preventing and/or treating a
                                                                                                                                                                                                                                                                                                               Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                   /product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                   5T4 antigen coding DNA of the invention.
                                                                                             Redchenko I;
Location/Qualifiers
1. .1260
/*tag= a
                                                                                                                                                    Disclosure; Page 67; 73pp; English.
                                                                                (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                       disease, particularly cancer.
                                                       13-FEB-2003; 2003WO-GB000670
                                                                    13-FEB-2002; 2002GB-00003419
                                                                                             Kingsman S,
                                                                                                         WPI; 2003-637141/60
                                                                                                                P-PSDB; ADB97520
                              WO2003068816-A1
                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                             Carroll M,
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New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.

Kingsman S;

Carroll M, Harrop R, WPI; 2003-663795/62

P-PSDB; ADB97455

OXFO-) OXFORD BIOMEDICA UK LTD 13-FEB-2002; 2002GB-00003420. 13-FEB-2003; 2003WO-GB000618.

Disclosure; Page 49; 63pp; English.

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The invention relates to a Major Histocompatibility Complex (MHC) class of II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or mucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, TAA, tumour-associated antigen, anti-tumour, cytostatic,
immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1260
9
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1087 GCCCTGATAGGTGCCATTTTCTTACTG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuileGlyAlailePheLeuLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-774-176-21 (1-9) x ADB97452 (1-1260)
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40.00
100.0$
100.0$
100.0$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA27058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
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AKKEKEKEK
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

101 40.00 100.0% 100.0%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

1087 GCCCTGATAGGTGCCATTTTCTTACTG 1113

ADB97452 standard; DNA; 1260

RESULT 12 ADB97452 04-DEC-2003 (first entry)

ADB97452;

exaxex.

1 AlaLeulleGlyAlailePheLeuLeu 9

US-10-774-176-21 (1-9) x ADB97513 (1-1260)

/product= "5T4"

WO200136486-A2

/\*tag= a

```
Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune
                                                                                                                                                                                                                                                       Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0'U; 0 Other;
                                                                                                                                                                                                                                                                                            Example 2; Page 78; 79pp; English.
                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                      99GB-00001739.
                                                                                                                           98GB-00025303
                                                                                                  99WO-GB003859
                                                                                                                                                                                                      Carroll MW, Myers KA;
                                                                                                                                                                                                                              WPI; 2000-387735/33
                                                WO200029428-A2
                         Homo sapiens.
                                                                                                  18-NOV-1999;
                                                                                                                                       27-JAN-1999;
30-JUL-1999;
                                                                                                                           18-NOV-1998;
                                                                         25-MAY-2000
```

Carroll MW, Ellard FM;

Kingsman A, Kingsman SM, Bebbington CR,

WPI; 2001-343805/36.

Myers KA;

P-PSDB; AAB83839,

(OXFO-) OXFORD BIOMEDICA UK LTD

02-MAR-2000; 2000GB-00005071.

99WO-GB003859. 2000GB-00003527.

18-NOV-1999; 15-FEB-2000;

13-NOV-2000; 2000WO-GB004317

Disclosure, Fig 26, 118pp, English.

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The specification describes the use of a single chain antibody (SCFV), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the pervention and treatment of a disease condition. The SCFV antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. Including arthribody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, ardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce SCFV of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferative disorder; infection; inflammatory condition; or immunotherapy; foetal cell; maternal blood; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetal abnormality; foetal sex determination; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1090 GCCCTGATAGGCGCCATCTTCCTACTG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaLeuileGlyAlailePheLeuLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-774-176-21 (1-9) x AAF89736 (1-1263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK87174 standard; cDNA; 1263 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.00
100.0%
100.0%
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK87174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK87174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                        1263
9
0
0
0
                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of canine 5T4 protein.
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AAF89736 standard; DNA; 1263

RESULT 14

ઠે 원 AAF89736

(first entry)

23-JUL-2001

AAF89736;

US-10-774-176-21 (1-9) x AAA27058 (1-1263)

101 40.00 100.0% 100.0%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores:

g

Canis

Location/Qualifiers

вр.

Canis

Key

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the professed in colontal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell conficients in factorions, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in disgnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, issues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The isolating foetal may then be subject to biochemical or genetic mapping used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                       /*tag= a
/product= "ST4 protein"
            Location/Qualifiers
1. .1263
                                                                                                                                                                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 67; 68pp; English.
                                                                                                                                                                                                                                                                                                                     Carroll M;
                                                                                                                                                                                                13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                                       13-NOV-2000; 2000WO-GB004317.
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P-PSDB; AAU98693.
                                                                                                                                                                                                                                                                                                                     Drury N,
                                                                                                                  WO200238612-A2
                                                                                                                                                       16-MAY-2002
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                    Key
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Matches:
Conservative:
Mismatches:
Indels:
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Alignment Scores:

Search completed: May 27, 2006, 10:38:34 Job time : 378.5 secs

Perfect score:

Sequence:

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Run

Scoring table:

Searched:

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AC128294 Rattus no
AC106962 Rattus no
AC172361 Bos tauru
AC137516 Sequence
AC126539 Mus muscu
AC15639 Mus muscu
          AX316088 Sequence
AX82164 Sequence
DD161112 Novel Ant
AX467373 Sequence
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 32642 12-SEP-2002;
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Sequence 32642 from Patent WO02070737,
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Alignment Scores:
Pred. No.:
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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CQ687716
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-Q=/abss/ABSSWEB spool/US10774176 - LOOPEXXT=0
-UNITS=bits -START=1 - END=-1 - MATRIX=blosund2 - TRANS=human40.cdi -LIST=45
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-YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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CQ920916 Sequence
BD249733 Polypepti
                                                                                                                     (without alignments)
257.039 Million cell updates/sec
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                                                                                                      ; Search time 3358.6 Seconds
               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                         nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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99b_par::*
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95b_v::*
95b_v::*
95b_n::*
                                                                                                       May 27, 2006,
                                                                                                                                                                                               1 ALIGAIFLL 9
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Database :

Sequence Homo sapi Sequence Primer fo

Sequence

Homo sapi Rattus no Homo sapi Mus muscu Sequence

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Macaca fa

Sequence

PAT 03-FEB-2004

Score

Result No.

4 4 4 0 0 0

us-10-774-176-21.p2n.rge

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Canis sp.
Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 15-SEP-2000
MILES WILLIAM CARROLL, KEVIN ALAN MYERS
C12N15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065,
C07K19/00,
C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carroll, M.W. and Myers, K.A.
Polypeptide
Patent: WO 0029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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    /organism='Canis sp.

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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Methods for prognosis and treatment of solid tumors
Patent: W04097052-A 2116 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
                                                                                                                                                                   linear
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JP 2002530060-A/3
17-SEP-2002
18-NOV-1999 JP 2000582415
18-NOV-1998 GB 9825303.2,27-JAN-1999
JL-1999 GB 9917995.4
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Carroll,M.W. and Myers,K.A.

Polypeptide

Patent: JP 2002530060-A 3 17-SEP-2002;

OXFORD BIOMEDICA LTD
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JP 2002530060-A/3.
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PN JP 20025300
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PF 18-NOV-1995
PR 18-NOV-1995
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DB:
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CQ920916
LOCUS
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SOUNCE
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AUTHORS
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BD249733
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DRIGIN

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And Zerfusen, b. D.

Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigens, and Methods of Use
Muralidhara Padigaru, Suresh Shenoy, Remesh Kekuda, Vladimir Gusev,
Pascale Pochart, Mei Zhong, Juca Rastelli, Peter Mezes, Glennda
Smithson, Xiaojia Guo, Valerie Gerlach, Stacie Casman, Ferenc
Boldog, Li Li, Bryan Zerhusen, Velizar Tchernev, Esha Gangolli, Corine
Vernet, Carol Pena, Catherine Burgess, Xiaohong Liu, Kimberly
Spytek, Linda Gorman, Steven Spaderna, Edward Voss, Uriel
Malyankar, David Anderson, Meera Patturajan, Charles Miller, Raymond J
Taupier Jr
OS Homo sapiens
Pr 08-MAR-2002
PP 08-MAR-2002
PP 08-MAR-2001
PP 08-MAR-2001
PP 06/294889, 11-MAY-2001
PR 19-UUN-2001
PR 60/294889, 11-MAY-2001
PR 60/294899, PR 19-UNA-2001
PR 60/
                                                                                                                                                                                                                       Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigens, and Methods of Use.
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1. (bases 1 to 1156)
Padigaru,M., Shenoy,S.G., Pochart,P.F., Kekuda,R., Gusev,V.Y., Zhong,M., Jr.R.J.T., Casman,S.J., Li,L., Miller,C.E., Patturajan,M., Anderson,D. W., Malyankar,U.M., Voss,B.Z., Spaderna,S.K., Gorman,L., Spytek,K.A., Liu,X., Burgess,C.E., Pena,C.E., Gerlach,V., Smithson,G., Mezes,P.D., Rastelli,L., and Zerhusen,B.D.
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60/287424,
60/281194,
60/280822,
60/291190,
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60/304354,
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60/29485,09-MAR-2001 US
60/28590,03-MAR-2001 US
60/281675,04-APR-2001 US
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60/333272,14-NOV-2001
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                                                                         Gaps:
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                                                                                                                                        1 AlaLeuIleGlyAlaIlePheLeuLeu
                                                                                                      x AX829164 (1-927)
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JP 2005508604-A/23.
Homo sapiens (human)
Homo sapiens
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100.0%
100.0%
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02-APR-2001
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12-MAR-2001
08-MAR-2001
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14-NOV-2001
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22-MAR-2001
                  Percent Similarity:
Best Local Similarity:
                                                                                                        US-10-774-176-21 (1-9)
                                                   Query Match
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DD161112
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KEYWORDS
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                                                                                                                                                                                                                                                                               Canis sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                           PAT 14-DEC-2001
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mack, D.H., Gish, K.C. and Afar, D.
Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer

Batent: WO 02039377-A 57 01-AUG-2002;

BOS Biotechnology, Inc. (US)

Location/Qualifiers

1. .927

/mol type="Homo sapiens"
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                                                                                                                                                                             linear
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Sequence 57 from Patent W002059377.
AX829164

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                                                                                         Sequence 3 from Patent EP1160323.
   Gaps:
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                                  US-10-774-176-21 (1-9) x AX025013 (1-901)
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                                                                                                                                                                                                                              AX316088.1 GI:17899280
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Best Local Similarity:
Query Match:
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AUTHORS
TITLE
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AX316088
LOCUS
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AX829164
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PAT 10-DEC-2003

linear

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Felis catus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis
                                                                                                                                                                                                                                                                                                                               Carroll, M.M., Kingsman, S.M. and Redchenko, I.M. MHC class I peptide epitopes from the human 5t4 tumor-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll,M.O., Harrop,R.O. and Kingsman,S.O. MHC class II peptide epitope of 5t4 antigen Patent: WO 03068015.A i 21-AUG-2003; Oxford Biomedica (UK) Limited (GB)

1. .1260
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Matches:
Conservative:
Mismatches:
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  Mismatches:
Indels:
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers

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AX821548
AX821548.1 GI:39724930
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AX821533
AX821533.1 GI:39724929
                                Gaps:
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Best Local Similarity:
Query Match:
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ACCESSION
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KEYWORDS
SOURCE
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VERSION
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AUTHORS
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AUTHORS
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AX821533
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PI charles e miller, meera patturajan, david w anderson, uriel m PI
malyankar,
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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corine a m vernet,esha a gangolli,velizar t tchernev,bryan d
zerhusen
                                                                                           PI muralidhara padigaru, suresh g shenoy, pascale f-g pochart, remesh kekuda,
                                                                                                                              vladimir y gusev, mei zhong, raymond j taupier jr, stacie j
                                                                                                                                                                                      edward z voss, steven k spaderna, linda gorman, kimberly PI
                                                                                                                                                                                                                 xiaohong liu, catherine e burgess, carol e a pena, valerie
60/332172, PR
60/335301, PR
60/325430, PR
60/34570, PR
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60/33184,31-OCT-2001 US
60/330380,27-SEE-2001 US
60/325681,12-SEE-2001 US
60/318462,03-JAN-2002 US
60/337165,08-MAR-2002 US
60/3121903
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Myers, K., Drury, N. and Carroll, M.
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AX467373
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PAT 10-DEC-2003

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PAT 14-DEC-2001
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Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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POLYPEDIGE
PACENT: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOWEDICA LTD (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W.,
Ellard, F.M. and Myers, K.A.
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synthetic construct
other sequences; artificial sequences.
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Patent: WO 0136486-A 14 25-MAX-2001;
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AX316086
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1 (bases 1 to 1263)

Carroll, M. and Myers, K.A.
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CI2N15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065, C07K19/00,
C12N15/00
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Patent: JP 2002330060-A 1 17-SEP-2002;
OXFORD BIOMEDICA LID
OS Homo sapiens (human)
PD 17-202530060-A/1
PD 17-25P-2002
PP 18-NOV-1999 GB 982303.2,27-JAN-1
30-JUL-1999 GB 9813995.4
PI MILES WILLIAM CARROLL, KEVIN ALAN MYE
PC C12N15/09, A61K39/00, A61K48/00, A61P35
PC C07K19/00,
PC C07K19/00,
PC C12N15/00
PC C12N15/00
PC POlypeptide Location/Qualifiers
FT SOURCE (1.1253)
FT C12N15/00 CC POLYPEPTIGE LOCATION/Qualifiers
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JP 2002530060-A/1.
Homo sapiens (human)
Homo sapiens
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BD249731
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AX025011
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Search completed: May 27, 2006, 19:35:24
Job time : 3359.6 secs
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                 Homo sapiens
Bukaryotes, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia, Butheria, Euarchontoglires, Primates; Catarrhini,
Hominidae, Homo
                                                                                                                                Carroll, M.W. and Myers, K.A.

5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DBC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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AX467371
Sequence 1 from Patent EP1160323.
AX316086
AX316086.1 GI:17899278
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Aas61372 Soybean 2
Aas98600 Human col
Abs40605 Bovine ES
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Adb97525 DNA encoc
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ACL56146
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99GB-00001739.
99GB-00017995.
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27-JAN-1999;
30-JUL-1999;
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Mouse;
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Adi26160 Human cDN
Adi26158 Human cDN
                                                                                          (without alignments)
249.339 Million cell updates/sec
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                                                                             ; Search time 377.5 Seconds
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          GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                        using frame_plus_p2n model
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ADI26160
ADI26158
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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genesegn2005s:*
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cancer;

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Result No.

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TTAT. The TAT 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been included were incoulated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit en immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                          Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autodimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosuus; asthma; allergic rhinitis; systemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                            The present sequence encodes the mouse 574 tumour-associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding protein that promotes STAT6 activation #63
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
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Matches:
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                                                                                                                             Example 2; Page 78; 79pp; English
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2003JP-00137505.
2003US-0470836P.
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2002JP-00377326.
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                Myers KA;
                                               WPI; 2000-387735/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003104277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-2002;
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              Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD126160;
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or succeptibility to a disease related to expression or activity of the compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant composition, antibodies and antisense molecules are useful composition. Composition, antibodies and antisense molecules are useful composition composition, authority and antisense molecules are useful composition diseases, inflammation, autoimmune diseases, diabetes, allergic diseases, inflammation, autoimmune diseases, diabetes, allergic disease associated with STAT6 activation and/or prevention for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, oscheamitis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activation or inhibition of STAT6. The present sequence represents a cuivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                               New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA encoding protein that promotes STAT6 activation #62.
  Muramatsu S, Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;
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Matches:
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Indels:
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Honda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI26158 standard; cDNA; 2557 BP
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  Matsuda A,
                                                                                                                                                             diabetes and cancer.
                                     WPI; 2004-122214/12
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Best Local Similarity:
                                                          P-PSDB; ADI26161
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  Sugahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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DB:
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mouse; murine; cancer; psoriasis; ulcerative colitis; inflammation; ischaemic heart disease; thrombosis; immune disorder; bacterial disorder; viral disorder; ds; gene.

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administaring the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as altergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention for treating diseases. Compositions are also useful in rheumatoid attritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activity. The protein or nucleic acid is effectively useful for screening compounds for treating and appreventing disease associated with excessive compounds for treating and preventing disease associated with excessive activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                          signal transducer and activator of transcription 6 activation noting purified protein, for diagnosing and treating disease ociated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                             Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2557 BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;
                                                                                                                                                                                             Honda G, Muramatsu S,
                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 123; 1368pp; English
                                                            2002US-0385912P.
2002JP-00377326.
2002US-0436467P.
                                                                                                           15-MAY-2003; 2003JP-00137505
16-MAY-2003; 2003US-0470836P
               05-JUN-2003; 2003WO-JP007123
                                              2002JP-00164257
                                                                                                                                                                                           Sugahara T, Matsuda A,
                                                                                                                                                                                                                           WPI; 2004-122214/12.
                                                                                                                                                                                                                                                                                                                         diabetes and cancer.
                                                                                                                                                           (ASAH ) ASAHI KASEI
                                                                                                                                                                                                                                          P-PSDB; ADIZ6159
                                                            06-JUN-2002;
26-DEC-2002;
27-DEC-2002;
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                                             05-JUN-2002;
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                                                                                                                                                                                                                                                                                            promoting
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New mouse nucleic acid molecules and polypeptides, useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischemic heart

Claim 1; SEQ ID NO 612; 263pp; English.

disease or thrombosis.

Hayashizaki Y, Kamiya M;

Hestir K,

Lee E,

Williams LT, Chu K, WPI; 2004-431966/40.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

2003US-0493356P

2002US-0431158P. 2002US-043145P. 2002US-0431606P. 2003US-0476621P. 2003US-0476632P. 2003US-0485217P. 2003US-0485359P.

08-JUL-2003; 08-JUL-2003; 38-AUG-2003;

08-AUG-2003;

09-JUN-2003; 09-JUN-2003;

24-OCT-2003; 2003WO-US033948

15-NOV-2002;

04-DEC-2002; 05-DEC-2002; 05-DEC-2002;

WO2004046310-A2.

Mus sp.

03-JUN-2004

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The invention comprises 744 novel mouse DNA sequences (genes). The DNA sequences of the invention are useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischaemic heart disease, thrombosis, mamune disorders, bacterial disorders and viral disorders. The present nucleic acid represents a mouse DNA sequence of the invention. NOTE: The present DNA sequence is not shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN; SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding; 240017 region G3; 318013 region A3; 515002 region G2; ds.
                                                                                                                                                                    Sequence 2557 BP; 610 A; 794 C; 688 G; 465 T; 0 U; 0 Other;
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Conservative:
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Query Match:
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Matches:
Conservative:
Mismatches:

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Best Local Similarity:

Query Match:

Percent Similarity:

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Indels:

BP

AD035939 standard; DNA; 2557

AD035939/c RESULT

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AD035939;

Novel mouse gene sequence #612.

26-AUG-2004 (first entry)

PheLeuThrGlyAsnGlnMetThrVal 9

US-10-774-176-20 (1-9) x ADI26158 (1-2557)

soybean

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The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myotonic muscular dystrophy; acanthosis; nigricans; retinopathy; nephropathy; artherosclerosis; peripheral arterial disease; cancer; adenocarcinoma; leukaemia; breast cancer; prostate cancer; colon cancer; ovarian cancer; autolmmune disease; inflammation; immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 335913 BP; 114582 A; 53398 C; 53027 G; 114906 T; 0 U; 0 Other;
                                                                                                                                                                     New purified nucleic acid for producing a soybean plant having a cyst nematode resistance and for use in plant breeding programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHIP; Pleckstrin homology domain-interacting protein; NDRP; ds;
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IRS; signal transducer and activator of transcription, STAT,
transgenic animal; diabetes mellitus type 2; hyperglycaemia,
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Conservative:
Mismatches:
                                                             Parnell LD;
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                                                                                                                                                                                                                                    Claim 2; Page 400-595; 1353pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-774-176-20 (1-9) x AAI61372 (1-335913)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS98600 standard; DNA; 140036 BP
                                                               Parsons JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genomic DNA for PHIP/NDRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2001; 2001WO-CA000673.
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(FARH/) FARHANG-FALLAH J.
(CHEN/) CHENG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the specification
                                                             Wang ML,
                   (MONS ) MONSANTO CO.
                                                                                                       2001-425872/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                             P-PSDB; AAM42215
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                                                           Hauge BM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 335913 BP; 114579 A; 53403 C; 53026 G; 114905 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                  New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs.
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Matches:
Conservative:
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                                                                                                                             35-JAN-2001; 2001WO-US000552
                                                                                                                                                                       07-JAN-2000; 2000US-0174880P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the specification
                                                                                                                                                                                                                                                          Wang ML,
                                                                                                                                                                                                                                                                                                    WPI; 2001-425872/45
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                                         WO200151627-A2
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  Glycine max.
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substrate;

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The invention relates to an isolated Pleckstrin homology domain interacting protein (PHIP) that recruits proteins of the insulin receptor substrate (TRS) family, and signal transducer and activator of transcription (STAT) transcription factors, to receptors that interact with and phosphorylate the proteins and STAT transcription factors, the nucleic acid encoding PHIP (nPHIP), a nucleic acid which binds to nPHIP or regions of it, analogues, fragments or allelic variants of PHIP or newtons and inferentiation-related protein (NDRP) nucleic acid sequence infiferentiation-related protein (NDRP) nucleic acid sequence or neuronal differentiation-related protein (NDRP) nucleic acid sequence or its exons as given in the specification, expression vectors and host calls approach an already expressing PHIP The nucleic acids, and a transgenic animal not already expressing PHIP. The nucleic acids, and a transgenic animal not already expressing PHIP. The nucleic acids, and a transgenic animal not already expressing PHIP. The nucleic acids, and a transgenic animal not already expressing PHIP. The nucleic acids, and a transgenic animal not already expressing PHIP. The nucleic acids, and a transgenic animal not already expressing PHIP. The nucleic acids, and a transgenic animal and already expressing PHIP.
                                                                                                                                                         Novel Pleckstrin homology domain interacting protein recruiting proteins of insulin receptor substrate family, and signal transducer and activator of transcription factors to their receptors, useful to treat diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, colon cancer, ovarian cancer and many others given in the specification, autoimmune disease, inflammation and immunodeficitiency. The protein is also useful for discovering or testing compounds which may be either enhancers or inhibitors of PHIP function. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated with an insulin receptor (e.g. diabetes mellitus type 2, hyperglycaemia, myotonic muscular dystrophy, acanthosis, nigricans, retinopathy, nephropathy, artherosclerosis, peripheral arterial disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 140036 BP; 48500 A; 25843 C; 22499 G; 43194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or cancer (e.g. adenocarcinoma, leukaemia, breast cancer, prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibodies are useful for diagnosis and treatment of a
                               Cheng A;
                                                                                                                                                                                                                                                                                          Disclosure; Page 99-133; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is genomic DNA encoding PHIP and NDRP
                               Rozakis-Adcock M, Farhang-Fallah J,
                                                                                              WPI; 2002-041586/05.
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Length: Matches: Conservative: Mismatches: Indels: Gaps: 1.93e+04 39.00 100.0% 87.5% 84.8% Percent Similarity: Best Local Similarity: Query Match:

JS-10-774-176-20 (1-9) x AAS98600 (1-140036)

œ 1 PheLeuThrGlyAsnGlnMetThr

ABX40605 standard; cDNA; 343 BP ABX40605; 

20-FEB-2003 (first entry)

Bovine EST associated with lactation/muscle/fat deposition #5770

Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

Bos Taurus

JS2002137139-A1

26-SEP-2002

24-SEP-2001; 2001US-00960352

Differential expression; diagnosis; therapy; drug screening; cancer; neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;

Human colon cancer differentially expressed polynucleotide, SEQ ID:2281.

ACL56146 standard; cDNA; 505

RESULT 9 ACL56146 24-MAR-2005 (first entry)

ACL56146;

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lactation or muscle and fat deposition designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a tissue, where hybridisation between the marker nucleic acid and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting the level or pattern of the complementary nucleic acid, where the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid; where the detection of the complementary nucleic acid is predictive of the determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids, Note: The
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                             New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence was not shown in the specification but was obtained in
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 5770; 245pp; English
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    99US-0115707P
                         11-JAN-2000; 2000US-00480902
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                                                               (BYAT/) BYATT J C. (MATH/) MATHIALAGAN
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12-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                           The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which are differentially expressed in colon cancer cells. The invention also crelates to vectors and host cells comprising a differentially expressed polynucleotide of the invention; a method for detecting a cancerous cell by detection of a gene product of the polynucleotides; a method of treating a gene product of the polynucleotides; a method of treating an individual with cancer by administration of a modulator of a gene product of the polynucleotides; and an isolated antibody that specifically binds to a polypeptide encoded by one of the 9672 polynucleotides responsed in a polynectides; and methods are useful for the detection of cancerous cells; for the diagnosis, prognosis and management of cancer; for the control of agents that modulate the phenotype of cancerous cells; for the identification of therapeutic targets for cancer chemotherapy; cond for the treatment of cancer, especially colon cancer and metastasized colon cancer, but also breast or pancreatic cancer. The polynucleotides are also useful as a source of probes or primers for use in diagnostic methods. The differentially expressed polynucleotides or their encoded proteins can additionally be used as vaccines to modulate primary immune responses for the prevention or treatment of cancer. The present sequence corresponse for the preventially expressed polynucleotide which is differentially expressed to concurr for mean of the printed specification, but was obtained in colon cancer. Note: The sequence data for this patent did concern for the preventially and concern the sequence data for this patent did colon cancer.
                                                                                                                                                                                                                                                            New isolated polynucleotides, which are differentially expressed in colon cancer cell, useful for treating cancer, e.g. colon cancer, breast cancer, or pancreatic cancer.
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Matches:
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                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2281; 97pp; English
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                                                                                                                13-MAY-2004; 2004WO-US015421.
                                                                                                                                              03-JUN-2003; 2003US-0475872P.
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                                                         WO2005000087-A2.
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                               Homo sapiens.
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                                                                                     06-JAN-2005
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, issues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The solating foetal about form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                     Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
CDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "5T4 protein"
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                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1260
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD BIOMEDICA UK LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2001; 2001WO-GB005004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.00
88.9%
77.8%
82.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200238612-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-2002.
                                                                                                                                                                                                                                                   Felis sp.
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ADB97513
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ADB97513 standard; DNA; 1260 BP

286 TTCCTCACCGGCAATCAGCTGGCCGTG 312

ADB97452 standard; DNA; 1260

ADB97452

ADB97452;

1 PheleuThrGlyAsnGlnMetThrVal

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The invention relates to a novel Major Histocompatibility Complex (MHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope string comprising the 5T4 epitope; a nucleic acid sequence encoding the 5T4 epitope or a polyepitope string of the 5T4 epitope or a polyepitope string of the 5T4 epitope or a cell; a cell pulsed with the 5T4 epitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope or preventing a disease or peptising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising the presence of the 5T4 epitope or its encoding comprising the 5T4 epitope and/its encoding nucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 5T4 epitope in conjunction with an MHC class or molecule. The 5T4 epitope or its encoding nucleic acid and the vector system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for diagnosing or monitoring the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone presence of the 5T4 epitope or its nucleic acid. The T cell line or clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           major histocompatibility complex class I peptide epitopes from human tumor-associated antigen, useful for preventing and/or treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is useful in the manufacture of a medicament for treating and/or preventing a disease. This polynucleotide sequence represents the feline 5T4 antigen coding DNA of the invention.
                                                                                                                              Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                         /product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redchenko I;
                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1260
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD BIOMEDICA UK LID
                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2003; 2003WO-GB000670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002; 2002GB-00003419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease, particularly cancer
                                                        04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131
38.00
88.9%
77.8%
82.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingsman S,
                                                                                            Feline 5T4 antigen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-637141/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ADB97520.
                                                                                                                                                                                                                                                                                                                                                  WO2003068816-A1
                                                                                                                                                                                                             Inidentified
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                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll M,
                  ADB97513;
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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the felline 5T4 protein.
                                                                                                                    gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                              /product= "Feline ST4 antigen protein"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-774-176-20 (1-9) x ADB97452 (1-1260)
                                                                                                                                                                                             Location/Qualifiers
1. 1260
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 49; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Kingsman S;
                                                                                         DNA encoding feline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                          (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002; 2002GB-00003420
                                                                                                                                                                                                                                                                                                                                           13-FEB-2003; 2003WO-GB000618
                                                        (first entry)
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38.00
88.9%
77.8%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
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                                                                                                                                                                                                                                                                             WO2003068815-A2
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                                                                                                                                                                   Unidentified
                                                          04-DEC-2003
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Length: Matches: Conservative: Mismatches:

Indels: Gaps:

Best Local Similarity:

Query Match:

Percent Similarity:

US-10-774-176-20 (1-9) x ADB97513 (1-1260)

Location/Qualifiers
1. .1263
/\*tag= a
/product= "5T4"

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hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                    Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
            sequence of canine 5T4 protein.
                                                                                                                                                                                               WO200136486-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                      25-MAY-2001
            Nucleotide
                                                                                                                                                                                                                                                                                                                                                           Myers KA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                          Canis
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ID ABK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metaerasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen is sequence to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                          Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                Human, TAA, tumour-associated antigen, anti-tumour, cytostatic,
immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                         Human 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 TTCCTTACCGGCAACCAGCTGGCCGTG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PheLeuThrGlyAsnGlnMetThrVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-774-176-20 (1-9) x AAA27058 (1-1263)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 78; 79pp; English.
                                  AAA27058 standard; DNA; 1263 BP.
                                                                                                                                                                                                                                                                                                                                 OXFO-) OXFORD BIOMEDICA UK LTD
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                                                                                                                                                                                                                                                                                  98GB-00025303.
99GB-00001739.
99GB-00017995.
                                                                                                                                                                                                                                                           99WO-GB003859.
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                                                                                  (first entry)
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88.9%
77.8%
82.6%
                                                                                                                                                                                                                                                                                                                                                          Carroll MW, Myers KA;
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-387735/33.
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Best Local Similarity:
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                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                           18-NOV-1999;
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27-JAN-1999;
                                                                                                                                                                                                                                                                                                           30-JUL-1999;
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                                                                                  22-AUG-2000
                                                                                                                                                                                                                                   25-MAY-2000
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                                                          AAA27058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
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          RESULT 13
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                        AAA27058
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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                           Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PheLeuThrGlyAsnGlnMetThrVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-774-176-20 (1-9) x AAF89736 (1-1263)
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                                                                                                                                                                                                                                   OXFO-) OXFORD BIOMEDICA UK LTD
                                                                       18-NOV-1999; 99WO-GB003859.
15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
13-NOV-2000; 2000WO-GB004317.
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88.9%
77.8%
82.6%
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P-PSDB; AAB83839.
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the profortuleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in disquastic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, issues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The calsation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel canine or feline 574 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                         Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                          cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                 /product= "5T4 protein"
                                                                                                                                                                                                                                                        Location/Qualifiers
1. .1263
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 67; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2000; 2000WO-GB004317.
                                                     07-OCT-2002 (first entry)
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                   ABK87174;
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Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
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88.9%
77.8%
82.6%
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Pred. No.:
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US-10-774-176-20 (1-9) x ABK87174 (1-1263)

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27, 2006, 10:38:27 May Search completed: May Job time: 417.5 secs

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BC087011 Rattus no BC088198 Mus muscu AX961912 Sequence AX961914 Sequence AX061914 Sequence AX061914 Sequence AX061914 Sequence AC158516 Mus muscu AC158516 Mus muscu AC128294 Rattus no AC128563 Rattus no AC12839 Mus muscu AC12879 Mus muscu AC12879 Mus muscu AC12879 Mus muscu AC12879 Homo sapi CR387991 Danio rer AL66077 Ralstonia AC118131 Rattus no AX196296 Sequence AC1887991 Danio rer AL646077 Ralstonia AC118736 Xenopus f AX87434 Xenopus f AX87434 Xenopus s AX87434 Xenopus s AX87436 Mus muscu CR54854 Homo sapi AC136746 Human DNA AC167999 Bos tauru AC16193 Homo sapi AC16199 Bos tauru
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILES WILLIAM CARROLL, KEVIN ALAN MYERS
C12N15,09, 461K39/00, 461K48/00, 461P35/00, C07K7/06, C07K14/065, C12N15/00,
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Carroll,M.W. and Myers,K.A.
Polypeptide
Patent: JP 2002530060-A 2 17-SEP-2002;
OXFORD BIOMEDICA LTD
OS Mus musculus (mouse)
PD 17-SEP-2002
PP 18-NOV-1999 JP 2000582415
PF 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9925303.2,27-JAN-1997
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PC C12LNIS/09, AGIK39/00, AGIK48/00, AGIP3;
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BD249732.1 GI:33059502
JP 2002530060-A/2.
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AX025012 Sequence
AX316087 Sequence
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257.039 Million cell updates/sec
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                                                                           ; Search time 3358.6 Seconds
           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                     - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Result Š.

Total number of Minimum DB seq Maximum DB seq

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Sequence:

OM protein

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Scoring table:

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AF063939
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Patent: WO 0029428-A 2 25-MAY-2000;
Patent: WO 0029428-A 2 25-MAY-2000;
CARROLL MILEA WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
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AF063939 GI:6650211
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Sukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                  5t4 tumour-associated antigen for use in tumour immunotherapy Patent: BP 116023-A 2 05-DEC-2001; Oxford Biomedica (UK) Limited (GB) Location/Qualifiers
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Ninkina,N.N. and Buchman,V.L.
Structure and expression of the rat 5T4 gene
2 (bases 1 to 2333)
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC087011 2361 bp mRNA linear ROD 13-DEC-2004
Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone
MGC:9332 IMAGE:7193411), complete cds.
HHLELASNHFLYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KYLHNSTLERWGGLAHVRPLDNNPWYCDCYWADMVSMLKETEVVPDKRRLTCRPPEK
MRNRGLDLTSSDLDCDATLPGSLOTSYVFGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPSLTNLSSNSDV"
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Submitted (02-DEC-2004) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Matches:
Conservative:
Mismatches:
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Tissue Procurement: Howard Jacobs
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Rattus norvegicus
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                                                                                      1645. .2333
/gene="5T4"
2315. .2320
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Director MGC Project.
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/gene="5T4"
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46.00
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                                                                                                                                      polyA_signal
                                                                                                                                                                                                                             Alignment Scores:
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Meb site: http://www-shgc.stanford.edu contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTVLPAGAFARQPPLADLAVLNLSGNHLKEVGAGAFEHLPGLRRLDLSHNPLTNLSAF
TFAGSNVSVSTPSPLLELILNHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
HHLELASNHFLYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
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MRNRGLLDLTSSDLDCDATLÞQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSLPSSSTS"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 2423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Heart, rat (Brown Norway)"
Clone_lib="NIH MGC_234"
|lab_host="DH108"
|note="Vector: pExpress1"
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/clone="MGC:93332 IMAGE:7193411"
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Tpbg protein"
/protein id="AAH87011.1"
/b xref="G1:5626820"
/db xref="GeneID:83684"
/db_xref="RGD:621453"
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db_xref="RGD:621453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: 5T4"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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PAAFIASGSAQPPPAERCPAACECSBARTYKCVNRNILEVPADLPPYVRNIETTGNQ
MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGIRRLDLSHNPLTNLSAF
AFAGSNASYSAPSPLEELILMHIVPPEDQRQNGSFEGWYAAALRSGLALRGL
TCLELASNHPLFLPRDILEAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KVLHNSTLAEWGGHAVKVFLDNNPWVCDCYWADWYWLKETEVVPBKARLTGAFPEK
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NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
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YRGSBNASVBSPLEELILNHIVPPEDQRQNGSFEGWYAFERGWVAAALRSGLALRGGL
TRLELASNHFLPLFADLLAQLPSLRYLDLSNSLVSLTYASFRALTHLESLHLEDDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LRRCT; Region: Leucine rich repeat C-terminal
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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/note="unnamed protein product"
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Indels:
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Matches:
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/gene="Tpbg"
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Query Match:
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Pred. No.:
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ORGANISM
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Alasmar, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.K.
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopking, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Sarses, M.B., Bonaldo, M.F., Casavant, T.L.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wanzhy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA squences
N. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Mansen,N., Ho,S.-L., Karlins,R., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Peargoon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6758854.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbe.r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Bequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
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FEATURES

PAT 14-JAN-2004

and Myers, K.A. leucine-rich

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                                                                                                                                                                                                                                                                                                                                 Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson Institute for Cancer Research, Christie Hospital, Wilmslow Road, Manchester, M2O 9BX, UK Imanumater, M2O 9BX, UK Imanumater Location/Qualifiers
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                            King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, Organisation of the mouse and human 5T4 oncofoetal leucine-riglycoprotein genes and expression in foetal and adult murine
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Mus musculus (house mouse)
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
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Mus musculus 5T4 oncofetal trophoblast glycoprotein gene.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Stat6 activation gene
Patent: WO 03104277-A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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Sequence 125 from Patent W003104277.
AX961914
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AC158516 167046 bp DNA linear ROD 21-JUN-2005
Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 167046) Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-MAY-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                     1 (bages 1 to 167046)
Adams, S., Cotton, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
2. (bases 1 to 167046)
Wilson, R.K.
Direct Submission
  7942
9 9 0
0 0
0 0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                     Gaps:
                                                                                                                        PheLeuThrGlyAsnGlnMetThrVal 9
                                                                                             US-10-774-176-20 (1-9) x MMU012160 (1-7942)
                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                               ACI58516 AC117768
AC158516.2 GI:63025421
23.5
46.00
100.0%
100.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson, R.K.
Direct Submission
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                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                    sequence.
                                                                                                                                                   4067
                                                       Query Match:
                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                             RESULT 10
AC158516/c
                                                                                                                                                                                                      LOCUS
  Pred. No.:
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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JOURNAL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciutognathi, Muroidea, Murinae, Rattus.

1 (bases 1 to 210237)
Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Anin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas V., Carter, K., Cavazos, I., Ceasar, H., Center, A., D'Souza, L.,
Claveband, C., Cockrell, R., Cock. C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE. AC128294
AC128294.3 GI:25083347
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                             The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male GSTBL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                                                   Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Sequence derived from PCR product of genomic DNA" 31565. 31779 /note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Sequence derived from one plasmid subclone."
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Mismatches:
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-774-176-20 (1-9) x AC158516 (1-167046)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP24-511A23"
/clone_lib="RPCI-24"
16685._.16712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                  MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                      SOURCE INFORMATION:
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Pred. No.:
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality as 230); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The stanishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is

NOTICE:

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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eavee, K., Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Faracto, C.M., Gabisi, A., Garta, R., Garcia, A., Garrer, T., Garza, M., Gabregeorgie, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Guevara, W., Gunarathe, P., Haaland, W., Hamil, Co., Hamilton, C., Holgues, M., Hollins, B., Howells, S., Hulyk, S., Hung, J., Idlebird, D., Jackson, A., Jackson, L., Jackson, L., Jang, H., Johnson, B., Hogues, M., Karjethy, S., Kally, S., Lu, X., March, M., Mandou, B., Maptin, M., Martin, R., Martin, R., Martin, R., Mahindartne, M., Martin, R., Martin, R., Mandou, B., Mayon, P., Martin, R., Martin, R., Martin, S., Marchi, S., Morce, S., Mandayor, J., Woore, S., Morgan, M., Moore, S., Mandayor, J., Pater, M., Perez, A., Perez, A., Perez, A., Perez, A., Perez, A., Perez, A., Perez, M., Pe
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On Nov 19, 2002 this sequence version replaced gi:23265004.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole contigs within a contigs caffold that consist entirely of whole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end sequences and whole genome
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: CH230-176H20
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Rat Genome Sequencing Consortium.
Direct Submission
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Direct Submission
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AUTHORS
TITLE
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JOURNAL
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AUTHORS REFERENCE

COMMENT

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 210237: contig of 210237 bp in length.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Rattus.
1 (bases 1 to 239076)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
                 Assembly program: Phrap, version 0.990329
Consensus quality: 201781 bases at least Q40
Consensus quality: 203921 bases at least Q30
Consensus quality: 205310 bases at least Q20
Estimated insert size: 205531, sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
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AC106962.5 GI:25139469
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Conservative:
Mismatches:
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complement(206062. .206961)
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/note="wgs_end_extension
clone_end:T7"
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clone_end:Sp6"
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-176H20"
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clone_end:Sp6
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/note="clone_boundary
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SOURCE
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Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:22857070.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgum sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the facture table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 239076)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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JOURNAL
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TITLE

COMMENT

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ACL30132 189229 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-129E18, WORKING DRAFT SEQUENCE, 4
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                    Assembly program: Phrap; version 0.990329
Consensus quality: 228642 bases at least Q40
Consensus quality: 23269 bases at least Q30
Consensus quality: 234041 bases at least Q20
Estimated insert size: 231522; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 234710: contig of 234710 bp in length
4711 234810: gap of unknown length
4811 235924: contig of 1114 bp in length
5925 236024: gap of unknown length
6025 237314: contig of 1290 bp in length
7315 237414: gap of unknown length
7315 237414: gap of unknown length
10cation/Qualifiers
1 239076: contig of 1662 bp in length.
1 239076
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                Center: Baylor College of Medicine
Center code: BCM
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235925. .236024
                                                                                                                                                            Center project Information
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Best Local Similarity:
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                           table.
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us-10-774-176-20.p2n.rge

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Narany, Danaie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baladrin, D., Bandaranike, D., Barber M., Barneted, B., Barneted, B., Brown, M., Blanken, C., Barch, P., Carer, C., Burch, P., Birch, M., Cree, A., D'Soura, L., Caderna, V., Carcer, C., Cave, C., Coyle, M., Cree, A., D'Soura, L., Caderna, V., Carcer, C., Coyle, M., Cree, A., D'Soura, L., Caderna, C., Cowkell, R., Chen, Z., Chu, J., Chave, C., Coyle, M., Cree, A., D'Soura, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Daragher, L., Dugan, Eccetco, M., Eugene, C., Ding, Y., Dinh, H., Divya, K., Dragbar, M., Eugene, C., Ding, Y., Dinh, H., Divya, K., Dragbar, M., Garler, M., Havlak, P., Hawes, A., Handle, M., Haddun, S.L., Hodgen, M., Henderson, L., Jaco, M., Mall, C., Hamilton, K., Havlak, P., Hawes, A., Hulyk, S., Hune, J., Dinson, R., Jolivet, A., Jackson, L., Jaco, M., Liu, Y., Liu, Y., Lu, X., Mar, J., Morris, S., Marghathy, S., Kelly, S., Kelly, S., Kally, S., Kally, S., Kally, S., Kally, S., Martin, K., Martin, R., Martin,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchoncoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 189229)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig sacifold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Atlas 3.0;
Consensus quality: 158286 bases at least Q40
Consensus quality: 161560 bases at least Q30
Consensus quality: 163846 bases at least Q20
Estimated insert size: 170094; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                          shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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1195 184294: gap of unknown length

1295 185535: contig of 1341 bp in length

1316 185735: gap of unknown length

1316 186344: contig of 1209 bp in length

131744: gap of unknown length

131744: gap of unknown length

131745 189229: contig of 2185 bp in length.

1017 Location/Qualifiers
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Web site: http://www.hgsc.bcm.tmc.edu/
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Matches:
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                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                              Project Information
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/db_xref="taxon:10116"
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complement(182186.
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10 (Dasses I to 22844)
11 (Dasses I to 22844)
12 (Dasses I to 22844)
13 (Dasses I to 22844)
14 (Dasses I to 22844)
15 (Dasses)
15 (Dasses)
16 (Dasses)
17 (Dasses)
18 (Dasses)

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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_ENRICHED.
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Mismatches:
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                         Indels:
                                                     Gaps:
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88.9$
93.5$
12
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Best Local Similarity:
                      Query Match:
DB:
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DEFINITION
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AUTHORS
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Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tr 77030, USA On Sep 19, 2002 this sequence version replaced gi:21909333. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using A.Las (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                       Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 228414)
Rat Genome Sequencing Consortium.
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 206214 bases at least Q40
Consensus quality: 209397 bases at least Q30
Consensus quality: 211141 bases at least Q30
Estimated insert size: 227271; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
Center project name: GYPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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206830. .208310
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/db xref="taxon:10116"
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/note="wgs_contig"
/n4485. .206729
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2420. .4597
/note="wgs_contig"
200269. .202348
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106730. .206829
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226457
Worley, K.C.
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Submitted (13-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 2, 2002 this sequence version replaced gi:22539250.
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Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-OCT-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 179668)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Musinae; Mus. 1 (Dases 1 to 179668) Maligorski,J., Bielicki,L., Creason,K., Spalding,L., The sequence of Mus musculus BAC clone RP24-351117 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC124399 179668 bp DNA linear ROD 13-NOV-:
Mus musculus BAC clone RP24-351117 from chromosome 10, complete
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
               /note="wgs_contig"
213674. .220116
/note="wgs contig"
220403. .223650
/note="wgs contig"
223701. .224742. /note="wgs_contig"
/setimated length=unknown
226357. .226456
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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McPherson, J.D. and Waterston, R.H.
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 208661. .210473
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The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CS7BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the entire insert of the clone. This clone is overlapped by AC121871.
                 Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                         Center project name: M BB0351117
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                                                                --- Summary Statistics
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    179668
/organism="Mus musculus"

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/rpt_family="MER1_type"
4755. .5164
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/db_xref="taxon:10090"
/chromosome="10"
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/rpt_family="MaLR"
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/rpt_family="ERVL"
3239. .3384
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/rpt_family="ERVK"
49. .271
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/rpt_family="ERVL"
6476. .6874
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2299. .2444
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7871. .8002
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Center code: WUGSC
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Center: Washington University Genome Sequencing Center

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1998;
27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000
  AAA27059
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-MODEL=frame+_p2n.model -DEV=xlh
-QcAbss/AssWEB spool/US10774176/runat_26052006_091441_24976/app_query.fasta_1
-QcAbss/AssSWEB spool/US10774176/runat_26052006_091441_24976/app_query.fasta_1
-DB=N Geneseq -OFWT=fastap - SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORN=ext -HEAPSIZE=500 -MINLEN=0 -MAXEN=2000000000 -HOST=abss02h
-USER=USI0774176_QCGN_1 1_2389_Qrunat_26052006_091441_24976 -NCPU=6 -ICPU=3
-NO WMAP -NGS_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_INSOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Adi26160 Human cDN
Adi26158 Human cDN
                                                                                                                                                                             (without alignments)
249.339 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                      May 27, 2006, 09:34:35 ; Search time 377.5 Seconds
                       version 5.1.8
- 2006 Biocceleration Ltd.
                                                                                                             using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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12 ADI26160
12 ADI26158
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7.0
7.0
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                                                                                                                                                                                                                                                                                                                                                       Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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genesegn2004bs:*
genesegn2005s:*
                       GenCore (c) 1993
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geneseqn2003ds:*
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seq length: 200000000
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Match Length DB
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2557
2557
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                                                                                                               nucleic search,
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
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Database :

Score

Result Š 4 4 4

Fri Jun

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(TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to mestrais in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding
                                                                                Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systemic lupus erythematosus; sepsis; asthma; allergic rhinitis;
ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                    The present sequence encodes the mouse 574 tumour-associated antigen
                                                                                                                                                                                                                                                                                                                        the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; gene; human; signal transducer and activator of transcription STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; th hyperactive disease; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding protein that promotes STAT6 activation #63.
                                                                                                                                                                                                                                                                                                                                                                                            Seguence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AACCTGCTGGAGGTGCCGGCGGATCTA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AsnLeuLeuGluValProAlaAspLeu
                                                                                                                                     Example 2; Page 78; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002US-0385912P.
2002UP-00377326.
2002US-0436467P.
2003UP-00137505.
2003US-0470836P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI26160 standard; cDNA; 2557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2003; 2003WO-JP007123.
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44.00
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                                               WPI; 2000-387735/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #O2003104277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-2004
               Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI26160;
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9
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1281 9 0 0 0

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune disease, diabetes, chyperlipidaemia, infections disease associated with STAT6 activation and/or prevention of the treating disease. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive compounds for treating and preventing disease associated with excessive decipation of STAT6. The present sequence represents a decipation of STAT6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; albS. ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                      purified protein, for diagnosing and treating disease with activation/inhibition of transcription factor e.g.
                                                                                                               and activator of transcription 6 activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA encoding protein that promotes STAT6 activation #62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human cDNA encoding a protein which promotes STAT6 activation.
Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2557 BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;
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Matches:
Conservative:
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Muramatsu S,
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                                                                                                                                                                                                                           Claim 4; SEQ ID NO 125; 1368pp; English
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Honda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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  Matsuda A,
                                                                                                                 New signal transducer
                                                                                                                                                                                   diabetes and cancer.
                                               WPI; 2004-122214/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                      P-PSDB; ADI26161
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  Sugahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                         promoting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STATS). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The mucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATS activation. A transformant composition. Some protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATS activation such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STATG activation and/or prevention of Th1 hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepsitis and AIDS. The protein has efficient promoting STATG activity. The protein nor nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATG. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                    promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                            signal transducer and activator of transcription 6 activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                            Ishizawa K;
                                                                                                                                                                                                                                                                            Muramatsu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 123; 1368pp; English.
                                                                                                                                                                                                                                                                            Honda G,
                                                                                   06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002US-043647P.
15-MAY-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
                     05-JUN-2003; 2003WO-JP007123
                                                                  2002JP-00164257
                                                                                                                                                                                                                                                                          Matsuda A,
                                                                                                                                                                                                                             (ASAH ) ASAHI KASEI KK
                                                                                                                                                                                                                                                                                                                       WPI; 2004-122214/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                            P-PSDB; ADI26159
                                                                05-JUN-2002;
                                                                                                                                                                                                                                                                     Sugahara T,
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Sequence 2557 BP; 512 A; 730 C; 696 G; 619 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
                                               Indels:
                                                         Gaps:
         39.1
44.00
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100.0%
                            Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                               Query Match:
DB:
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US-10-774-176-19 (1-9) x ADI26158 (1-2557)

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796 AACCTGCTGGAGGTGCCGGCGGATCTA 822
AsnLeuLeuGluValProAlaAspLeu 9
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Novel mouse gene sequence #612. AD035939 standard; DNA; 2557 26-AUG-2004 (first entry) AD035939 AD035939/c 1D AD03593 XX AC AD0359: XX 26-AUG XX XX RESULT

mouse; murine; cancer; psoriasis; ulcerative colitis; inflammation; ischaemic heart disease; thrombosis; immune disorder; bacterial disorder; viral disorder; ds; gene. 2002US-0426916P. 2002US-0431158P. 2002US-0431445P. 2002US-0431606P. 2003US-0476621P. 2003US-0476632P. 2003US-0485217P. 2003US-0485359P. 2003US-0493332P. 24-OCT-2003; 2003WO-US033948 2003US-0493356P WO2004046310-A2 09-JUN-2003; 08-AUG-2003; 09-JUN-2003; 08-JUL-2003; 15-NOV-2002; 08-AUG-2003; 04-DEC-2002; 03-JUN-2004 Mus sp 

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Hayashizaki Y, Kamiya M; Hestir K, Lee E, Williams LT, Chu K,

WPI; 2004-431966/40.

New mouse nucleic acid molecules and polypeptides, useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischemic heart disease or thrombosis.

Claim 1; SEQ ID NO 612; 263pp; English.

The invention comprises 744 novel mouse DNA sequences (genes). The DNA sequences of the invention are useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischaemic heart disease, thrombosis, immune disorders, bacterial disorders and viral disorders. The present nucleic acid represents a mouse DNA sequence of the invention. NOTE: The present DNA sequence is not shown in the specification, but has been retrieved from the WIPO website.

Sequence 2557 BP; 610 A; 794 C; 688 G; 465 T; 0 U; 0 Other;

2557 9 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 39.1 44.00 100.0% 100.0% 1100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred. No.:

US-10-774-176-19 (1-9) x ADO35939 (1-2557)

105 AACCTGCTGGAGGTGCCGGCGGATCTA 79 σ 1 AsnLeuLeuGluValProAlaAspLeu

ABX40605 standard; cDNA; 343 BP (first entry) 20-FEB-2003 ABX40605; ABX40605 

RESULT

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Bovine EST associated with lactation/muscle/fat deposition #5770

Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

oncofoetal leucine-rich glycoprotein; 574; tumour;

(first entry)

/\*tag= a /product= "5T4 protein"

1. .1260 /\*tag= a

Location/Qualifiers

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Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                             cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic;
                                                                      cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                 cancer immunotherapy; foetal cell; maternal blood; cyto foetal abnormality; foetal sex determination; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers K, Drury N, Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-557449/59.
P-PSDB; AAU98694.
                                                                                                                                                                                                                                                                                                                                          WO200238612-A2
                                 07-OCT-2002
                                                                                                            Feline; cat;
                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2002
ABK87175;
                                                                                                                                                                                                          Felis sp.
                                                                                                                                                                                                                                                Key
The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are if in the call having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the call to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cissue comprising a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating amarker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for geneme mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constant sequence used sequence tag) nucleic acids in the present sequence as one of the constant sequence as one applied in a bovine and analysis, cattle constant sequence as one as the constant sequence as one of the constant sequence as one as the constant sequence as one as and an analysis of the constant sequence as one as and an analysis of the constant sequence as one as and an analysis of the constant sequence as one as and an analysis of the constant sequence as one as an analysis of the constant sequence as and an analysis of the constant sequen
                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 343 BP; 40 A; 146 C; 108 G; 49 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                         Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 5770; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USPTO web
                                                                                                                                                                                                                                                                                                         Tao N,
                                                                                                              24-SEP-2001; 2001US-00960352.
                                                                                                                                                 12-JAN-1999; 99US-0115707P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the
                                                                                                                                                                                                                                                                                                         Byatt JC, Mathialagan N,
                                                                                                                                                                                                        (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                          WPI; 2003-110599/10.
                                                                                                                                                                                                                                            (TAON/) TAO N.
WARR/) WARREN W C.
                                   US2002137139-A1
                                                                        26-SEP-2002
 Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 514, and the concofoetal leucine-rich glycoproteins known as 514, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell concerning to the invention and or treatment of tumours or other diseases associated with cell concerning to preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in disquestic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, this seues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The contain and in part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AACCTGACCGAGGTGCCCGCGGACCTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AsnLeuLeuGluValProAlaAspLeu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-774-176-19 (1-9) x ABK87175 (1-1260)
Claim 4; Page 68; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
39.00
88.9*
88.9*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
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Length: Matches: Conservative: Mismatches:

47.8 39.00 88.94 88.94

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

.. 9

Indels:

Gabs:

131 AACTTGACCGAGGTGCCGGCCGACCTG 157

ABK87175 standard; cDNA; 1260 BP.

RESULT 6
ABK87175
ID ABK8

1 AsnLeuLeuGluValProAlaAspLeu

US-10-774-176-19 (1-9) x ABX40605 (1-343)

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New major histocompatibility complex class I peptide epitopes from human 574 tumor-associated antigen, useful for preventing and/or treating a
                                                                 Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                   Location/Qualifiers
1. .1260
/*tag= a /*tag= //product= "Feline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5T4 antigen coding DNA of the invention.
                                                                                                                                                                                                                                                     Redchenko I;
                                                                                                                                                                                                                                                                                                                                Disclosure; Page 67; 73pp; English
ADB97513 standard; DNA; 1260 BP
                                                                                                                                                                                                                                   (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                  13-FEB-2002; 2002GB-00003419.
                                                                                                                                                                                                                                                                                                              disease, particularly cancer.
                                                                                                                                                                                                 13-FEB-2003; 2003WO-GB000670
                                 (first entry)
                                                                                                                                                                                                                                                  Carroll M, Kingsman S,
                                                 Feline 5T4 antigen DNA.
                                                                                                                                                                                                                                                                    WPI; 2003-637141/60.
                                                                                                                                                                                                                                                                             P-PSDB; ADB97520
                                                                                                                                                              WO2003068816-A1
                                                                                                   Unidentified
                                04-DEC-2003
                                                                                                                                                                               21-AUG-2003
                ADB97513;
                                                                                                                    Key
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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further provides a polypelicope string comprising the 5T4 epitope; a nucleic acid compression of the 5T4 epitope; a vector system capable of delivering the 5T4 epitope; and the 5T4 epitope string of the 5T4 epitope acid to a cell julsed with the 5T4 epitope, a polypelitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease of a mathod for treating and/or preventing a disease of a mathod for treating and/or preventing a disease of a specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope and/its encoding nucleic acid; a method comprising the 5T4 epitope has cytostatic activity. The vaccine inclear acid in a subject; and a T cell line or clone capable of system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for disquasing or system or cell is useful in the prevention and/or treatment of a disease, presence of the 5T4 epitope or its encoding nucleic acid and the vector system or cell is useful in the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or treating the treating and/or treating the treating treating the treating the treating treating treating treating treati

Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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Conservative:
Mismatches:
Indels:
Length:
Matches:
207
39.00
88.9%
88.9%
                  Percent Similarity:
Best Local Similarity:
Query Match:
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gene; ds, feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                /product= "Feline 5T4 antigen protein"
0
                                  238 AACCTGACCGAGGTGCCCGCGGACCTG 264
                           1 AsnLeuLeuGluValProAlaAspLeu 9
             US-10-774-176-19 (1-9) x ADB97513 (1-1260)
                                                                                                                                                            Location/Qualifiers
                                                                                                           DNA encoding feline 5T4 protein.
                                                                   ADB97452 standard; DNA; 1260 BP
                                                                                                                                                                                                                          13-FEB-2003; 2003WO-GB000618
                                                                                              (first entry)
                                                                                                                                                                  1. .1260
/*tag= a
                                                                                                                                                                                              WO2003068815-A2
                                                                                                                                             Unidentified
                                                                                              04-DEC-2003
                                                                                                                                                                                                            21-AUG-2003
                                                                                 ADB97452;
                                                                                                                                                            Key
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New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.

Kingsman S;

Carroll M, Harrop R, 2003-663795/62

WPI; 2003-663795, P-PSDB; ADB97455

(OXFO-) OXFORD BIOMEDICA UK LTD 13-FEB-2002; 2002GB-00003420

Disclosure; Page 49; 63pp; English.

The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA coding for the feline 5T4 protein.

Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
                  39.00
88.9%
88.9%
88.6%
                                        Similarity:
                             Percent Similarity:
Best Local Similari
Alignment Scores:
                                                 Query Match:
         Pred. No.:
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US-10-774-176-19 (1-9) x ADB97452 (1-1260)

0

Gaps:

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Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                          Canine; dog; oncofoetal leucine-rich glycoprotein; 574; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                                                                               cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                        241 AACCTGACCGAGGTGCCCGCGGACCTG 267
                                US-10-774-176-19 (1-9) x AAF89736 (1-1263)
                                                         1 AsnLeuLeuGluValProAlaAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                              ABK87174 standard; cDNA; 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2001; 2001WO-GB005004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-557449/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers K, Drury N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAU98693
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200238612-A2
                                                                                                                                                                                                     07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2002.
                                                                                                                                                                         ABK87174;
                                                                                                                                                                                                                                                                                                                                   Canis sp.
                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                 ABK87174
                                                                                     용
                                                                                                                                                             The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bebbington CR, Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                          Nucleotide sequence of canine 5T4 protein.
                                238 AACCTGACCGAGGTGCCCGCGGACCTG 264
     Φ
1 AsnLeuLeuGluValProAlaAspLeu
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 26; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD BIOMEDICA UK LID.
                                                                                                                                                                                                                                                                                                                                     1. .1263
/*tag= a
/product= "5T4"
                                                                                        AAF89736 standard; DNA; 1263 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-GB003859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingsman A, Kingsman SM,
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-343805/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB83839
                                                                                                                                                                                                                                                                                                                                                                                             WO200136486-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1999;
                                                                                                                                                23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers KA;
                                                                                                                                                                                                                                                                                          Canie sp.
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/\*tag= a /product= "5T4 protein"

Carroll M;

Location/Qualifiers

.1263

(first entry)

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The present invention relates to the isolation of canine and feline concoocal leucine-rich glycoproteins known as 574, and the concoocal leucine-rich glycoproteins known as 574, and the polymucleotide sequences encoding them. The 574 proteins are expressed in golymucleotide sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell compositions may also broliferation, infections, and inflammacory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracted plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The solucion process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).

The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Claim 1; Page 67; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
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Length:
Matches:
Conservative:
Mismatches:

208 39.00 88.9% 88.9%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores: Pred. No.:

Indels:

34141 CTTCTGGAGGTGCCTGCAGATCTG 34164

RESULT 12

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are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (ii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (vii) for neutralizing the carcinoma; and (xi) for determining carcinoma associated (CA) gene copy number in addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586Al, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 295096 BP; 75726 A; 62659 C; 64620 G; 85924 T; 0 U; 6167 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
80400
                Conservative:
Mismatches:
Indels:
Matches:
                                                                                                                                                               241 AACCTGACCGAGGTGCCCGCGGACCTG 267
                                                                      Gaps:
                                                                                                                                         1 AsnLeuLeuGluValProAlaAspLeu 9
                                                                                                       US-10-774-176-19 (1-9) x ABK87174 (1-1263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 331; Opp; English.
                                                                                                                                                                                                                                                   ACN44068 standard; DNA; 295096 BP
                                                                                                                                                                                                                                                                                                                                                            Mouse genomic sequence mCG13636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                       18-NOV-2004 (first entry)
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88.9%
88.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-328604/31.
                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003073826-AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                        ACN44068;
                                              Query Match
DB:
                                                                                                                                                                                                                                    ACN44068
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The invention relates to human tumour-associated antigenic target (TAT)

polypeptides, and their related nucleic acids. The TAT polypeptides are

overexpressed in cancer tissues compared to normal tissues, and may thus

serve as effective targets for the diagnosis and treatment of cancer in

mammals. The invention also relates to nucleic acid and polypeptide

sequences at least 80% identical to the TAT nucleic acids and

polypeptides; expression vectors and host cells comprising a TAT nucleic

acid; an antibody specific for a TAT polypeptide; usion proteins comprising a

CMT polypeptide; and methods and compositions for the treatment or

diagnosis of cancer in mammals. TAT polypeptides, uncleic acids,

antibodies, antagonists, binding molecules and compositions are useful

for diagnosing or treating a cell proliferative disorder associated with

colorectal cancer, lung cancer, liver cancer, bandear

cancer, pancreatic cancer, cervical cancer, cancers of the central

concer, pancreatic cancer, cervical cancer, cancers of the central

concer, pancreatic ancer, cervical cancer, cancers of the central

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                                                                                                                                              Tumour-associated antigenic target (TAT) cDNA DNA325682, SEQ ID NO:3633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
                                                                                                                                                                                          Tumour-associated antigenic target; TAT; human; overexpression; ctumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; certral nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1641 BP; 376 A; 426 C; 442 G; 397 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                   gene therapy; cytostatic; gene; ss.
                ACN39471 standard; cDNA; 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-2003; 2003WO-US028547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002US-0414971P
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang Z, Zhou Y;
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37.00
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                                                                                                       18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-2004
                                                              ACN39471;
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ACN39471
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295096

Length:

1.59e+05 38.00 100.0% 100.0% 86.4%

Best Local Similarity:

Query Match:

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:

Matches: Conservative: Mismatches: Indels:

Gaps:

US-10-774-176-19 (1-9) x ACN44068 (1-295096)

2 LeuLeuGluValProAlaAspLeu 9

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The invention relates to a cancer cell-specific apoptosis inducing agent comprising, as an active ingredient, a compound which inhibits stabilization of a chromosome, or a compound which suppresses the expression of a gene chosen from APE2, ATR, BRCA1, Chk1, Cdc5, Cdc6, Cdc7, Cdc45, Cdt1, C3A, CSB, Ctf18, DDB1, DDB2, DNA2, DUT, Elg1, Endov, Cdc7, Cdc45, Cdt1, C3A, CSB, Ctf18, DDB1, DDB2, DNA2, DUT, Elg1, Endov, Ligase1, Mad2, MBH1, FBH1, ERN1, Geminin, Hus1, KNTC2, NNC80, MCMT, Cdc6, Ligase1, Mad2, MBH2, PMC3, MCM3, MCM5, MCM5, MCM6, MCM7, MCM8, MCM10, MCM7, Cdc6, Cdc6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer cell-specific apoptosis inducing agent useful as anticancer agent, comprises as active ingredient, compound that inhibits stabilization of chromosome or compound that suppresses expression of gene e.g. APE2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA interference; gene silencing; 88; carcinoma; cytostatic; apoptosis; chromosome stabilization; cancer; DNA damage.
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                                                                                                                              Human TIMELESS homolog, cDNA SEQ ID 632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 632; 181pp; Japanese.
Gaps:
                                                                                               1 AsnLeuLeuGluValProAlaAspLeu 9
                                                   JS-10-774-176-19 (1-9) x ACN39471 (1-1641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENECARE RES INST CO LTD.
                                                                                                                                                                                                                                                  AED22740 standard; cDNA; 1753 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-2005; 2005WO-JP006914.
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                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2005097189-A1
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                                                                                                                                                                                                                                                                                                   AED22740;
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is a double-stranded RNA (siRNA, short interfering RNA), antisense oligonuclectide, a variant protein having dominant negative character with respect to protein encoded by the gene, an antibody and a low molecular weight compound which binds to the protein encoded by the gene. The compounds are useful as anticancer agents. (M1) is useful for manufacturing a pharmaceutrical composition comprising the compound. The compound is useful for elucidating the mechanism of inducing cancer cell specific apoptosis and is highly cancer cell specific, has few or no side effects as an anticancer agent and damage produced in chromosomal DNA is repaired. The present sequence is a CDNA representing a gene target for the compounds of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrinimmune (PMT) activity. The microarray is useful in diagnosing a condition associated with PMI activity, such as CPS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray, psychoneuroendocrinimmune; chronic fatique;
non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expressed sequence tag. Note the ID NO of up to 3314 but only sequences up
                                                                                                                                                                                                                                   Sequence 1753 BP; 407 A; 457 C; 480 G; 409 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                           x AED22740 (1-1753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648 AATATTCTCCATGTTCCAGCTGACCTT
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specificatio mentions SEQ II
SEQ ID NO 1829 are provided.
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88.9‡
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                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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The invention relates to a cancer cell-specific apoptosis inducing agent comprising, as an active ingredient, a compound which inhibits stabilization of a chromosome, or a compound which inhibits catabilization of a chromosome, or a compound which suppresses the expression of a gene chosen from ARE2, ART, BRCA1, Chk1, Cdc5, Cdc6, Cdc7, Cdc45, Cdt1, CSA, CSB, Ctf18, DDB1, DDB2, DNA2, DUT, Elg1, EndoV, EB91, ERM1, FRBN, Geminin, Hus1, KNTC2 (NDE80), KNB0, Ligasel, Mad2, MBD4, MGm3, MGm4, MGm5, MGm6, MGm7, MGm8, MGm10, MGMT, MLH3, Mms4, MPG, MSH2, Mus2, PKN, NEIL2, NEIL2, NFH1, Orc1, Orc3, PRM19, PCNA, Pifl, PmS1, PMS1, PMS2, PKN, Polap180, Pola Pp10, Pola Spp1 (Primza), Polb, Pold pl25, Pole Dpb3, Pole Dpb4, Pole Pol2, Pol1, Pol1, CC Rad54, Rad51, Rad1, Rad18, Rad23A, Rad23B, Rad51, Rad51D, TMBLESS, Tin2, Topoisomerase I, Topoisomerase IIIa, Topoisomerase IIIa, Topoisomerase IIIb, Ubc13, UNG, XAB2, XPC, XPF, XPG, Xrc2 and XRCC4. Also included are an anticancer agent comprising (I) as an active ingredient, screening (M1) apharmaceutical composition (involving screening the compound which a carrier? III, the compound which is the compound which a carrier? III, the compound which a carrier?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer cell-specific apoptosis inducing agent useful as anticancer agent, comprises as active ingredient, compound that inhibits stabilization of chromosome or compound that suppresses expression of gene e.g. APE2, BRCA1, Cdc7, NEIL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA interference, gene silencing; ss; carcinoma; cytostatic; apoptosis; chromosome stabilization; cancer; DNA damage.
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Sequence 3627 BP; 926 A; 894 C; 1039 G; 768 T; 0 U; 0 Other;
                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                         Indels:
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                                                                      Alignment Scores:
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XX AED27337

XX AED7

XX AED7
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purification, chromatin structure maintenance and telomere structure maintenance. The compound, which suppresses the expression of the genes is a double-stranded RNA (siRNA, short interfering RNA), antisense oil gonucleotide, a variant protein having dominant negative character with respect to protein encoded by the gene, an antibody and a low molecular weight compound which binds to the protein encoded by the gene. The compounds are useful as anticancer agents. (MI) is useful for manufacturing a pharmaceutical composition comprising the compound. The compound is useful for elucidating the mechanism of inducing cancer cell specific approasis and is highly cancer cell specific, has few or no side effects as an anticancer agent and damage produced in chromosomal DNA is repaired. The present sequence is a CDNA representing a gene target for
                        damage check point, sister chromatid aggregation or isolation, base excision repair, mismatch excision repair, mucleotide excision repair, homologous-recombination restoration, non-homologous terminal binding restoration, double-stranded MN-cleavage repair, DNA post replication repair (DNA damage tolerance), DNA crosslinking damage repair, DNA protein crosslinking damage repair, DNA protein crosslinking damage repair, DNA
chromosome replication of DNA, chromosome DNA reproduction reaction, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3627 BP; 925 A; 893 C; 1039 G; 768 T; 0 U; 2 Other;
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Matches:
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Title: Perfect score:

Sequence:

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Scoring table:

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BC087011 Rattus no
BC058198 Mus muscu
AX2961912 Sequence
AX061914 Sequence
AJ012160 Mus muscu
AC158294 Rattus no
AC128294 Rattus no
AC106962 Rattus no
AB003707 Maldane c
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AC12545 Rattus no
AC124497 Mus muscu
BV291648 S23296207
AX867373 Sequence
AX821533 Sequence
AX821548 Sequence
AX149553 Sequence
AX149553 Sequence
AX149553 Sequence
AX167371 Sequence
AC156143 Bos tauru
AC156143 Bos tauru
AC156143 Caenorhab
Continuation (22 o
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Continuation (7 of
AC165022 Bos tauru
AC156065 Bos tauru
AC172361 Bos tauru
AC508260 Pyrocysti
X96895 H. sapiens s
AV089992 Toxoplasm
AC090023 Homo sapi
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AC193824 Homo sapi
AL161773 Human DNA
AC025409 Homo sapi
AC166006 Colobus g
AC021127 Homo sapi
AC108909 Mus muscu
AC132450 Mus muscu
AC122888 Mus muscu
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1 (bases 1 to 1281)
Carroll,M.W. and Myers,K.A.
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MILES WILLIAM CARROLL, KEVIN ALAN MYERS
CLANIS/09,A61K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,C12N15/00,
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Patent: JP 2002530060-A 2 17-SEP-2002;
OXFORD BIOMEDICA LTD
OX Mus musculus (mouse)
PN JP 2002530060-A/2
PD 17-SEP-2002
PP 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9825303.2,27-JAN-:
PR 18-NOV-1999 GB 9917995.4
NILES WILLIAM CARROLL,KEVIN ALAN WYIP
PC C12N15/09, A61K39/00,A61K48/00,A61P3;
PC C12N15/00,
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AC084440
CR382128_2
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AC093824
AL161773
AC25409
AC166006
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AC12888
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AC156065
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JP 2002530060-A/2.
Mus musculus (house mouse)
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      υυυυ
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-Q=/abss/ABSSWEB spool/US10774176/runat_26052006_091443_24987/app_query.fasta_1
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-NORM=STORT=10 - GGN - TRREADS=1 - SG052006_091443_24987 - NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 - XGAPOP=10 - XGAPEXT=7
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AX025012 Sequence
AX316087 Sequence
                                                                                                                                   May 27, 2006, 09:51:03 ; Search time 3358.6 Seconds (without alignments) 257.039 Million cell updates/sec
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                      GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd
                                                                                                 using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , C
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Database :

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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATÉRIE: WO 0029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB)
                   ce 1.1281
/organism='Mus musculus (mouse)'.
Location/Qualifiers
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AX316087
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/organism="Mus musculus"
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/db xref="GI:665012"

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MTVL.PAGRARAPPALALAVLAVLASGHHLKBYGAGAREHLPGLARLDLSHNPLTNLSAF

TRAGSNVSVSTPSPLLELILNHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arvelysy 2333 bp mRNA linear ROD 01-JAN-2000 Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA, complete cds.
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Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Bucchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 2333)
Minkina, N.N. and Buchman, V.L.
Structure and expression of the rat 574 gene
Unpublished
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                      Carroll, M.W. and Myers, K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 2 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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/dev stage="newborn"
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPELAGGSAQPPPARCCPACECSEARTYKKVNRNILEVPADLPPYVRNLETTGNQ
MTVLPAGAFARQPPLADLAVLNLSGNHLKEVGAGAFEHLPGLRRLDLSHNPLTNLSAF
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HHLELASNHFLYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KVLHNSTLAEMQGLAHVRVFLDNNPWVCDCYWADWSWLKETEVVPDKARLTCAFPEK
MRNRGHLDLTSSDLDCDATLPQSLQTSYVFLGTVLALIGAIFLLVLYLBRKGIKKWMH
NIRDACRDHMGGYHYRYEINADPRLTNLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="RGD:621453"
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                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 186 Row: o Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                    /mol type="mkNA"
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/db_xref="GeneID:83684"
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/db_xref="RGD:621453"
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/codon_start=1
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butfeard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z361 bp mRNA linear ROD 13-DEC-2004 Rattus norvegicus trophoblast glycoprotein, mRNA (cDNA clone MGC:93332 IMAGE:7193411), complete cds.
HHLELASNHFLYLPRDLLDQLPSLKHLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KYCHNSTLERWGGLAHVRVFLDNNPWYCDCYVADMVSHLKETEVVPDKARLTCAFPEK
MRNRGLLDLTSSDLDCDATLPOSLQTSYVFLGIALALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPSLTYNLSSNSDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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Matches:
Conservative:
Mismatches:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
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                                                                                                                              /gene="574"
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/gene="574"
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Direct Submission
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/gene="Tpbg"
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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Altschul, S.F., Zeeberg, B., Buetow, K. H., Schaefer, C. M., Schuler, G. D.,
Altschul, S.F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heich, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
McKernan, K. J., Malek, J. A., Gunarane, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Poung, A. C., Shevchenko, Y.
Butfard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,
Butterfield, Y. S., Krzywinski, M. I., Skalaka, U., Smailus, D. E.,
Generation, and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, K.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, N.L., Granite, S., Guan, X., Gupca, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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402. 1682
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammilia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Patent: WO 03104277-A 123 18-DEC-2003,
Asahi Kasei Kabushiki Kaisha (JP)
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Euteleostomi;

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                                                                                                                                                                                                                                                                                                         Submitted (23-OCT-1998) Myers K.A., CRC Immunology Group, Paterson Institute for Cancer Research, Christie Hospital, Wilmslow Road, Manchester, M20 9BX, UK
                                                                                                                                                  King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
            AJ012160.1 GI:3805948
5T4 gene; 5T4 oncofetal trophoblast glycoprotein.
Mus musculus (house mouse)
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Location/Qualifiers
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AJ012160
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
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YCHNSTLEARQCLAHVKPLDNNPWVCDCYMDMVAMLKETEVVPDKRRLTCAFPEK
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Mus musculus 5T4 oncofetal trophoblast glycoprotein gene.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugahara,T., Mateuda,A., Honda,G., Muramatsu,S. and Ishizawa,K.
Stat6 activation gene
Patent: WO 03104277-A 125 18-DEC-2003;
ABahi Kasei Kabushiki Kaisha (JP)
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Matches:
Conservative:
Mismatches:
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Sequence 125 from Patent WO03104277.
AX961914
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Matches:
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Mus musculus
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Best Local Similarity:
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Pred. No.:
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                                                                                    No.:
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TITLE
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                                ORIGIN
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AC158516 167046 bp DNA linear ROD 21-JUN-2005
Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
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Direct Submission
Submitted (21-JUN-2005) Genome Sequencing Center, Washington
Submitted (21-JUN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
MO 63108, Liss sequence version replaced gi:61656412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, R.K.
Birect Submission
Submitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 167046)
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Submitted (04-MAY-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Murinae, Murinae, Mus.

( bases 1 to 167046)

Adams, S., Cotton, M. and Haglund, K.

The sequence of Mus musculus BAC clone RP24-511A23
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
       7 9 4 2
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Length:
Matches:
Conservative:
Mismatches:
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Web Bite: http://genome.wustl.edu
botnact: submissions@watson.wustl.edu
Summary Statistics
                                                                                     Indels:
                                                                                                                                                                                                                     4019 AACCTGCTGGAGGTGCCGGCGGATCTA 4045
                                                                                                     Gaps:
                                                                                                                                                                              AsnLeuLeuGluValProAlaAspLeu 9
                                                                                                                                          JS-10-774-176-19 (1-9) x MMU012160 (1-7942)
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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AC158516.2 GI:63025421
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   39.2
44.00
100.0%
100.0%
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                                         Percent Similarity:
Best Local Similarity:
                                                                                     Query Match:
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KEYWORDS
SOURCE
ORGANISM
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Muroidea; Muridae; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

E. (Dases 1 to 210237)
Anjen, C., Allen, H., Alsbrooks, S., Amin, A., Anginano, D., Allen, C., Allen, V., Aoyagi, A., Anghrooks, S., Bara, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Burat, K., Carderons, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, Coyle, M., Cree, A., D'Souza, I., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                   MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                           The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male GSPBL/6J mouse spleen and/or brain genomic DNA. The Clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Sequence derived from PCR product of genomic DNA" 31565. .31779
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/note="Sequence derived from one plasmid subclone."
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HTG; HTGS_PRASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mismatches:
Indels:
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/db_xref="taxon:10090"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP24-511A23"
/clone_lib="RPCI-24"
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Best Local Similarity:
Query Match:
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Pred. No.:
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AC128294/c
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VERSION
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemietry, or covered by high quality data (i.e. phred quality as 230); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The sasembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is

Center project name: M\_BB0511A23 Drafting center: WIBR

NOTICE:

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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Bean, C., Eranger, C., Evanger, C., Franger, E., Fonger, M., Escotto, M., Engag, N., Forbes, L., Foster, M., Fester, P., Franger, C. M., Gabisl, A., Ganta, R., Garcia, A., Garner, T., Gazza, M., Gebregorgie, E., Geer, K., Gall, R., Garcia, A., Garner, T., Gazza, M., Gunazatne, P., Hanaland, W., Hamilton, C., Hamilton, K., Harrandez, P., Hander, P., Hawes, A., Henderson, N., Hernandez, J., Handells, S., Hluyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, A., Jackson, L., Jacob, L., Jangh, H., Johnson, B., Obhnson, R., Johnson, R., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Levan, J., Levan, J., Kovar, C., Karpathy, S., Kally, S., Khan, Z., Khan, J., Kovar, C., Liu, W., Lul, W., Loulsegd, H., Lozado, R. J., Lu, X., Mar, J., Mangum, B., Manhindartne, M., Mannoud, M., Malloy, K., Mangum, R., Mandum, B., Martin, K., Martin, R., Martine, E., Morean, M., Morgan, M., Morzis, K., Morzis, S., Munidasa, M., Norris, S., Mordan, M., Norris, S., Munidasa, M., Norris, S., Mordan, M., Norris, S., Norden, C., Papaternak, S., Paul, M., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, M., Ren, Y., Reigh, R., Reigh, R., Reilly, M., Ren, Y., Reiger, M. A., Reigh, R., Reilly, M., Ren, Y., Reiger, M. A., Ken, S., Scherr, A., Sodersten, B., Song, Y., Sharter, Beyovic, D., Primas, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., John, H., Stefinle, M., Strong, R., Yare, J., Warley, R., Weigh, N., Walas, R., Wals, Y., Walas, R., Wals, W., Wang, W., Wals, Y., Wals, W., Wals, Y., Wals, W., Wals, Y., Walsh, W., Wals, W., Wals, Y., Walsh, W., Wals, W., Walsh, W.,
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On Nov 19, 2002 this sequence version replaced gi:23265004.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GZGV
Center clone name: CH230-176H20
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Rat Genome Sequencing Consortium.
Direct Submission
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Worley, K.C.
Direct Submission
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COMMENT

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Z39076 bp DNA linear HTG 20-NOV-2002 unordered pieces. 4
                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mefazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Solurognath; Muroidea; Murinae; Rattus.

1 (bases 1 to 239076)
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Assembly program: Phrap; version 0.990329
Consensus quality: 201781 bases at least Q40
Consensus quality: 203921 bases at least Q30
Consensus quality: 205310 bases at least Q20
Estimated insert size: 205531; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 210237: contig of 210237 bp in length.
Location/Qualifiers
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Mismatches:
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/note="clone_boundary
clone_end:Sp6
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clone_end:T7"
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clone_end:Sp6"
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/db_xref="taxon:10116"
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208907. .210237
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/note="clone_boundary
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AC106962/c
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Fri Jun

COMMENT

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Maldane cristata mRNA for elongation factor-lalpha, partial cds.
AB003707
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NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Annelida; Polychaeta; Scolecida; Capitellida;
                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329
Consensus quality: 228642 bases at least Q40
Consensus quality: 232269 bases at least Q30
Consensus quality: 234041 bases at least Q20
Bstimated insert size: 231522; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234710: contig of 234710 bp in length 234810: gap of unknown length 235924: contig of 1114 bp in length 235014: contig of 1120 bp in length 237314: contig of 1290 bp in length 237414: gap of unknown length 239076: contig of 1662 bp in length.
                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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Matches:
Conservative:
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/mol_type="genomic DNA"
/db_Xref="taxon:10116"
/clone="CH230-87110"
                                               ----- Genome Center
Center: Baylor College of Medicine
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                                                                                                                                      Contact: hgsc-help@bcm.tmc.edu
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us-10-774-176-19.p2n.rge

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Center project Information
Center project name: GHWQ
Center clone name: CH230-11811
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IVGVNKMDNTEPPYSGPRFDEIKKEVGGYIKKIGYNPDTVPFVPISGWHGDNMLEKSD
KMSWYNGMOVKKVDKKEYKGYTLMDLDNIDPPRRPTDKALRLDLQDVYKIGGIGTVP
VGRVETGVLKPGMVYTFAPPHITTEVKSVEMHQALTBAEPGDNVGFNIKNVSVKDVR
RGNVCGDSKNDPPAGTEFERSOVIILMHPGQIQAGYAPVVDGHTAHIACRFKELLEKI
DRRSGKKLEDNPAHVKSGDACIVEMVPGKSMCVEAFVNYAP"
                                                                                                                                                                                                                                                                        Ocean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1. .>1125
/codon_start=1
/product="elongation factor-lalpha"
/protein_id="BAA25736.1"
/db_xref="C1:3063355"
/translation="QEMGKGSFKYAWVLDKLKABRERGITIDIALWKFETSKYYVTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC098662 236951 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-11811, *** SEQUENCING IN PROGRESS
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Muzny, D.Marie., Mctzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyadi, A., Ayodii, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blart, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Clacko, J., Chavaz, D., Chen, G., Cookrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
                                                                                                                                                                                                                                                             Submitted (07-MAY-1997) Shigeaki Kojima, University of Tokyo, Ocea Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164, Japan (E-mail:kojimaetrout.ori.u-tokyo.ac.jp, Tel:03-5351-6473, Pax:03-5351-6471)
                      1 (sites)
Cydima,S.
Paraphyletic status of Polychaeta suggested by phylogenetic
analysis based on the amino acid sequences of elongation factor-1
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                           Phylogenet. Evol. 9 (2), 255-261 (1998)
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mismatches:
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Matches:
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/db_xref="taxon:73384"
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Maldanidae, Maldane
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41.00
100.0%
88.9%
93.2%
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Direct Submission
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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Fangan, A., Egorato, M., Eugene, C., Evana, C.A., Falls, T., Fang, F., Fangan, A., Eascato, M., Elagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gablai, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregoergis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Hadland, W., Hamil, Co., Hamilton, C., Hamilton, K., Handler, J., Hongerson, N., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Herderson, M., Hernandez, M., Gores, M., Garreit, M., Gunaratne, J., Jang, H., Johnson, R., Johnson, R., Johnson, K., Jokkson, J., Gackson, L., Jang, H., Johnson, R., Johnson, R., Jokkson, J., Karpetty, S., Kelly, S., Lopez, J., Liu, M., Liu, W., Liu, Y., Louisege, H., Locado, R.J., Lu, X., Ma., J., Mandludartne, M., Mahroud, M., Malloy, K., Mangum, A., Mandum, B., Mapua, P., Martin, R., Mart
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.uc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- Genome Center
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2 (bases 1 to 236951)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Center code: BCM
Web Bite: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
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AUTHORS
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JOURNAL
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                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC125765 244451 bp DNA linear HTG 19-NOV-2002 Rattus norvegicus clone CH230-231L11, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 24451)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,
               Assembly program: Atlas 3.0; Consensus quality: 204463 bases at least Q40 Consensus quality: 208139 bases at least Q30 Consensus quality: 210836 bases at least Q20 Estimated insert size: 216195; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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|clone="CH230-11811"
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--- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-774-176-19 (1-9) x AC098662 (1-236951)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AsnLeuLeuGluValProAlaAspLeu 9
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80470. .82578
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225406, ,226786
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88.9%
93.2%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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AC125765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
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SOURCE
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ORIGIN

LOCUS

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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Nov 19, 2002 this sequence version replaced gi:23907923.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delagado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Degado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Bagan, A., Bacotch, R., Bagan, M., Plagg, M., Plagg, M., Parag, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Probes, L., Foster, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Genera, M., Gebregeorgis, E., Haeland, M., Hamll, C., Hamllton, K., Harrandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hallyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, A., Jacob, L., Labow, H., Lews, D., Liu, J., Liu, M., Liu, Y., Lonlseged, H., Longacre, S., Lopez, J., Liu, J., Liu, M., Liu, Y., Lonlseged, H., Loraado, R., Martin, R., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (30-UUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 24451)
Rat Genome Sequencing Consortium.
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
Center project Information
Center project name: GZFE
Center clone name: CH230-231L11
Center clone name: CH230-231L11
Center clone program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 237334 bases at least Q40
Consensus quality: 240866 bases at least Q30
Consensus quality: 240866 bases at least Q20
Estimated insert size: 244791; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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US-10-774-176-19 (1-9) x AC125765 (1-244451)

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244451

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.92e+03 41.00 100.0% 88.9% 93.2%

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

Pred. No.:

Gaps:

Search completed: May 27, 2006, 19:35:48 Job time : 3381.6 seca

Sequence:

Run on:

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Abx76333 Lung canc
Adb80503 Ovarian c
Adn38723 Cancer/an
Abx87175 cDNA enco
Adb97452 DNA enco
Adb97452 DNA enco
Adb97452 DNA encod
Add56199 Human LRR
Add56209 Human LRR
Add56209 Human LRR
Adj56299 Human LRR
Add56200 Human LRR
Add56197 Human LRR
Add36200 Human LRR
Add36200 Human LRR
Add36310 Tumour-as
Adv35098 Human cDN
Add13631 Full leng
Add1761 Fibrotic
Ads87175 DNA encod
Aak44254 Human ful
Ad130831 Full leng
Ad130831 Full leng
Ad130831 Full leng
Ad130831 Full leng
Ad13083 Full leng
Ad13083 Bacterial
Ad13083 Bacterial
Ad177826 SfUCPa de
Ag477782 Subcloned
Aaf89736 Nucleotid
Abk87174 cbnA enco
Acd93536 Human col
Aa897174 DNA encod
Adul1677 Solid tum
Abt 0771 Breast ca
Abx76333 Lung canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ads64173 Bacterial
Adt46017 Bacterial
Ads63789 Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse, TAA, tumour-associated antigen, anti-tumour, cytostatic; immunostimulant, vaccine; carcinoma, colorectal cancer, gastric cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                   ABK87175
ADB97513
ADB97452
AAA27058
AAD56199
                                                                                                                                                                                               ADJ56299
ACC51052
ABX76332
AAD56197
ADD56200
ADN38721
ADL06473
ADN03961
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ADT42735
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ACD93536
                                              ADU11677
ABT07721
                                                                      ABX76333
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AED17761
AAS87175
AAK94253
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ADI26162
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                                      AAS87174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA27059 standard; DNA; 1281 BP
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   AAA27059;
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                          Aaa27059 Mouse 5T4
Adi26160 Human CDN
Adi26158 Human CDN
                                                                                                 (without alignments)
249.339 Million cell updates/sec
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                                                                                    May 27, 2006, 09:34:35 ; Search time 377.5 Seconds
             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                            nucleic search, using frame plus p2n model
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That. The TAN 1914 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastrasis in colorectal and gastric cancer. 574 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been inculated with a virus expression vector containing the present sequence. The 574 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject. The present sequence appears in GenBank at accession number AJ012160
                                                                                                          Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                 The present sequence encodes the mouse 5T4 tumour-associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1281 BP; 246 A; 410 C; 354 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                    Example 2; Page 78; 79pp; English.
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Length: Matches: Conservative: Mismatches: Indels: US-10-774-176-18 (1-9) x AAA27059 (1-1281)

919 TACATGGCTGACATGGTGGCTTGGCTT 945 1 TyrMetAlaAspMetValAlaTrpLeu 9 ВР ADI26160 standard; cDNA; 2557 (first entry) 22-APR-2004 ADI26160; 

Human cDNA encoding protein that promotes STAT6 activation #63.

se; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmunodisease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

Homo sapiens

WO2003104277-A2

18-DEC-2003

05-JUN-2003; 2003WO-JP007123

2002US-0436467P. 2003JP-00137505. 2003US-0470836P. 2002US-0385912P. 2002JP-00377326. 05-JUN-2002; 06-JUN-2002; 26-DEC-2002; 27-DEC-2002;

ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; sichaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.

WO2003104277-A2.

18-DEC-2003

Human cDNA encoding protein that promotes STAT6 activation #62.

Ž (ASAH ) ASAHI KASEI

16-MAY-2003

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant or promote STAT6 activation. A transformant composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosums, septem.

C Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, ischemmic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activation or inhibition of STAT6. The present sequence represents a compounds for treating and preventing hyperactively useful for screening compounds for treating and preventing hyperactively useful for screening compounds for treating and preventing hyperactively activation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
                                                                                             Ltransducer and activator of transcription 6 activation purified protein, for diagnosing and treating disease with activation/inhibition of transcription factor e.g.
  Muramatsu S, Ishizawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 513 A; 729 C; 696 G; 619 T; 0 U; 0 Other;
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                                                                                                                                                                                                    Claim 4; SEQ ID NO 125; 1368pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x ADI26160 (1-2557)
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Honda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР.
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Matsuda A,
                                                                                                  signal transducer
                                                                                                                                                            diabetes and cancer.
                                     WPI; 2004-122214/12.
P-PSDB; ADI26161.
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Best Local Similarity:
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Sugahara T,
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                                                                                                                      promoting
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compounds which inhibit or programmer and an antigen. The nucleic acid is useful for expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions antibodies and antisense molecules are useful for the treating a disease associated with STATE activation such as allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful creating disease associated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arrhitis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, is chaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AlDS. The protein has efficient promoting STATE activity. The protein or nucleic acid is effectively useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                            New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activation or inhibition of STAT6. The present sequence repurer
human cDNA encoding a protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                      Ishizawa K;
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                                                                                                                                                                                                                                                                                                   Muramatsu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID NO 123; 1368pp; English
                                                                                                                                                                                                                                                                                                   Honda G,
                                                                                           06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002UP-00377336.
27-DEC-2002; 2002US-043647P.
15-MAY-2003; 2003US-04135595.
16-MAY-2003; 2003US-0470836P.
                          05-JUN-2003; 2003WO-JP007123
                                                                                                                                                                                                                                                                                                   Sugahara T, Matsuda A,
                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASEI KK
                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-122214/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADI26159
                                                                      05-JUN-2002;
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Length: Matches: Conservative: Mismatches: Indels: 9.6 50.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-774-176-18 (1-9) x ADI26158 (1-2557)

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1474 TACATGGCTGACATGGTGGCTTGGCTT 1500 TyrMetAlaAspMetValAlaTrpLeu

AAF89736 standard; DNA; 1263 23-JUL-2001 (first entry) \*\*\*\*\*\*\*

Nucleotide sequence of canine 5T4 protein.

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which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The Scr antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The Scr antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacter
Single chain antibody, ScFv; inflammatory disease; arthritis, cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes the use of a single chain antibody (ScFv),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encodes a 5T4 protein, which is used to produce ScFv of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ellard FM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Carroll MW,
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Matches:
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                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related diseases, and other immune
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/product= "5T4"
                                                                                                                                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LTD
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2000GB-00005071.
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P-PSDB; AAB83839.
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02-MAR-2000;
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the proposition of polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used in disquestic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating feetal cells from maternal blood. The isolation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                         Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; call prollferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                     cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present sequence encodes canine 5T4 protein
                                                                                                                                                                                                                                                 /*tag= a
/product= "ST4 protein"
                                                                                                                                                                                               Location/Qualifiers
1. .1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, Page 67, 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2001; 2001WO-GB005004
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAU98693
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07-OCT-2002
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Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
         41.7
45.00
100.0%
88.9%
90.0%
                             Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                Query Match:
DB:
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US-10-774-176-18 (1-9) x ABK87174 (1-1263)

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1 TyrMetAlaAspMetValAlaTrpLeu 9
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RESULT 6 ACD93536

ACD93536 standard; cDNA; 299 BP.

ACD93536;

(first entry) 23-SEP-2003

Human colon cancer cell expressed cDNA #1948.

Open reading frame detection, genome sequencing, colon cancer; breat cancer; breat cancer; antibiotic resistance; antibiotic non-colorance, congenital disease; agriculture; food crop genome, resistance gene, retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; gene; ss.

Homo sapiens.

US2002155438-A1. 

24-OCT-2002

99US-00406117. 27-SEP-1999;

98US-00196716. 20-NOV-1998;

(SIMP/) SIMPSON A J G. (NETO/) NETO E D. (BREN/) BRENTANI R R.

Brentani RR; Simpson AJG, Neto ED,

WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of ndividual

Example 9; Page 302; 959pp; English.

The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer; (1) at low stringency, preparing wingle aligonucleotide primer; (1) at low stringency, preparing wingle astranded cDNA by reverse transcribing mRNA with (1), amplifying contacting, preparing contolled modernee from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, nucleotide sequence of an organism. mRNA is obtained from mammalian controll which is associated with a pathological condition e.g. a nucleotide sequence of an organism. mRNA is obtained from mammalian controll which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of copulations of subjects and can be used to carry our genetic analyses of parge or small populations. further, it can be used to study living systems to determine if, e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with an individual or population more or less likely to be afflicted with an individual or population more or less likely to be passed to offspring the study of whether the conditions are likely to be passed to offspring through over or sperm. The method can also be used in the study of whether the conditions are likely to be passed to offspring through over or sperm. The malyses for pathological conditions can be studied in this way compared to determine if the pathogens which integrate into the genome, such as critical out in all animals, plants of present, deferent approaches to critical parameter of determination of the pathogens which integrate into the genomes wifice or mutations, which may require different approaches to critypanosomes different types of Plasmodium, et

us-10-774-176-18.p2n.rng

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a clypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in cappersity responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
Sequence 299 BP; 75 A; 84 C; 78 G; 62 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #22978.
                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                     Gaps:
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                                                                                                                                                        1 TyrMetAlaAspMetValAlaTrpLeu
                                                                                                                              x ACD93536 (1-299)
                                                                                                                                                                                                                                     AAS87174 standard; cDNA; 453 BP
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23-AUG-2000; 2000US-00649167.
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                                    52.2
41.00
88.9%
77.8%
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                                                                                                                              US-10-774-176-18 (1-9)
                                                             Percent Similarity:
Best Local Similarity:
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                        Alignment Scores:
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The invention describes a method comprising comparing an expression profile of at least one gene in a peripheral blood sample of a patient to at least one gene in a peripheral blood sample of a patient to the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an unsupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, the majority of the second class of patients has a second clinical outcome. Also described are: a system comprising (i) a memory or a cutome. Also described are: a system comprising (i) a memory or a storage medium including date that represent an expression profile of at least one gene in a peripheral blood sample of a patient who has a solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic, gene therapy; expression profile, solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                           0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
                                                                                                                                           Sequence 453 BP; 108 A; 111 C; 113 G; 121 T;
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23-JAN-2004; 2004US-0538246P.
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Immerman F, Dorner AJ;
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41.00
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(STRA/) STRAHS A.
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DB:
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tumour, (ii) at least another storage medium including data that tegresent at least one reference expression profile of the gene, (iii) a program capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the expression profile, and (iv) a processor capable of executing the comprision profile of patients who have the solid tumour correlate with clinical outcomes of the patients who have the solid tumour prognosis genes, where each of the solid tumour prognosis genes, where each of the solid tumour prognosis genes, where each of the solid tumour prognosis genes, where poth the first and second classes of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients has a second class of patients has a first clinical outcome. And the second class of patients has a second clinical outcome. The method, system, and array are useful for prognosing and treating solid tumours. This sequence represents a solid tumours prognosis gene of the invention. Note: The sequence acts for this patent did not form part of the program part of the program of the patients of the patients has a second class of the patients a solid tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development.
                                                                                                                                                                                                                                                                                                                              directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                      Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other;
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Matches:
Conservative:
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09-APR-2001; 2001US-00829472.
09-APR-2001; 2001US-028698P.
04-MAY-2001; 2001US-0288590P.
29-MAY-2001; 2001US-0294443P.
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41.00
88.9%
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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   8888888888888888888888888
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer calls. Genes identified by the cargon of the invention can be used in diagnostic purposes and also as the argent of the invention can be used in diagnostic purposes and also as cargets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT0763 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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                                                                                                                 Claim 9; Page 372; 414pp; English.
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2001US-0339245P.
2001US-0350666P.
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88.9%
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     cancer nucleic acids.
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Best Local Similarity:
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10-MAY-2001;
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersenativity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                       Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                        Claim 22; Page 336; 453pp; English
                                                                                                          expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 41.00 88.9\$ 77.8\$ 82.0\$ Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-774-176-18 (1-9) x ABX76333 (1-927)

1 TyrMetAlaAspMetValAlaTrpLeu 9 RESULT 11 셤 8

ADB80503 standard; DNA; 927 ADB80503; ADB80503 

ВЪ

Ovarian cancer-associated transcript #34. (first entry) 04-DEC-2003

cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.

Homo sapiens

Location/Qualifiers /\*tag= Key

WO2002102235-A2

27-DEC-2002

18-JUN-2002; 2002WO-US019297,

18-JUN-2001; 2001US-0299234P. 27-AUG-2001; 2001US-0315287P. 05-SEP-2001; 2001US-0317544P.

13-NOV-2001; 2001US-0350666P. 12-APR-2002; 2002US-0372246P. 

(EOSB-) EOS BIOTECHNOLOGY INC

Gish KC; Mack DH,

WPI; 2003-167431/16. P-PSDB; ADB80504.

Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.

Claim 10; Page 297; 332pp; English.

The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids used for the detection method of the invention.

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 41.00 88.9% 77.8% 82.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: Score:

US-10-774-176-18 (1-9) x ADB80503 (1-927)

559 CACATGGCAGACATGGTGACCTGGCTC 585 σ 1 TyrMetAlaAspMetValAlaTrpLeu ð

RESULT 12 ADN38723 ADN38723;

ADN38723 standard; cDNA; 927

17-JUN-2004 (first entry)

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41

fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory disease, autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; Human; differential expression; cancer; angiogenic disorder; 

detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; valnerary; gene therapy; vaccine; gene; ss.

Homo sapiens.

22-MAY-2003

13-NOV-2002; 2002WO-US036810.

(first entry)

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Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                     Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 74-75; 99pp; English.
                                                                                                                                                                                                                                  22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                     21-OCT-2002; 2002WO-US033540.
                              Human LRRCAPS related DNA #5.
                                                                                                                                                                                                                                                                                                                                              Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                              Belvin M, Schleithoff L,
                                                                                                                                                                                                                                                                                                 (EXEL-) EXELIXIS INC.
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                                                                                                                                        WO2003035831-A2.
                                                                                                           Homo sapiens.
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and methods are useful for disgnosing, prognosing and treating antibodies and methods are useful for disgnosing, prognosing and treating antibodies and methods are useful for disgnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart diseases, attended are useful to wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
                                                                                                                                                                                                                                                                                                                               Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a nucleic acid sequence of the invention
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                                                                                                                                                                                                                                                                                                                               Aziz N, Ginsburg WM, Murray R, Watson SR,
                                                                                         2002US-0347349P.
2002US-0355250P.
2002US-0356714P.
2002US-0359077P.
                                                                                                                                                       2002US-0368809P.
2002US-0370110P.
2002US-0372246P.
2002US-0386614P.
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                                              2001US-0335394P.
2001US-0340376P.
2002US-0347211P.
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2002US-0397845P.
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P-PSDB; ADN38724.
                                                                             38-JAN-2002;
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Mack DH,
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Plowman GD, Funke RP, Lioubin MN,

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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comportsing a purified Leucine rich repeat, capridous related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; noctropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility;
                                                                                                                                                                                                                                                                                                            Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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Length:
Matches:
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Mismatches:
Indels:
Gaps:

178 41.00 88.9% 77.8% 82.0%

Best Local Similarity: Percent Similarity:

Query Match: OB:

CACATGGCAGACATGGTGACCTGGCTC 585 1 TyrMetAlaAspMetValAlaTrpLeu 9

AAD56198 standard; DNA; 973

RESULT 13 **AAD56198**  AAD56198

US-10-774-176-18 (1-9) x ADN38723 (1-927)

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neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; mecabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
obesity; infectious disease; anorexia;
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2001US-0275601P.
2001US-0276000P.
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2001US-0277833P.
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2001US-0288066P.
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2001US-0304354P.
2001US-0309198P.
netabolic disorder; diabetes;
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2001US-0274281P.
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2001US-0333272P
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14-MAR-2001;
16-MAR-2001;
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12-MAR-2001;
13-MAR-2001;
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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disease, Alzheimer's disease, Parkinson's disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in
                                                                                                                                                      Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                                                                                                                      New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feline, cat, oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0 U; 0 Other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 114-115; 619pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic or diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK87175 standard; cDNA; 1260
                03-DEC-2001; 2001US-0338092P-04-DEC-2001; 2001US-0337185P-03-JAN-2002; 2002US-0345705P-08-MAR-2002; 2002US-00093463.
2001US-0337426P
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88.9$
77.8$
82.0$
                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, and asthma.
                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                  WPI; 2002-732824/79.
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Best Local Similarity:
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  03-DEC-2001;
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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell conforming in animals, proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in disgnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, issues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
cancer immunotherapy, foetal cell, maternal blood, cytostatic, foetal abnormality, foetal sex determination, gene, 88.
                                                                                                   Location/Qualifiers
1. .1260
/*tag= a
/product= "5T4 protein"
                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 68; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Carroll M;
                                                                                                                                                                                                                                                                                                                                    13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                            13-NOV-2001; 2001WO-GB005004.
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P-PSDB; AAU98694.
                                                                                                                                                                                                                                                                                                                                                                                                                    Myers K, Drury N,
                                                                                                                                                                                                           WO200238612-A2
                                                                                                                                                                                                                                                   L6-MAY-2002
                                                               Felis sp.
                                                                                                       Ke.
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 248 41.00 88.9% 77.8% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

JS-10-774-176-18 (1-9) x ABK87175 (1-1260)

898 CACATGGTGGACATGGTGGCCTGGCTC 924 1 TyrMetAlaAspMetValAlaTrpLeu 9 :::||| ||||||||||||

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Search completed: May 27, 2006, 10:38:49 Job time : 379.5 secs

Scoring table:

Minimum DB Maximum DB

Searched:

Perfect score:

Title:

Sequence:

OM protein

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AC128294 Rattus no
AC106962 Rattus no
AX149553 Sequence
AX467371 Sequence
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294208 H sapiens f
CQ920916 Sequence
DD161112 Novel Ant
AX821543 Sequence
AX821543 Sequence
AX821543 Sequence
AX821548 Sequence
AX822511 Sequence
AX025011 Sequence
CQ731678 Sequence
CQ731678 Sequence
DD174290 METHODS O
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CQ78274 Sequence
AX047786 Homo sapien
AX961916 Sequence
AX047786 Homo sapien
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AC158516 Mus muscu
AF063939 Rattus no
BC087011 Rattus no
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordato; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                AY328023 Symbiont
Continuation (210
                                                                                                                                                       Continuation (22 DQ157839 Triticum
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C12N15/09, AG1K39/00, AG1K48/00, AG1P35/00, C07K7/06, C07K14/065, C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                           CQ782726 SAK074790 BC037161 B
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Potent: JP 2002530060-A 2 17-SEP-2002;
CXFORD BIOMEDICA LTD
OX Mus musculus (mouse)
PD 17-SEP-2002
PP 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9925303.2,27-JAN-1999 GB 30-JUL-1999 GB 9917995.4
PI MILES WILLIAM CARROLL, KEVIN ALAN WYERS
PC C12N15/09, A61K39/00, A61K48/00, A61P35/00, CO7K7/PC C12N15/00,
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AP008211 209
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HSJ492P14
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JP 2002530060-A/2.
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1000.0 2423
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  RESULT 1
BD249732
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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-NO FWAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPPOP=6 -FGAPEXT=7
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AX025012 Sequence
AX316087 Sequence
                                                                                 ; Search time 3358.6 Seconds
  (without alignments)
257.039 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
             GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.

    nucleic search, using frame_plus_p2n model

                                                                                                                                                                                                                                                      6366136 segs, 31973710525 residues
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Database

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Score

Result No.

Homo sapi Macaca fa Homo sapi

Human DNA Mouse DNA Mouse DNA

Homo sapi Homo sapi

Sequence

Pred. No.:

PEATURES

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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      дествения поставлять пременения 2423 рр мкма linear ROD 21-OCT-2003 musculus trophoblast glycoprotein, mRNA (cDNA clone MGC:68145 IMAGE:5353871), complete cds.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Submitted (15-SEP-2003) National Institutes of Health, Mammalian
Submitted (15-SEP-2003) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                5t4 tumour-associated antigen for use in tumour immunotherapy Patent: BP 116033-A 2 05-DEC-2001; Oxford Blomedica (UK) Limited (GB) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Matches:
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Best Local Similarity:
Query Match:
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Pred. No.:
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JOURNAL
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PUBMED
AUTHORS
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JOURNAL
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BC058198
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide
Patent: WO 029428-A 2 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
                    Location/Qualifiers
1. .1281
/organism='Mus musculus (mouse)'.
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Conservative:
Mismatches:
Indels:
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    .1281
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    ..1281
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    /mol_type="genomic DNA"
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AX316087
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Sequence 2 from Patent WO0029428.
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                                                                                Location/Qualifiers
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Mus musculus
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      Polypeptide
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Best Local Similarity:
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Best Local Similarity:
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REFERENCE AUTHORS TITLE JOURNAL

FEATURES

RESULT 2 AX025012 LOCUS

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Pred. No.:

Score:

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PAT 14-JAN-2004

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Euteleostomi;

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VFAGSNASVSAPSPLEELILNHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
TRLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
KVLHNSTLAEWGGLAHVKVFLDNNPWYDCYMADMVAMLKETEVVPDKARLTCRFPEK
MRNRGLLDLNSSDLOEDAVLPQSLQTSYVFIGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHNEGYHKYEINADPRLYNLSSNBOV"
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSVPSSSTS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene Patent: WO 03104277-A 123 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muroidea; Muridae; Mus.
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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Sequence 123 from Patent WO03104277.
AX961912
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/db_xref="taxon:10090"
556".1836
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                     Indels:
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/organism="Mus musculus"
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/db_xref="G1:40881323"
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                                                                                       (1-2423)
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                                                                                     x BC058198
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Best Local Similarity: 100.0%
Query Match: 100.0%
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AUTHORS
TITLE
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AX961912
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AX961914
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                                                                                                                                                     Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R. W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karline, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Peargeon, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse." /clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFAGSNASVSAFSPLEELILMHYPPEDORONGSFEGNVAFEGNVAAALRSGLALRGL
TCLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHEDNAL
KYLHNSTLABMGGLAHVKYPLDNNPWYCDCYNADMVAMLKETEVVPDKARLTCAFPEK
MRNRGLLDLNSSDLDCDAVLPSOLGTSYVFIGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                      found
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MTVLPAGAFARQPPLADLEALNLSGNHLKEVCAGAFEHLPGLRRLDLSHNPLTNLSAF
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                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: p Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755854.
Location/Qualifiers
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protein [Function unknown]"
/db xref="CDD:COG4886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="LRRCT; Region: Leucine rich repeat C-terminal
                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2423
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Matches:
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402_.1682
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    .2423
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="FVB/N"

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|db_xref="MGI:1341264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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  Contact: MGC help desk
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/gene="Tpbg"
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PAT 14-JAN-2004

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                    /bound_r
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Best Local Similarity:
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VFAGSNASVGAPSPLEELILMHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
TRLELASNHPLPLPRDLLAQLPSLTK.LDLRNNSLVSLTYASFRNLTHLESLHLBBNAL
KVLHNSTLLEMQGLAHVKVELDNNPMVCDCYMADMVAMLKETEVVPDKARLTCEPPEK
MRNRGLLDLMSSDLOCDAVLPQSLQFSYVFLGTVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
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Mus musculus 5T4 oncofetal trophoblast glycoprotein gene.
AJ012160
                                                                                                                                                                                                                                                                    /trānslation="MPGAGSRGPSAGDGRLRLARLALVLLGWVSASAPSSSVPSSSTS
PADFLASGSAQPPPAERCPAACECSEAARTVKCVNRNLLEVPADLPPYVRNLFLTGNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (13-0CT-1998) Myers K.A., CRC Immunology Group, Paterson
Institute for Cancer Research, Christie Hospital, Wilmslow Road,
Manchester, M20 9BX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      King, K.W., Sheppard, F.C., Westwater, C., Stern, P.L. and Myers, K.A. Organisation of the mouse and human 5T4 oncofoetal leucine-rich glycoprotein genes and expression in foetal and adult murine
                      Sugahara, T., Matsuda, A., Honda, G., Muramatsu, S. and Ishizawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5T4 gene; 5T4 oncofetal trophoblast glycoprotein. Mus musculus (house mouse) Mus musculus
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                /note="unnamed protein product" /codon_start=1
                                  State activation gene
Patent: WO 03104277-A 125 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:10090"
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                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                   /proteIn_id="CAF06466.1"
/db_xref="GI:40881325"
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/clone_lib="Lambda Dash"
3108. 3113
/bound_moiety="Spl"
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/strain="129/Sv"
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MTVLPAGAPARQPPLADLEALNLSGNHLKEVCAGAPEHLPGLRRLDLSHNPLTNLSAF
VFAGSNASVSAPSPLEELILNHIVPPEDQRQNGSFEGMVAFEGMVAAALRSGLALRGL
TRLELASNHFLFLPRDLLAQLPSLRYLDLRNNSLVSLTYASFRNLTHLESLHLEDNAL
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Mus musculus BAC clone RP24-511A23 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                          KVIJINSTIJAEWQGIAHVKVPIDNNPWYCDCYMADMVAWIKETEVVPDKARLTCAFPEK
MRNRGLLDINSSDLDCDAVLPQSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKMMH
NIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV"
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1 (bases 1 to 167046)

1 (bases 1 to 167046)

1 The sequence of Mus musculus BAC clone RP24-511A23

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="5T4 oncofetal trophoblast glycoprotein"
5713. 5718
5713. 5718
/gene="5T4"
/gene="5T4"
/gene="5T4"
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Mismatches:
Indels:
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Matches:
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moiety="Sp1"
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AC158516.2 GI:63025421
                                     /gene="514"
3152. .34"
                                                                                                     /gene="5T4"
3779.
                                                                                        /gene="5T4"
3451. .5779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="5T4"
3866. .5056
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                           gene="5T4
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

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AUTHORS REFERENCE

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AF063939 2333 bp mRNA linear ROD 01-JAN-2000
Rattus norvegicus 5T4 oncofetal antigen homolog (5T4) mRNA,
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MTVLPAGAFARQPPLADLAVLNLSGNHLKEVCĀGĀFĒHLPGLRRLDLSHNPLTNLSĀF
TFAGSNVSVSTPSPLLELILNHIVPPEDQRQNGSFEGMVAĀFEGMVĀĀALRSGLALRGL
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KVLHNSTLEBRØGLAHYRVELDNNPWYCDCYNADMYSMLKETEVVPDKARLTCARPEK
MRNGELDLTSSDLDCDATLPGSLOTSYVELGIVLALIGAIFLLVLYLNRKGIKKWMH
NIRDACRDHMEGYHYRYEINADPSLTNLSSNSDV"
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Submitted (06-MAY-1998) School of Biomedical Sciences, University
of St. Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                              142336. .142347
/note="Sequence derived from one plasmid subclone."
/note="Unresolved simple sequence repeat."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure and expression of the rat 5T4 gene Unpublished
                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:

    .2333
/organism="Rattus norvegicus"

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/db_xref="taxon:10116"
/tissue_type="cerebellum"
/dev_stage="newborn"
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/db_xref="GI:6650212"
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Ninkina, N.N. and Buchman, V.L.
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/codon_start=1
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/gene="5T4"
2315. .2320
/gene="5T4"
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This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinuclectide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                              Direct Submission
Submitted (04-MAY-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 167046)
Wilson, R.K.
Birect Submission
Direct Submission
Oniversity School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
MO MAY 4, 2005 this sequence version replaced gi:61656412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male CS7BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                          Submitted (19-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 167046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence derived from PCR product of genomic DNA" 31565. .31779 /note="Unresolved simple sequence repeat." 46804 46721. .4680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: M_BB0511A23
Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .16712
(bases 1 to 167046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:
                        Wilson, R.K.
Direct Submission
                                                                                                                                                           Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        minima]
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source

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Rattus norvegicus clone CH230-176H20, WORKING DRAFT SEQUENCE. AC128294
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929143. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alen, C. Alder, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Angeriano, B., Angeriano, B., Angeriano, B., Angeriano, B., Baden, H., Barnetead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Brant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Clacko, J., Chavez, D., Chen, G., Cok, C., Coyle, M., Cree, A., D'Souza, L., Devila, M.L., Davis, C., Davy-Carrell, L., De Anda, C., Dederich, Dolly M.L., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                          /clone="MGC:93332 IMAGE:7193411"
/tissue_type="Heart, rat (Brown Norway)"
/clone_lib="NIH_MGC_234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2361
8
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HTG: HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                   /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1282 TACATGGCTGACATGGTGTCTTGGCTT 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                           note="Vector: pExpress1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAH87011.1"
/db_xref="G1:56268820"
/db_xref="GeneID:83684"
/db_xref="RGD:621453"
                                                                                                                                                                                                                                                                                                                                        /note="gynonym: 5T4"
/db_xref="GeneID:83684"
/db_xref="RGD:621453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-774-176-18 (1-9) x BC087011 (1-2361)
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                                                                                                                                                                                                                                                    lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="Tpbg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 210237)
                                                                                                                                                                                                                                                                                                       . .2361
gene="Tpbg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "gene="Tpbg"
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47.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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VERSION
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SOURCE
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                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emmail: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
conA Library Preparation: Express Genomics
conA Library Preparation: Express Genomics
Conter, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 186 Row: o Column: 24
                                                                                                                                                                                                                                                                                                                                                                                                op mRNA linear ROD 13-DEC-2004
glycoprotein, mRNA (cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Submitted (102-108C-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                BC087011 2361 bp mRNA Rattus norvegicus trophoblast glycoproté (MGC193332 IMAGE:7193411), complete cds.
                                                                                                                                                                                                                                                                                  1282 TACATGGCTGACATGGTGTCTTGGCTT 1308
                                                                                                                                                   Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                         TyrMetAlaAspMetValAlaTrpLeu
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                                                                              Percent Similarity:
Best Local Similarity:
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          Alignment Scores:
Pred. No.:
                                                                                                                               Query Match:
DB:
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BC087011
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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AUTHORS
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COMMENT
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TITLE

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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Bana, C. Brans, C., Fang, F. Fang, F. Fanger, F. Escotto, M., Engene, C., Evans, C., Falls, T., Fang, F. Franger, F. Fanger, C. Reaser, C.M., Ganta, M., Garta, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garrar, M., Gurara, W., Gunaratene, P., Haaland, W., Hamil, C., Hamilton, K., Hamilton, K., Handler, P., Hawe, P., Hawe, J., Hamilton, K., Hamilton, K., Harler, P., Handerson, N., Hernandez, J., Hacob, L., Jang, H., Hame, J., Idlebird, D., Jackson, A., Jackson, L., Jang, H., Ghanson, B., Ochnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, W., Liu, Y., Loulsegd, H., Lozado, R., Lu, X., Man, J., Manshindartne, M., Mannoud, M., Malloy, K., Mangum, A., Mandhartne, M., Mannoud, M., Malloy, K., Mandy, M., Mandhindartne, M., Mannoud, M., Malloy, K., Mant, L., Liu, Y., Liu, Y., Loulsegd, H., Lozado, R.J., Lu, X., Martin, R., Martin, Marti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission.

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23265004.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley,K.C.
Direct Submission
Submission
Submission
Submission
Submission
Submission
To Journan Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 210237)
Rat Genome Sequencing Consortium.
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Center clone name: CH230-176H20
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COMMENT

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC106962 239076 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-87110, WORKING DRAFT SEQUENCE, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurcopathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 239076)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Assembly program: Phrap, version 0.990329
Consensus quality: 201781 bases at least Q40
Consensus quality: 203921 bases at least Q30
Consensus quality: 205310 bases at least Q30
Consensus quality: 205310 bases at least Q30
Estimated insert size: 205531, sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC106962 GI:25139469
AC106962.5 GI:25139469
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
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clone_end:T7"
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clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-176H20"
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208<u>9</u>07. .210237
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/note="clone_boundary
clone_end:T7
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SOURCE
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shotgun sequence only contigs will be indicated in the feature
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Allen,C., Allen,H., Alabrooks,S., Amin,A., Anguiano,D., Anguiano,D., Anguiano,T., Anguiano,T., Anguiano,T., Anguiano,T., Anguiano,T., Anguiano,T., Anguiano,T., Baladon,H., Banate,T., Barantead,M., Barantead,M., Blanki,D., Barantead,M., Barantead,M., Barantead,M., Blanki,T., Blanki,T., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesarth, Core,T., Dederon,E., Chardon,C., Charant,C., Davy-Cartroll,T., Calderon,E., Charant,C., Dederich,D., Delgado,C., Craves,D., Chen,G., Chara,D., Davy-Garroll,T., Davial,B., Barantead,E., Dederich,D., Delgado,C., Derger,H., Secotto,M., Elagy,M., Potgan,A., Duthin,H., Davial,B., Eaves,K., Egan,A., Bacotto,M., Elagy,M., Rothes,L., Folls,T., Fara,G., Fraser,C., Gener, T., Carza,M., Guracto,T., Garac,M., Harrandez,M., Handerson,N., Harrandez,M., Handerson,N., Harrandez,M., Handerson,N., Harrandez,M., Guracto,M., Manghi,M., Katt,C., Liu,Y., Londson,M., Hawat,D., Katt,C., Leats,D., Liu,J., Liu,W., Liu,Y., Londson,M., Martin,M., Mandun,M., Martin,M., Martin,M
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The sequence in this assembly is a combination of BAC based reads and whole genome shortgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (14-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 239076)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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TITLE
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AUTHORS
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JOURNAL
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REFERENCE

JOURNAL

COMMENT

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 08-JUN-2001
                                                                                                                                                                                                                                                                                                            Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711 234710: contig of 234710 bp in length
711 234810: gap of unknown length
9812 235924: contig of 1114 bp in length
9825 236024: gap of unknown length
9825 237414: gap of unknown length
9815 237414: gap of unknown length
9815 239765: contig of 1290 bp in length
9815 239076: contig of 1662 bp in length.
9826 2502110/Qualifiers
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                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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Mismatches:
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/mol_type="genomic DNA"
/db xref="taxon:10116"
Center: Baylor College of Medicine
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Matches:
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Sequence 14 from Patent WO0136486.
AXI49553
AXI49553.1 GI:14347991
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235925. .236024
                                                                                             ----- Project Information
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                                                                     Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                   Center project name: GOPI
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complement (3307. .3804)
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Piel,J., Hoefer,I. and Hui,D.
Direct Submission
                                    GI:44662898
                                                                                                                                                                                                                                                                                             (bases 1 to 75778)
                                                                                                       Bacteria.
1 (bases 1 to 75778)
                                                                                                                                                                                                                                                                                                                        Direct Submission
                                     AY328023.1
                                                                                                                                                                                                                                                                                  14973122
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Symbiont bacterium of Paederus fuscipes putative isocitrate dehydrogenase kinase/phosphatase gene, partial cds, and putative dioxygenase, putative pederin biosynthesis mixed type I polyketide synthase/nonribosomal peptide synthetase gene cluster, hypothetical
           Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W.,
Ellard, F.M. and Myers, K.A.
Antibodies
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Indels:
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers

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protein, putative RNA methylase, hypothetical protein, and putative aldehyde dehydrogenase genes, complete cds. AY328023 AY059471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 75778)
Piel,J., Hofer,I. and Hui,D.
Evidence for a symbiosis island involved in horizontal acquisition of pederin biosynthetic capabilities by the bacterial symbiont of
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Chote="symbiosis island"

complement (802. .938)

/note="putative transposase pseudogene"

/note="hypothetical protein pseudogene, similar to PA1689

from Pseudomonas aeruginosa"
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Jena
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Institute for Chemical Ecology, Winzerlaer Str. 10, Jena 07745,
                                                                                                                                                                                                                                                                                                             A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of Paederus beetles
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14002-14007 (2002)
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On Mar 3, 2004 this sequence version replaced gi:23307838.
Location/Qualifiers
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fuscipes
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J. Bacteriol. 186 (5), 1280-1286 (2004)
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symbiont bacterium of Paederus
symbiont bacterium of Paederus
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Job time : 3371.6 secs
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complement(6372. .7310)
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transl_table=11
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/transl_table=1
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/transl_table=
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/gene="pedD"
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/gene="pedD"
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11341. .12162

gene

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GYCSLLIKPLITALING TABLILLY SET 19 THE SECONDESSAY OF THE SECONDESSAY O
                                                                                                                                                                                                 /trānslation="MQTAIADVEKVATLYDSAEGQVGPILFGGHMHWGYWDEVTGEGN
FANNAERLAQIMIAKAPIKAGQKFTDMGCGFGESALKLAKAKGCFVDGITISKEQQLS
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GSTLLLITDLPLLPESTEAFKEFVWEHIHSRFWSREDYPELLAEAEFELIEIDDITDNV
MPWLEPKLKEAIELHRPQVEAIIPNDTEKAIDDWLYLFFYMSENLGYMIVMAKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGGFIPDIRGFDPAFFNIPGAEAITLDPRQRLLLMSAYQTLNDAGYASQALRQSKTGV
FVALQDNEYLQLLADAGIDPGQWYAQTCLLANRISYFFDWRGTSEVVDAQCPGAAVAI
HRAVSALRNGEIELALVGAANLLLRPEPFVLLSESGQLSESASVHSFGAQAQGHLRAE
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REGYVQFYRVMLDIRSRGVGSSKPLAEPRADLQLISMADAMDHAYPFPWYNRDLGRAPA
EDLAPI FQYAFBYQNYFSAQDLKLFNQSYRESLGYMFLEBFYQBGBYELALBYBGBI
DFALNLKFNPTLYRMATIARMAEHLLILAEHAIDAPLSPCRELTMLSERERHLLLHEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tränslation="MSVNIHQQLKEIEDALLNNSGVAVTLDVESSDKLRKREAEDSPE
AIAIVGLSGYFPQSASVDEFWRHLDQDATLIEEIPDSRFDWRKVFDPTGERPGSSCSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATTEPYPSCCFHQLFEKQARAMPQAIAAIFQEQRLSYAELDERSERLAIYLQQCGVQ
PNRIVAVCLERSLDMLVALIGIARSGAAWLPLDPNYPDDRLRFMLSDSQAQLLLTEBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDKTAAIVSQAVGERLQIVAMDGHWPEIERQARTSELQMRDDPRNLAYVIYTSGSTG
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CATDKLNDSEALQGEI ERLQPTVMQATPSTWTLL FHGGWNNRQGVKI LCGGEPLPPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon start=1
/transl table=11
/product="mixed type I polyketide synthase/nonribosomal
peptide synthetase"
methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAS47564.1"
/db_xref="GI:44662946"
                                                         /protein_id="AAS47560.1"
/db_xref="G1:44662942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-774-176-18 (1-9) x AY328003S21 (1-75778)
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score:

Title: Perfect

Sequence:

protein

δ

Run on:

Scoring table:

Minimum DB 8 Maximum DB 8

Searched:

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Addis 21 Cancer/an Addis 25 Human tum Adno 361 Human tum Adres 48 Breast ca Acris 8510 Tumour-as Advis 508 Human cDN Addis 9115 DNA encod Aak94253 Human ful Addis 913 Full leng Aak94264 Human cDN Addis 913 Full leng Aak 9136 Nucleotid Abk 87175 CDNA enco Abk 87175 CDNA enco Abk 87175 CDNA enco Adb 97513 Feline 57 Addis 59 Solid tum Addis 19 Solid tum
                            Adn38723 Cancer/an
Add56198 Human LRR
Abv99349 Human LRR
Aaa27058 Human 5T4
Ad56199 Human LRR
Ad56199 Human LRR
Ad56197 Human LRR
Ad56197 Human LRR
Aad56197 Human LRR
Aad56197 Human LRR
                                                                                                                                                                                                                                                                                                                                             Adv73884 Human col
Abk51946 3'-untran
Acd12556 Human G-p
Aaa27059 Mouse 5T4
                                                                                                                                                                                                                                                                                                                                                                                                           Adc32089 Human pol
Adc32089 Human nov
Adr07185 Full leng
                                                                                                                                                                                                                                                                                                                                                                                       Adi26160 Human cDN
Adi26158 Human cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
           Abx76333 Lung canc
Adb80503 Ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                           Aai59574 Human pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Open reading frame detection; genome sequencing; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer cell expressed cDNA #1948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                 ADL06473
ADN03961
ADN25981
ACN385198
ACN365098
AAC94253
AAC94253
AAC94253
AAC94253
AAC94253
AAC94253
AAC94253
AAC94253
AAC94253
AAC94254
AD126162
AD126162
AD13519
AD126156
                                                                                                                                                                                                                                                                                                                                                                                                            AAI61358
ADC32089
         ABX76333
ADB80503
ADN38723
                                                                        AAD56199
ADJ56299
ACC51052
ABX76332
AAD56197
AAD56200
                                                                                                                                       ADN3872
                                                              AAA27058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACD93536 standard; cDNA; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00406117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00196716
                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
 US2002155438-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-2002
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACD93536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
ACD93536
  -MODEL-frame+ p2n.model -DEV=x1h
-Q=/abs9/ABSSWEB spool/US10774176/runat 26052006 091441 24976/app query.fasta 1
-Q=/abs9/ABSSWEB spool/US10774176/runat 26052006 091441 24976/app query.fasta 1
-Q=/abs9/ABSSWEB spool/US10774176/runat 26052006 091441 24976/app query.fasta 1
-USTS-B-MINGATCH=0.1 -LOPELT=0 -LOPETT=0
-UNITS-B-LIG STRATE-1 -END=-1 -MATRIX-B-LOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-USTS-B-CONTONIN=EXT -HEAPSIZE=500 -MINIEN=0 -MAXLEN=200000000 -HOST=abss02h
-USTS-B-CSTORM=EXT -1 2389 @runat 26052006 091441 24976 -NCPU=6 -ICPU=3
-NO WMAP -NGS SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0,5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acd93536 Human col
Aas87174 DNA encod
Adul1677 Solid tum
                                                                     ; Search time 377.5 Seconds
  (without alignments)
249.339 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
         version 5.1.8 - 2006 Biocceleration Ltd.
                                                    using frame_plus_p2n model
                                                                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                                                                          5244920 segs, 3486124231 residues
                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ACD93536
5 AAS87174
13 ADU11677
                                                                                                                                                                      0.5
7.0
7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                        May 27, 2006, 09:34:35
           GenCore (c) 1993
                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geneseqn2003cs:*
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geneseqn2002bs:*
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                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                 US-10-774-176-17
52
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Match Length DB
                                                                                                                                      HMADMVTWL 9
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                                                    nucleic search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299
453
475
                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                               Command line parameters:
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100.0
100.0
                                                                                                                                                                                                                                               Potal number of
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Database :

Score

Result Š. 522

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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism comprising contacting mRNA from cell of organism comprising contacting mRNA with (1), amplifying single-stranded cDNA by reverse transcribing mRNA with (1), amplifying single-stranded cDNA by reverse transcribing mRNA with (1), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, nucleotide sequence of an open reading frame; for preparing a contig, all or part of a genome of an organism; and for sequencing all or nucleotide sequence of an open reading frame; for preparing a contig, all or part of a genome of an organism; and for sequencing colon cancer or breast cancer cell. The method is useful for analyses of or human cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of populations further, it can be useful for analyses of systems to determine if, e.g. there have been genetic shifts which render of systems to determine if, e.g. there have been genetic analyses of congenital diseases, and the risk of affliction to a foctus, as well as the study of whether the conditions are likely to be passed to offspring through ove or sperm. The method can also be used in the study of whether the conditions are likely to be passed to offspring through ove or sperm. The analyses for pathological conditions can be congenitated out in all animals, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be genomes can also be studied in this way. Similarly, the method permits and the area of the pathogens which may require which may require with the area. The method is a similar to a such a such a such a contaction of the patho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially eliminates sequencing of non-coding portions. This sequence represents a polymucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                              Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of
                                                                                                                  Brentani RR
                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 302; 959pp; English
SIMPSON A J G.
NETO E D.
BRENTANI R R.
                                                                                                                  Simpson AJG, Neto ED,
                                                                                                                                                                       WPI; 2003-182626/18
                                                          (BREN/)
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78 G; 62 T; 0 U; 0 Other; Sequence 299 BP; 75 A; 84 C;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                               CACATGGCAGACATGGTGACCTGGCTC 221
                                                                                               US-10-774-176-17 (1-9) x ACD93536 (1-299)
           0.389
52.00
100.0%
100.0%
                                                Similarity:
                                    Percent Similarity:
Alignment Scores:
                                                             Query Match:
                                               Best Local
```

AAS87174 standard; cDNA; 453 BP (first entry) 13-FEB-2002 RESULT 2 AAS8717

ADU11677 standard; DNA; 475

ADU11677

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in displandable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot acid sequences AAS644504 represent novel human diagnostic cativity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 453 BP; 108 A; 111 C; 113 G; 121 T; 0 U; 0 Other;
DNA encoding novel human diagnostic protein #22978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 22978; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217
                                                                                                                                                                                                                                                                                     23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                           HYSE-) HYSEQ INC
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                                                                                                                                          WO200175067-A2
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                                                                                                     Homo sapiens
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Solid tumour prognosis gene segid 2116.
                                                                                                                  Disclosure; Page; 111pp; English.
                                                  29-APR-2004; 2004WO-US013587.
                                                         29-APR-2003; 2003US-0466067P.
23-JAN-2004; 2004US-0538246P.
   27-JAN-2005 (first entry)
                                                                                           WPI; 2004-804779/79.
                                                                        (STRA/) STRAHS A.
                                    WO2004097052-A2
                                                                     (AMHP ) WYETH
                            Unidentified
                                                                                Strahs A, T
Immerman F,
                                           11-NOV-2004.
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Dorner AJ;

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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure and biosensor development. DNA sequences ABT07693 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets windic can be used in the areas of diagnostics, therapeutics, dary development, pharmacogenetics, protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ds; breast cancer; breast cancer-associated gene sequence; development; pharmacogenetics; biosensor development.
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                             Indels:
                                                                                                                                                                                                     180 CACATGGCAGACATGGTGACCTGGCTC 206
                                                        Gaps:
                                                                                                                                                                       1 HisMetAlaAspMetValThrTrpLeu
                                                                                                              (1-475)
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Best Local Similarity: 100.0%
Query Match: 100.0%
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N-PSDB; ABJ05564.
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                          Query Match:
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                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                      The invention describes a menhod compirang on expression profile of the at least one gene in a peripheral blood sample of a patient to at least one gene in a peripheral blood sample of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood monuclear cells (FBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes is a subcluster formed by an unsupervised clustering analysis of gene expression profile in PBMCs of a population of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, the majority of the first class of patients has a second clinical outcome. Also described are: a speciment and expression profile of a patient one gene in a peripheral blood sample of a patient where the cutomout. (ii) at least another storage medium including data that represent an expression profile of a cutomout. (iii) at least another storage modium including data that represent at least one reference expression profile of the gene, (iii) a program, where expression levels of the gene in peripheral blood sample of executing the program, where expression levels of the gene in peripheral blood cutomodear calls of patients who have the solid tumour forting data for solid tumour prognosis genes, where can fine a solid tumour prognosis genes is differentially expressed in peripheral blood comprising concentrated probes for solid tumour prognosis genes, where peach of the patients as compared to pBMCs of a second class of patients as econd classes of the invention. Note: The sequence data for this assert data for minical cutomory and where the f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention describes a method comprising comparing an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slonim DK;
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                                                                                                                                         cytostatic; gene therapy; expression profile; solid tur
peripheral blood mononuclear cell; PBMC; prognosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trepicchio WL, Burczynski ME, Twine NC,
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Matches:
Conservative:
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Score:

0.646 52.00 100.0%

Percent Similarity:

Alignment Scores:

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in creased or decreased expression in lung cancer samples. Lung cancer associated polypoptide, for compound that modulates a lung cancer-associated polypoptide, for inhibiting proliferation of a lung cancer-associated polypoptide, for cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful contracting lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lessions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchites in the genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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 Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                    CACATGGCAGACATGGTGACCTGGCTC 585
                                                                                                                               1 HisMetAlaAspMetValThrTrpLeu 9
                                                                                           US-10-774-176-17 (1-9) x ABT07721 (1-927)
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2001US-0290492P.
2001US-0339245P.
2001US-0350666P.
2001US-0334370P.
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P-PSDB; ABU56604.
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Percent Similarity:
Best Local Similarity:
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29-NOV-2001;
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                                   Query Match:
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Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                        post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
                                          T; 0 U; 0 Other;
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2001US-0315287P.
2001US-0317544P.
2001US-0350666P.
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27-AUG-2001;
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13-NOV-2001;
                                           Sequence 927
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                                                                        Alignment Scores:
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Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids used for the detection method of the invention.
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                                                                             Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
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Murray R, Watson SR,
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2001US-0334393P.
2001US-0335994P.
2001US-0340376P.
2002US-0347211P.
2002US-0347449P.
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2002US-0386614P.
2002US-0396839P.
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                                                                                                                                                        Best Local Similarity:
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                                                                                                                                           Percent Similarity:
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10-JAN-2002;
08-FEB-2002;
13-FEB-2002;
20-FEB-2002;
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05-JUN-2002;
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29-NOV-2001;
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Mack DH,
                                                                                                                                                                                                                                                                                                                                       ADN38723;
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies and host cells comprising a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modularors of activity or expression of the
polypeptides and mucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The
                           Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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LRRCAPS; cancer; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HisMetAlaAspMetValThrTrpLeu 9
                                                                                                Claim 8; SEQ ID NO 41; 1385pp; English
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Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human LRRCAPS related DNA #5
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52.00
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Best Local Similarity:
P-PSDB; ADN38724.
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01-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosupressive; osteopathic; antiparkinsonian; cancer; antinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoletic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopolesis; wound healing; anglogenesis; ds.
              Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                                                                 gene therapy. The present sequence is human LRRCAPS related DNA
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Matches:
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                                                                                  Example 5; Page 74-75; 99pp; English
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2001US-0274219P.
2001US-027422P.
2001US-0274849P.
2001US-0275235P.
2001US-0275279P.
2001US-0275579P.
2001US-0275579P.
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Best Local Similarity:
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08-MAR-2001;
08-MAR-2001;
09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
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13-MAR-2001;
14-MAR-2001;
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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek RA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Pedigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                      2001US-0277327P
2001US-0277338P
2001US-0277338P
2001US-0277338P
2001US-027835P
2001US-0278854P
2001US-0278854P
2001US-0278854P
2001US-0278336P
2001US-0278336P
2001US-0280202P
2001US-0280802P
2001US-0280802P
2001US-0280802P
2001US-0280802P
2001US-0280802P
2001US-0280802P
2001US-0280802P
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2001US-0288342P.
2001US-0288528P.
2001US-0291190P.
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2001US-0291240P.
2001US-0294485P.
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2001US-0299027P.
2001US-0299303P.
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2001US-0318770P.
2001US-0325430P.
2001US-0325681P.
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2001US-0332272P.
2001US-0333184P.
2001US-0333272P.
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2001US-0309198P.
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2001US-0337426P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders, and asthma.
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P-PSDB; ABP70071.
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14-NOV-2001; 2
21-NOV-2001;
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15-MAY-2001;
16-MAY-2001;
16-MAY-2001;
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31-OCT-2001;
14-NOV-2001;
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14-NOV-2001;
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16-AUG-2001;
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Claim 16; Page 114-115; 619pp; English.

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX associated disorder. The NOVX calong sequences and proteins are useful for treating, preventing or diagnosing diseases, anorexia, cancer associated disorder, neurodegenerative disease, Alzheimer's disease, diabetes, cancer, neurodegenerative disease, anorexia, cancer associated cachexia, cancer, neurodegenerative disease, Alzheimer's disease, parkinson's disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with chronic disease or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antipolesis that bind immunospecifically to NOVX substances for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic or diagnostic methods
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

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Conservative:
                                      Mismatches:
          Length:
Matches:
                                                 Indels:
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        1.71
52.00
100.0%
100.0%
                                       Best Local Similarity:
                            Percent Similarity:
Alignment Scores:
                                                Query Match:
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US-10-774-176-17 (1-9) x ABV99349 (1-1156)

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1 HisMetAlaAspMetValThrTrpLeu 9
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AAA27058 standard; DNA; 1263 22-AUG-2000 (first entry) AAA27058; AAA27058 

Human 5T4 tumour-associated antigen gene.

Human, TAA, tumour-associated antigen, anti-tumour, cytostatic, immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer,

Homo sapiens.

WO200029428-A2.

25-MAY-2000

99WO-GB003859.

18-NOV-1999;

98GB-00025303. 99GB-00001739. 99GB-00017995. 18-NOV-1998; 27-JAN-1999; 30-JUL-1999; (OXFO-) OXFORD BIOMEDICA UK LTD

Carroll MW, Myers KA;

WPI; 2000-387735/33.

Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.

Example 2; Page 78; 79pp; English

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The present sequence encodes the human 5T4 tumour-associated antigen carcinomas but has a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour induced were inoculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-blased activity, where a difference between the test agent-blased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
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LRRCAPS; cancer; gene therapy; ds.
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                                                                                                                                                                                                          Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD56199 standard; DNA; 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human LRRCAPS related DNA #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-2002; 2002WO-US033540.
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01-MAR-2002;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                 Query Match:
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expressed in MYCN activated cells. Specifically, it refers to polymucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a proto-oncogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of mucheic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the CDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an
for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to novel isolated cDNAs that are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA differentially expressed in MYCN activated cells SeqID 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss; MYCN activated cell.
                                                                   Sequence 1331 BP; 252 A; 447 C; 369 G; 263 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                          931 CACATGGCAGACATGGTGACCTGGCTC 957
                                                                                                                                                                                                     Gaps:
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                                                                                                                                                                                                                                      US-10-774-176-17 (1-9) x AAD56199 (1-1331)
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                                                                                                                                                                                                                                                                                                                                                                         ADJ56299 standard; cDNA; 2020 BP
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NUCHTERN J G.
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SHOHET J M.
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                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                  Alignment Scores:
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DB:
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Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the US Patent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bladder cancer associated cDNA sequence SEQ ID NO:192.
                                                                                       Sequence 2020 BP; 451 A; 591 C; 493 G; 485 T; 0 U; 0 Other;
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                                                      ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                ACC51052 standard; cDNA; 2053
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
12-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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                                                                                                                                                                         Percent Similarity:
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                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC51052;
                                                                                                                                                                                                            Query Match:
                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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                                                                                                                                                           Score:
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transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 * identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung cancer-associated polynucleotide, gene, ds; cytostatic, emphysema, antinflammatory; antiasthmatic, non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for detecting a lung cancer-associated
   methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polymucleotide that exhibits increased or decreased expression in lung cancer.
                                             T; 0 U; 0 Other;
                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                              Sequence 2053 BP; 461 A; 602 C; 499 G; 491
                                                                                                                                                                                                                                                            various screening and diagnostic methods, and/or antisense/inhibition applications
                                                                                                                                                                            Gaps:
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                                                                                                                                                                                                            x ACC51052 (1-2053)
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                                                                                                                                                                                                                                                                                                                                           BP.
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2001US-0339245P.
2001US-0350666P.
2001US-0334370P.
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Best Local Similarity:
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13-NOV-2001; 2
29-NOV-2001; 2
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                                                                              Alignment Scores:
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administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent blissed activity, and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, p53 pathway, Leucine rich repeat capricious related protein;
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                                                                                                                                                                                                  Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Conservative:
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15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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Francis-Lang H, Friedman
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                                                                                                                                                                  Invention
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composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS DNA
CC composition for diagnosing or treating caucts. .... CC gene therapy. The present sequence is human LRRCAPS DNA XX Sequence 2053 BP; 461 A; 602 C; 499 G; 491 T; 0 U; 0 Other;
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 3.22 52.00 100.0% 100.0% Alignment Scores:
Pred. No.:
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Query Match:
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US-10-774-176-17 (1-9) x AAD56197 (1-2053)

1 HisMetalahspMetValThrTrpLeu 9 ò

Search completed: May 27, 2006, 10:37:47 Job time : 381.5 secs

Novel Ant

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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BD249731 Polypepti
AX31608 Sequence
CQ731678 Sequence
DD174290 METHODS O
229083 Homo sapien
BD127282 Perence
AK074786 Homo sapien
BD127283 Primer fo
CQ782724 Sequence
BD127283 Primer fo
CQ782726 Sequence
BD127283 Primer fo
CQ782726 Sequence
BD127283 Primer fo
AK074790 Homo sapi
BC037161 Homo sapi
AJ012159 Homo sapi
AJ012159 Homo sapi
AL121977 Human DNA
AX467371 Sequence
AX149553 Sequence
AX149553 Sequence
AX14951 Papio anu
CR9731045 Sus scrof
AC149011 Papio anu
CR9731045 Sus scrof
AC11883 Rattus no
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AX821533 Sequence
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AX080009 Homo sapi
AC134803 Rattus no
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AC115358 Mus muscu
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AC172361 Bos tauru
AF063939 Rattus no
BC087011 Rattus no
AL136536 S.pombe c
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H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA32B9,
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AC159552 Bos tauru
AC159552 Bos tauru
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-APR-1997) The Sanger Centre, Wellcome Trust Genor
Campus, Hinxton, Cambridgeshire, CB10 iSA, UK. E-mail contact:
humquery@eanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
1 (bases 1 to 421)
Mungall,A.J., Huckle,E., Langford,C., Ross,M.T. and Hunt,S.E.
Direct Submission
Submitted (17-APR-1997) The Sanger Centre, Wellcome Trust Gen
 DD161112
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/chromosome="6"
/clone="SC6pA32B9"
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AC149011
AC149257
CR974572
CT573045
AC111883
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AX821533
AX821548
AC080009
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AC138109
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HSA012159
HSJ492P14
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AC172361
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Homo sapiens (human)
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   VERSION
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FEATURES
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       Command line parameters:

-MODEL=frame+_pin.model. -DEV=xlh
-Q=|abss/ABSWEB spool/US1074176/runat_26052006_091443_24987/app_query.fasta_1
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-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -MOST=abss04
-USFR=US10774176_@CGN 1 1 7524_@runat_26052006_091443_24987 -NCPU=6 -ICPU=3
-WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CQ920916 Sequence
AX829164 Sequence
                                                                                                                                               (without alignments)
257.039 Million cell updates/sec
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                                                                                                                            May 27, 2006, 09:51:03; Search time 3358.6 Seconds
                      GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                           - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                   6366136 segs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
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CQ920916
AX829164
                                                                                                                                                                                                                                                                                       Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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52
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9b_pl:**
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16-MAY-2001
12-MAR-2001
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                     /clone_Tib="SC6pA"
/dev_stage="adult"
/note="The estimated purity of the flow-sorted chromosome
6 library is >97%"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleos
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Burczynski, M.E., Twine, N.C., Slonim, D.K., Trepicchio, W.L., Strahs, A., Immerman, F. and Dorner, A.J.
Methods for prognosis and treatment of solid tumors
Patent: World 10097052-A 2116 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
Location/Qualifiers
          /tissue_type="EBV lymphoblastoid_cell_line"/clone_lib="SCGpA"
                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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CQ920916.
CQ920916.1 GI:56210857
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACATGGCAGACATGGTGACCTGGCTC 206
                                                                                                                                                                       Gaps:
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'sex="female"
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Mammalia Butheria; Buarchontoglifes; Filmates; Carafillini; Hominidae; Homo.

1 (bases 1 to 1156)

2 Padigaru, M., Shenboy, S. G., Pochart, P.F., Kekuda, R., Gusev, V.Y., Zhong, M., Jr. B.-T., Casman, S.J., Li, L., Miller, C.E., Patturajan, M., Anderson, D. W., Malyankar, U.M., Voss, E.Z., Patturajan, M., Anderson, D. W., Malyankar, U.M., Voss, E.Z., Patturajan, M., Anderson, D. W., Malyankar, U.M., Voss, E.Z., Patturajan, M., Anderson, D. W., Smithson, G., Mezes, P.D., Rastelli, L., Boldog, F.L., Guo, X., Vernet, C.A.M., Gangolli, E.A., Tchernev, V.T. and Zerhusen, B.D.

Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigonis, and Methods of Use Patent: JP 2005508604-A 23 07-APR-2005;

Muralidhara Padigaru, Suresh Shenoy, Rewisesh Kekuda, Vladimir Gusev, Pascale Pochart, Mei Zhong, Luca Rastelli, Peter Mezes, Glennda Smithson, Xiaojia Guo, Valerie Gerlach, Stacie Casman, Ferenc Boldog, Li Li, Bryan Zerhusen, Velizar Tchernev, Esha Gangolli, Corine Vernet, Carol Pena, Carherine Burgess, Xiaohong Liu, Kimberly Spytek, Linda Gorman, Steven Spaderna, Edward Voss, Uriel Malyankar, David Anderson, Meera Patturajan, Charles Miller, Raymond J Taupier Jr

OS Homo sapiens

PN JP 2005508604-A/23

PN JP 2005508604-A/23

PN 19-2001 US 60/299310, 18-JUN-2001 US 60/299027, PR

11-MAY-2001 US 60/299310, 18-JUN-2001 US 60/29999, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD161112 1156 bp DNA linear PAT 23-NOV-2005 Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigens, and Methods of Use.
                                                     compositions and methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60/294899, P
60/284849, P
60/288342, P
60/281194, P
60/280822, P
60/29109, P
60/29109, P
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                                                                                                                                                                                                                                                                                                                                                                                 927
Mack, D.H., Gish, K.C. and Afar, D.
Methods of diagnosis of breast cancer, com
screening for modulators of breast cancer
Patent: WO 02059377-A 57 01-AUG-2002;
EOS Biotechnology, Inc. (US)
Location/Qualifiers
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Mismatches:

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DD161112.1 GI:83967439
JP 2005508604-A/23.
Homo sapiens (human)
Homo sapiens
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AL Carroll, M.W. and Myers, K.A.

Polypeptide
AL Patent: JP 2005330060-A 1 17-SEP-2002;

OXFORD BIOWEDICA LTD
OS Home sapiens (human)

NA P 2005330060-A/1

PD 17-SEP-2002

PF 18-NOV-1999 JP 2000582415

PR 18-NOV-1999 GB 9825303.2,27-JAN-1999 GB 9901739.4 PR
10-JUL-1999 GB 917995.4

PR 18-NOV-1999 GB 917995.4

PR 18-NOV-1999 GB 9917995.4

PR 18-NOV-1999 GB 9917995.4

PR 12N15/09, AGIK39/00, AGIK48/00, AGIP35/00, CO7K19/06, CO7K19/00,

PC C12N15/00

PC C12N15/00

PC C12N15/00

PC C12N15/00

PC C12N15/00

PC C12N15/00

PC POlypeptide

FH Key

I. 1263

FT SOURCE

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Matches:
Conservative:
Mismatches:
Indels:

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       08-MAR-2001 US 60/274281,08-MAR-2001 US 60/274322, PR 50-MAR-2001 US 60/274194,02-APR-2001 US 60/280900, PR 50-MAR-2001 US 60/280901 US 60/280900, PR 50-MAR-2001 US 60/279995, PR 60/270901 US 60/277327,20-MAR-2001 US 60/277339, PR 19-MAR-2001 US 60/27731, 20-MAR-2001 US 60/277561, PR 13-MAR-2001 US 60/277321, 21-MAR-2001 US 60/27731, PR 22-MAR-2001 US 60/27731, 21-MAR-2001 US 60/27731, PR 22-MAR-2001 US 60/27731, PR 60/27731, 21-MAR-2001 US 60/27731, PR 22-MAR-2001 US 60/27791, PR 22-MAR-2001 US 60/27791, PR 60/2799303, 10-UL-2001 US 60/279944, PR 19-UL-2001 US 60/299303, 10-UL-2001 US 60/37944, PR 19-UL-2001 US 60/399303, 10-UL-2001 US 60/33944, PR 19-UL-2001 US 60/399303, 10-UL-2001 US 60/33271, PR 14-NOV-2001 US 60/333272, 14-NOV-2001 US 60/332371, PR 14-NOV-2001 US 60/33380, 21-CT-2001 US 60/335301, PR 19-CT-2001 US 60/33380, 21-SEP-2001 US 60/335301, PR 19-CT-2001 US 60/33380, 21-SEP-2001 US 60/335301, PR 19-CT-2001 US 60/33186, 01-SEP-2001 US 60/33186, 01-SEP-2001 US 60/33186, 01-SEP-2001 US 60/33189, 01-DEC-2001 US 60/33184, PR 10-DEC-2001 US 60/33184, PR 10-DEC-2001 US 60/33184, PR 10-DEC-2001 US 60/33180, 21-SEP-2001 US 60/331874, PR 10-DEC-2001 US 60/33180, 21-SEP-2001 US 60/3318770, PR 10-DEC-2001 US 60/33180, 21-SEP-2001 US 60/3318730, PR 10-DEC-2001 US 60/33184, PR 10-DEC-2001 US 60/3
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Location/Qualifiers
1. 1156
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/mol_type="unassigned DNA"
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
Query Match:
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casman,li
PI charle
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PAT 15-SEP-2000
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent: WO 0029428-A 1 25-MAY-2000;
Patent: WI MILES WILLIAM (GB); MYERS KEVIN
BIOMEDICA LTD (GB)
                                                                                                                DNA
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1. 1263
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1 HisMetAlaAspMetValThrTrpLeu 9
                                                                                                            AX025011 1263 bp
Sequence 1 from Patent WO0029428.
AX025011
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AX316086 LOCUS

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Mammatata; Butteria; Edutining Filmates; Catallining Mammatata; Butteria; Edutining Mammatata; Municata; Municata; Municata; Muck, D. H. and Agiz, N.

Mack, D. H. and Agiz, N.

Mack, D. H. and Agiz, N.

METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCRENING FOR MODULATORS OF BLADDER CANCER

A Patent: JP 2005514908-A 102 26-MAY-2005;
Protein Design Labs Inc

OS Homo Sapiens
PN JP 2005514908-A/102
PP 2005514908-A/102
PP 200514908-A/102
PP 03-JUL-2002 US 60/372246,13-NOV-2001 US 60/350666, PR 03-JUL-2001 US 60/302814
PI david h mack, natasha agiz

CC

FH Key

Location/Qualifiers.
                                                                                                                                                                                                    DD174290 2053 bp DNA linear PAT 19-DEC-2005 METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER.
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Z29083. I GI:435654
ST4 gene; ST4 oncofoetal antigen.
Thomo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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      Mismatches:
Indels:
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                                                                                                                        985 CACATGGCAGACATGGTGACCTGGCTC 1011
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                                                                                                       1 HisMetAlaAspMetValThrTrpLeu
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JP 2005514908-A/102.
Homo sapiens (human)
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Query Match: 100.0%
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AUTHORS
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Patent: BP 1160223-A 1 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                        DNA
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Sequence 17612 from Patent WO02068579.
CQ731678 GI:42308932

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                                                                                                                   Sequence 1 from Patent EP1160323.
AX316086
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Homo sapiens
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ORIGIN

PAT 18-SEP-2002

JOURNAL PUBMED REFERENCE

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Homo sapiens (human)
JP 2002017375-A/2713
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC

Primer for synthesizing full-length CDNA and use thereof FH Key

Location/Qualifiers
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                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                              Hominidae; Homo.
l Chases 1 to 2359)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Primers for synthesizing full length cDNA clones and their use
Patent: EP 1396543-A 2864 10-MAR-2004;
Research Association for Biotechnology (JP)
BD127282
Primer for synthesizing full-length cDNA and use thereof.
                                                                                                                                                                                                                                                                               Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2713 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-774-176-17 (1-9) x BD127282 (1-2359)
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                                           BD127282
BD127282.1 GI:23222227
JP 2002017375-A/2713.
Homo sapiens (human)
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APFLASAVSAQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
ALAVLPAGARRRPPLAELALALISSERIDEVRAGAFEHLLSENGLDLESINGLDLESINGLAGARILSPF
AFGSSNASVSARSPELVELILIHITYPEPEDERONRSFEGHVVAALLAGRALIGGIRELELA
SNHPLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNITHLESLHLEDNALKVLHNG
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LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKGIKKWMHNIRDAC
RDHMEGYHYRYEINADPRLTNLSSNSDV"
                                                                                                                                                                 Myers, K.A.
Direct Submission
Submitted (16-DEC-1993) Myers K. A., Paterson Institute for Cancer
Research, Immunology, Wilmslow Road, Manchester, M20 9BX, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /experiment="experimental evidence, no additional details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="transmembrane peptide"
/standard_name="transmembrane region"
/function="Anchorage of the protein to the cell membrane"
Myers, K.A., Rahi-Saund, V., Davison, M.D., Young, J.A., Cheater, A.J. and Stern, P.L.
Isolation of a cDNA encoding 5T4 oncofetal trophoblast
glycoprotein. An antigen associated with metastasis contains
leucine-rich repeats
                                                                                                                                                                                                                                                                                                                                                                               rissue_type="placenta"
/clone_lib="lambda gt11 library of J. Milan"
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/product="Leucine rich repeat region"
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                                                                                                  J. Biol. Chem. 269 (12), 9319-9324 (1994) 8132670
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/label=C-flank
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      clone="NT2RP2000694"
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19 2 (Dases 1 to 2359)
19 3 (Samission Tr. and Otsuki, T. and T
                                                                                                                                                                                                                                    /protein_id="Cap85958.1"
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AFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALLGELA
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                                                                                                                                                                                                                                                                                                                                                                                                                   SNHFLYLPRDVLAQLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNG
TLAELQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKMRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRGIKK"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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oligo capping; fis (full insert sequence).
Homo eaplens (human)
Homo eaplens
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location/Qualifiers
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APFLASAVSAQPPLDDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQ
LAVLPAGAFARRPPLAELAALNLSGSRLDBYRAGAFEHLFSLRQLDDLSHNPLADLSPF
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THFLYLPROVLAQLPSLHAHDLSNNSVYSFRNLTHLESLHLEDNAKVLHVG
TLAELQGLPHIRVFLONNPWVCDCHNADMYTWRKFEVYQGKORLTCAYPEKKRNRVL
LELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLAVLXNENNFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 14-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASSFSSS
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Patent: WO 03104277-A 127 18-DEC-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
426. .1688
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us-10-774-176-17.p2n.rge

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3 2361 bp DNA linear PAT 18-SEP-2002 for synthesizing full-length cDNA and use thereof.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
JP 2002017375-A/2714
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAVASHI, SHIZUKO ISHII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                           Hominidae, Homo.
1 (bases 1 to 2361)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
                                                                                                                                                                                                                                                                                                                                          Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2714 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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JP 2002017375-A/2714.
Homo sapiens (human)
Homo sapiens
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SHINICHI KOJIMA
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BD127283
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RESULT 15
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AUTHORS
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Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-774-176-17 (1-9) x BD127283 (1-2361) 0.0961 52.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: DB: ò 셤

Alignment Scores: Pred. No.:

Score:

ORIGIN

Search completed: May 27, 2006, 19:34:57 Job time : 3362.6 secs

Solid

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Aaa27060 Canine 5T
Abto7721 Breast ca
Abx7633 Lung canc
Adb80503 Ovarian c
Adb80503 Ovarian c
Adb80503 Ovarian c
Adb80753 Human NOV
Abx87175 CDNA enco
Adb97513 Feline 5T
Adb97513 Feline 5T
Adb97515 Nucleotid
Abx87174 CDNA enco
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Add126168 Human CDN
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Aec85321 Human cDN
Abk78385 Bacillus
Abk78397 Bacillus
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Adx27350 Plant ful
                                                                                                                                                                                                                                                                                                                                                                           ds, cytostatic, gene therapy, DKFZp5661133 activity inhibitor; breast cancer; differential expression.
                                                                                                                                                                                                                                                                                                                                                              Breast cancer differentially expressed gene product #199.
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                 ADD46508
ADX27350
                                                                                                                                                                                                                                                                                                                        BP.
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CHIR ) CHIRON CORP
WO2003057926-A1.
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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ADK11793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hansen R;
                                                                                                                                                                                                                                                                                                           RESULT 1
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 Adk11793 Breast ca
Acd93536 Human col
Aas87174 DNA encod
                                            ; Search time 377.5 Seconds
  (without alignments)
249.339 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
      GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                nucleic search, using frame_plus_p2n model
                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                        5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
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ACD93536
AAS87174
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database

Score

Result Š. 539

Total number of

Searched:

88

Minimum Maximum

Scoring table:

Perfect score:

Sequence:

OM protein

Run on:

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The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKF2p56G1133 activity. The methods are useful for treating cancer, e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention.
                                                               Inhibiting a cancerous phenotype of a cell, useful for treating breast sancer comprises contacting a cancerous mammalian cell with an agent for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 130 BP; 30 A; 41 C; 30 G; 29 T; 0 U; 0 Other;
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                                                                                                                               Inhibition of DKFZp566I133 activity.
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XXX ACD5
XXX ACD7
XXX ACC7
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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (1) at low stringency, preparing single oligonucleotide primer (1) at low stringency, preparing condamness and sequencing the product, and repeating the contacting, preparing conditions and amplifying steps with different primers and sequencing resulting conditions are sequenced from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism; and for sequencing concluded to the part of a genome of an organism; and for sequencing and or human cell which is associated with a pathological condition e.g. a nucleotide sequence of an organism. mNAM is obtained from mammalian concludes or sequence of an organism. mNAM is obtained from mammalian concludes or sequence of an organism. mNAM is obtained from mammalian concludes or mmall populations. further, it can be used to carry out genetic analyses of parge or small populations. further, it can be used to study living an individual or population more or less likely to be afflicted with an individual or population more or less likely to be afflicted with an individual or population more or less likely to be afflicted with as scorer, and so forth. The method can also be used in the study of the study of whether the conditions are likely to be passed to offspring through over or sperm. The analyses for pathological conditions can be carried out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as criviliance and also applied to eukaryotic pathogens, such as a trypanosomes different approaches to cundersone shiftes or mutations, which may require different approaches to polymucleotide isolated from h

G; 62 T; 0 U; 0 Other;

Sequence 299 BP; 75 A; 84 C; 78

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Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
         2
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2
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                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #22978.
                             Conservative:
Mismatches:
Indels:
          Length:
Matches:
                                                                                                                   TTCCTGGACAATCCCTGGGTCTGC 188
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                                                                                                        1 PheLeuAspAsnAsnProTrpValCys
                                                                                   US-10-774-176-16 (1-9) x ACD93536 (1-299)
                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                      AAS87174 standard; cDNA; 453
                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631
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                                          Best Local Similarity:
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                              Percent Similarity:
                                                                                                                                                                                                                                                                                      Homo sapiens.
Alignment Scores:
Pred. No.:
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                                                                                                                                                                                         AAS87174;
                                                    Query Match:
DB:
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99US-00406117 98US-00196716

27-SEP-1999; 20-NOV-1998;

24-OCT-2002.

JS2002155438-A1

Homo sapiens

Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of

Simpson AJG, Neto ED,

WPI; 2003-182626/18.

(SIMP/) SIMPSON A J G. BRENTANI R R.

(BREN/)

Example 9; Page 302; 959pp; English

individual

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed (II) are useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in rissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). In are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotides of other traits to assess by brodiversity and the polypeptide and polypeptides or other traits to assess to be application of mutations and polymerations of the polypeptide and polypeptides or other traits to assess to be application of mutations and polymerations of the polypeptide and polymerations of the polyperation of the polyperation of the polyperat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 22978; 103pp; English.
                                                                                                               Tang YT;
                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                         WPI; 2001-639362/73
                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                   P-PSDB; ABG22987
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Sequence 453 BP; 108 A; 111 C; 113 G; 121 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
                                                   Indels:
         0.396
59.00
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US-10-774-176-16 (1-9) x AAS87174 (1-453)

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1 PheLeuAspAsnAsnProTrpValCys 9
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ADU11677 standard; DNA; 475 27-JAN-2005 (first entry) RESULT 4 ADU11677 

ВР

Solid tumour prognosis gene seqid 2116.

cytostatic; gene therapy; expression profile; solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds.

Inident i fied

WO2004097052-A2

11-NOV-2004

29-APR-2004; 2004WO-US013587,

29-APR-2003; 2003US-0466067P. 23-JAN-2004; 2004US-0538246P.

(AMHP ) WYETH

STRA/) STRAHS A.

Slonim DK; Twine NC, Burczynski ME, Trepicchio WL, Dorner AJ; Strahs A, T. Immerman F,

WPI; 2004-804779/79.

A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.

Disclosure; Page; 111pp; English

The invention describes a method comprising comparing an expression profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the at least one gene, where the patient has a solid tumour, and each of the first and second classes of patients have the solid tumour, and coth the first and second classes of patients have the solid tumour, and appulation of patients who have the solid tumour, and appulation of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of at class to one paper in a peripheral blood sample of a patient who has a solid tumour, (ii) at least another storage medium including data that represent at least one reference expression profile to the reference expression profile, and (iv) a processor capable of executing the program capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the comprising concentrated probes for solid tumour prognosis genes, where each of the patients who have the solid tumour prognosis genes is differentially expressed in PBMCs of a first class of patients has a second classe of patients has a second class of patients has a second class of controme. The method, system, and array are useful for prognosis gene of the method, system, and array are useful for prognosis gene of the burnant prognosis genes and intention of parming the reference and tumour prognosis genes and patients has a solid tumour prognosis gene of the prainted proper expression between the patients has a second classe of patients and second classes of patients has a second clas in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences specification, but was obtained of the printed 

Sequence 475 BP; 119 A; 125 C; 117 G; 114 T; 0 U; 0 Other;

Matches: Conservative: Mismatches: Length: Indels: 0.418 59.00 100.0% 100.0% Similarity: Percent Similarity: Query Match: No.:

US-10-774-176-16 (1-9) x ADU11677 (1-475)

147 Trecresacaacaarceressrerse 173 σ 1 PheLeuAspAsnAsnProTrpValCys

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AAA27060 standard; DNA; 901 AAA27060 ID AAA2 XX AC AAA2

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                                                Canine; TAA; tumour-associated antigen; anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
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                              Canine 5T4 tumour-associated antigen gene.
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/product= "5T4 antigen"
                                                                                                           Location/Qualifiers
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           22-AUG-2000
                                                                                         Canis sp.
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WO200029428-A2

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The present sequence encodes the canine 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour idagnosis, targeting and immunotherapy. Mice in which tumours had been human or murine 5T4 gene sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen can be used to elicit an immune response, preferably CTL or an antibody response in a
                                                                                                                                                                                                                                                            Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
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drug development; pharmacogenetics; biosensor development
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                                                                                                                                                                                                                                                                                                                      Disclosure; Page 78-79; 79pp; English.
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                                   98GB-00025303.
99GB-00001739.
99GB-00017995.
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02-FEB-2001; 2001US-0265928P.
09-APR-2001; 2001US-00829472.
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                                                                                                                                                            Myers KA;
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Best Local Similarity:
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P-PSDB; AAY94351
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18-NOV-1999;
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The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer. And for detecting genes that are up or down-regulated in breast cancer calls. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datesets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07693 - ABT07761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                       useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast
                                                                                                                                                                                                                                                Detecting a breast cancer-associated transcript in a patient's cell,
                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 372; 414pp; English.
                                                                                        (EOSB-) EOS BIOTECHNOLOGY INC
09-APR-2001; 2001US-0282698P.
04-MAY-2001; 2001US-0288590P.
29-MAY-2001; 2001US-0294443P.
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                                                                                                                                                                                                                                                                                                               nucleic acids.
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Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

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Mismatches:
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ABX76333 

ABX76333 standard; DNA; 927 BP

ABX76333

02-APR-2003 (first entry)

cancer-associated polynucleotide #197. Lung

antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis. cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; Lung

Unidentified

WO200286443-A2

31-OCT-2002

18-APR-2002; 2002WO-US012476.

10-MAY-2001; 2001US-0290492P. 09-NOV-2001; 2001US-0339245P. 13-NOV-2001; 2001US-033666F. 29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P. 2001US-0284770P 

(EOSB-) EOS BIOTECHNOLOGY INC

Aziz N, Murray R;

WPI; 2003-093161/08. P-PSDB; ABU56604.

Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

Claim 22; Page 336; 453pp; English

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer associated polymucleotides and polymeptides are used for identifying a compound that modulates a lung cancer-associated polymeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atlectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchhectasis. The genes, polymucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences and as targets for screening for therapeutic compounds that modulate lung cancer-associated polymucleotides of the nvention

Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 0.886 59.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores Query Match: Pred. No.: Score:

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US-10-774-176-16 (1-9) x ABX76333 (1-927)

œ ADB80503

04-DEC-2003 (first entry) ADB80503; 

BP

ADB80503 standard; DNA; 927

Ovarian cancer-associated transcript #34.

cytostatic; gene therapy, vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.

Homo sapiens

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The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, and determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:41
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                       Location/Qualifiers
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27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-03544P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                     18-JUN-2002; 2002WO-US019297
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P-PSDB; ADB80504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                        WO2002102235-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                          27-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EOSB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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                             Key
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SECENTIAL SECTION OF THE SECTION OF
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
antibodies and chods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, and uterrine fibroids. They may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
        retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glynne R, Hevezi PA;
3, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a nucleic acid sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Wilson KE,
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Matches:
inflammatory disease; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Afar D, Aziz N, Ginsburg WM,
Mack DH, Murray R, Watson SR,
                                                                                                                                                                                                                                          2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                            2001US-0340376P.
2002US-0347211P.
                                                                                                                                                                                                                                                                                                                            2002US-0347349P.
2002US-0355250P.
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2002US-0372246P.
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59.00
100.0%
100.0%
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P-PSDB; ADN38724.
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Best Local Similarity:
Query Match:
                                                                                                                              WO2003042661-A2.
                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                             03-DEC-2001;
14-DEC-2001;
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29-MAR-2002;
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                                                                                                                                                              22-MAY-2003
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No.:
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Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinflammatory; cardiant; haemostatic; neuroprotective; anorectic; noctropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haemacopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                         ABV99349 standard; DNA; 1156 BP
                                                                                                       Human NOV8a coding sequence.
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                      WO200272771-A2.
                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001;
09-MAR-2001;
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                                                                             27-JAN-2003
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                                                   ABV99349;
RESULT 11
              ABV99349
                                       The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway modulating agent for preparing a for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent.
                                                                                                                                                                                                                                     Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy; d8.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                1 PheLeuAspAsnAsnProTrpValCys
                         US-10-774-176-16 (1-9) x ADN38723 (1-927)
                                                                                                                               AADS6198 standard; DNA; 973 BP
                                                                                                                                                                                                             Human LRRCAPS related DNA #5.
                                                                                                                                                                                                                                                                                                                                                       21-OCT-2002; 2002WO-US033540.
                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-2001; 2001US-0338733P.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
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59.00
100.0%
100.0%
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11
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                                                                                                                                                                                                                                                                                                      WO2003035831-A2.
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2001US-0274101P.
2001US-0274194P.
2001US-0274281P.
2001US-0274322P.
2001US-0274849P.
2001US-0275235P.
2001US-0275578P.
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2001US-0276776P.
2001US-0276994P.
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2001US-0277833P.
2001US-0278152P.
2001US-0278894P.
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2001US-0279036P.
2001US-0279344P.
2001US-0279995P.
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2001US-0280802P.
2001US-0280822P.
2001US-0280900P.
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2001US-0283675P.
2001US-0287424P.
2001US-0288066P.
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2001US-0288528P.
2001US-0291190P.
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08-MAR-2002; 2002WO-US007288
                                                                                                                                              001US-0275601P
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TTCCTGGACAACAATCCCTGGGTCTGC 567

PheteuAspAsnAsnProTrpValCys 9

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US-10-774-176-16 (1-9) x AAD56198 (1-973)

Percent Similarity: Best Local Similarity:

Query Match:

Gaps:

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99127-ABV99595 and ABP70049-ABP70149), where X is any unuber from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of medicament for treating a syndrome associated with a human disease, medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating. The NOVX coding sequences and proteins are useful for treating. Cancer, neurodegenerative disease, anorex-associated cacheria, cancer, neurodegenerative disease, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, cardiovascular disorders, fartility, bronchial aschma, AIDS, dyslipidemia, metabolic disorders, fartility, bronchial aschma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders associated with obesity, also no various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell profileration, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                       11 L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ;
FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM;
EA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK;
Z, Malyankar UM, Anderson DM, Patturajan M, Miller CE;
F RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 114-115; 619pp; English.
                                                                                                                                                                                                                                                      21-NOV-2001; 2001US-0332094P.
03-DEC-2001; 2001US-0337426P.
03-DEC-2001; 2001US-033718992P.
04-DEC-2001; 2001US-033718FP.
03-JAN-2002; 2002US-0346705P.
                                                       2001US-0318770P.
2001US-0325430P.
2001US-03350B0P.
2001US-0335301P.
2001US-0332172P.
2001US-0332172P.
2001US-033214P.
2001US-0333184P.
2001US-0333184P.
                                       2001US-0318462P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taupier RJ, Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-732824/79.
                                                                                                                                                                                                                                                                                                                                                                                                                           Rastelli L, Mezer
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                                                                                                27-SEP-2001;
18-OCT-2001;
31-OCT-2001;
                                                                                                                                                                                                 14-NOV-2001;
14-NOV-2001;
                                                           .2-SEP-2001;
                                                                                27-SEP-2001;
                                                                                                                                                          14-NOV-2001;
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Pena CEA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOBS EZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhong M;
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SQ Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:

Score:

Score:

Percent Similarity:

100.0\$

Mismatches:

Destruction:

100.0\$

Mismatches:

US-10-774-176-16 (1-9) x ABV99349 (1-1156) Qy 1 PheLeuAspAsnAsnProTrpValCys 9

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the proposition-rich glycoproteins known as 574, and the confootal leucine-rich glycoproteins the styressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The protein are useful for isolating foetal cells from maternal blood. The cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es). The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                            Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.
                                                                                                                                                                             cDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
Indels:
757 TICCTGGACAACAAICCCTGGGICTGC 783
                                                                                                                                                                                                                                                                                                                                                                                               /product= "5T4 protein"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1260
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 68; 68pp; English.
                                                                    ABK87175 standard; cDNA; 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2001; 2001WO-GB005004.
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59.00
100.0%
100.0%
                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200238612-A2
                                                                                                                                       07-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers K,
                                                                                                      ABK87175;
                                                                                                                                                                                                                                                                                                       Felis sp.
                                 RESULT 12
                                                    ABK87175
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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope of the 5T4 antigen. The invention further provides a polyepitope string comprising the 5T4 epitope erring of the 5T4 epitope; a vector system capable of delivering the 5T4 epitope mucleic acid to a cell; a cell pulsed with the 5T4 epitope, a polyepitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of mucleic acid in a subject; and a T cell line or clone capable of mucleic acid in a subject; and a T cell line or clone capable of mucleic acid in a subject; and a T cell line or clone capable of mucleic acid in a subject; and a call into or clone capable of mucleic acid in a subject; and a cell into acid and the vector system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for diagnosing or monitoring the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or preventing a disease. This polynucleotide sequence represents the feline or preventing a disease. This polynucleotide sequence represents the feline or string a disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New major histocompatibility complex class I peptide epitopes from human 5T4 tumor-associated antigen, useful for preventing and/or treating a
                                                                                                                                                                                                                                                                                                                               Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1260
/*tag= a
/product= "Feline 5T4 antigen protein"
                                    Redchenko I;
US-10-774-176-16 (1-9) x ABK87175 (1-1260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 67; 73pp; English.
                                                                                                                                                                ADB97513 standard; DNA; 1260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2003; 2003WO-GB000670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, particularly cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002; 2002GB-00003419
                                                                                                                                                                                                                                              04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s,
                                                                                                                                                                                                                                                                                          Feline 5T4 antigen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kingsman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-637141/60.
P-PSDB; ADB97520.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                         ADB97513;
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Seguence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;

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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy or as part of a vaccine. This polynucleotide sequence represents the DNA
                                                                                                                                                                                                                                                                                                                                  gene; ds; feline; Major Histocompatibility Complex class II; MHC; epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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                                     Conservative:
Mismatches:
                           Matches:
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                                                                    Indels:
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                                                                                                                                      Gaps:
                                                                                                            US-10-774-176-16 (1-9) x ADB97513 (1-1260)
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 49; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kingsman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding for the feline 5T4 protein
                                                                                                                                                                                                                                                                                                           DNA encoding feline 5T4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                         ADB97452 standard; DNA; 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2003; 2003WO-GB000618.
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                                   Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
Alignment Scores:
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                                                                                                                                                                                                                                                     ADB97452;
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                                                                                                                                                                                                            ADB97452
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The present sequence encodes the human ST4 tumour-associated antigen carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. ST4 antigen may therefore be useful in tumour idagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the present sequence. The ST4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen test can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor associated antigen, 5T4 capable of eliciting cytotoxic T\text{-lymphocyte} response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                              Human, TAA, tumour-associated antigen, anti-tumour, cytostatic,
immunostimulant, vaccine, carcinoma, colorectal cancer, gastric cancer,
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    Mismatches:
Indels:
Gaps:
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                                                                                       US-10-774-176-16 (1-9) x ADB97452 (1-1260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 78; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                            AAA27058 standard; DNA; 1263 BP
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99GB-00001739.
99GB-00017995.
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Best Local Similarity:
Query Match:
DB:
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27-JAN-1999;
30-JUL-1999;
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Length:
Matches:
Conservative:
Mismatches:
Indels:

1,25 59.00 100.0% 100.0%

Percent Similarity: Best Local Similarity: Query Match: DB:

No.:

PheLeuAspAsnAsnProTrpValCys 9

US-10-774-176-16 (1-9) x AAA27058 (1-1263)

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868 TICCIGGACAACAAICCCIGGGICIGC 894
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Search completed: May 27, 2006, 10:38:31 Job time: 379.5 secs

OM protein

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Sequence:

Searched:

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AC106962 Rattus no
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AC123523 Mus muscu
AC123533 Mus muscu
AC101205 Mus muscu
AC155913 Mus muscu
     AX822164 Sequence
AX81513 Sequence
AX8153 Sequence
AX81548 Sequence
AX8259731 Polypepti
AX025011 Sequence
AX149553 Sequence
AX146086 Sequence
AX16086 Sequence
BD249732 Polypepti
AX025012 Sequence
BD249732 Polypepti
AX055012 Sequence
CQ731678 Sequence
CQ731678 Sequence
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Z29083 Home sapien
AX961916 Sequence
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AX961916 Sequence
AX074791 Homo sapien
BC087011 Rattus no
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BC087011 Rattus no
BC087011 Sequence
AX961914 Sequence
AX961915 Homo sapi
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burczynski, M.E., Twine, N.C., Slonim, D.K., Trepicchio, W.L., Strahs, A., Immerman, F. and Dorner, A.J.
Methods for prognosis and treatment of solid tumors
Patent: WO 2004097052-A 2116 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
Location/Qualifiers
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AX961914
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Alignment Scores:
Pred. No.:
ACCESSION
VERSION
KEYWORDS
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BD249733 Polypepti
AX025013 Sequence
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257.039 Million cell updates/sec
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                                                       May 27, 2006, 09:51:03 ; Search time 3358.6 Seconds
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        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

    nucleic search, using frame_plus_p2n model

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Fgapop 6.0 , Fgapext
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Database

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Result Š. PAT 15-SEP-2000

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll, M.W. and Myers, K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 3 05-DEC-2001;
Oxford Biomedica (WK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                             Polypeptide
Batent: WO 029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB)
BIOMEDICA LTD (GB)
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AX025013
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mismatches:
Indels:
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Conservative:
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Gaps:
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BD249733
BD249733.1 GI:33059503
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Canis sp.
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PAT 14-DEC-2001

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DEFINITION

AX829164

RESULT

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

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Smithson, Xiaojia Guo, Valerie Gerlach, Stacie Casman, Ferenc
Boldog, Li Li, Bryan Zerhusen, Velizar Tchernev, Esha Gangolli, Corine
Vernet, Carol Pena, Catherine Burgess, Xiaohong Liu, Kimberly
Spytek, Linda Gorman, Steven Spaderna, Edward Voss, Uriel
Malyankar, David Anderson, Meera Patturajan, Charles Miller, Raymond J
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xiaojia guo,
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PI vladimir y gusev,mei zhong,raymond j taupier jr,stacie j
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PI charles e miller,meera patturajan,david w anderson,uriel
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60/27579,03-MAY-2001 U
60/288066,30-APR-2001 U
60/288002,02-APR-2001 U
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19-MAX-2001 US
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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I (bases 1 to 1156)

Padigaru,M., Shenoy,S.G., Pochart,P.F., Kekuda,R., Gusev,V.Y.,
Zhong,M., Jr.R.J.T., Caeman,S.J., Li,L., Miller,C.E.,
Patturajan,M., Anderson,D.W., Malyankar,U.M., Voss,E.Z.,
Spaderna,S.K., Gorman,L., Spytek,K.A., Liu,X., Burgess,C.E.,
Pena,C.E.A., Gerlach,V., Smithson,G., Mezes,P.D., Rastelli,L.,
Boldog,F.L., Guo,X., Vernet,C.A.M., Gangolli,E.A., Tchernev,V.T.
                                                                                                                                                                                                                                                                                                                                                                                                       compositions and methods
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelec
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Methods of diagnosis of breast cancer, com
screening for modulators of breast cancer
strent: WO 02059377-A 57 01-AUG-2002;
EOS Blotechnology, Inc. (US)
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                                       US-10-774-176-16 (1-9) x AX316088 (1-901)
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1263)
Carroll,M.W. and Myers,K.A.
Polypeptide
Patent: JP 2002530060-A 1 17-SEP-2002;
CXFORD BIOMEDICA LTD
OS Homo sapiens (human)
PN JP 2002530060-A/1
PD 17-SEP-2002
PP 18-NOV-1999 GB 9825303.2,27-JAN-1999 GB
30-JUL-1999 GB 9917995.4
PILES WILLIAM CARROLL,KEVIN ALAN MYERS
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Pelidae,
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MHC class I peptide epitopes from the human 5t4 tumor-associated
antigen
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Patent: WO 0238612-A 3 16-MAY-2002;
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Location/Qualifiers
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                                             1 PheLeuAspAsnAsnProTrpValCys 9
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TITLE
                                                                                                                  AX467373
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AX821533
                                                                                                      RESULT 7
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PAT 16-JUL-2002
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll,M.W. and Myers,K.A.
5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
                                                                 Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W., Ellard, F.M. and Myers, K.A.
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Matches:
Conservative:
Mismatches:
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/mol_type="unassigned DNA"
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            synthetic construct
synthetic construct
other sequences; artificial sequences.
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                                                                                           Antibodies
Patent: WO 0136486-A 14 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers

    1263
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Sequence 1 from Patent EP1160323.
AX316086
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Homo sapiens (human)
Homo sapiens
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AX316086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
C12N15/09,A61K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,
C07K19/00,
C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
1. 1263
/mol_type="unassigned DNA"
/mol_type="taxon:9606"
                                                              ce 1. 1263 /organism='Homo sapiens (human)'.
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Conservative:
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Gaps:
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Sequence 14 from Patent WO0136486.
AX149553.1 GI:14347991

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    /db_xref="taxon:9606"

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Sequence 1 from Patent W00029428.
AX025011
AX025011.1 GI:10184932
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                                          Polypeptide
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AX025011
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
Canis.
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1 (bases 1 to 1281)
Carroll, M.W. and Myers, K.A.
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Patent: JP 200250060-A 2 17-SEP-2002;
OS FORDA LIDE ALD
OS FORDA LIDE ALD
OS FORDA LIDE ALD
DO 17-SEP-2002
PP 19-NOV-1999 JP 2000582415
PP 18-NOV-1999 GB 9917395.4
PP 18-NOV-1999 GB 9917396.4
PP 18-NOV-1999 GB 9917
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1. 1281
/organism='Mus musculus (mouse)'.
Location/Qualifiers
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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    .1281
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Sequence 1 from Patent W00238612.
AX467371
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JP 2002530060-A/2.
Mus musculus (house mouse)
Mus musculus
                                                               AX467371.1 GI:21900602
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PN JP 20025300
PP 19-2002300
PP 18-NOV-1999
30-JUL-1999 GB
PC C12N15/09, A
PC C12N15/00,
PC CONTS/00,
PC POLYPEPTIGE
FF Key
FT SOUTCE
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BD249732
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Alignment Scores: 0.0433 Length: 1281

Pred. No.: 59.00 Matches: 9

Scoret: 59.00 Matches: 9

Percent Similarity: 100.0$ Conservative: 0

Best Local Similarity: 100.0$ Mismatches: 0

Query Match: 100.0$ Indels: 0

DB: 2
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US-10-774-176-16 (1-9) x BD249732 (1-1281)

Search completed: May 27, 2006, 19:35:22 Job time : 3359.6 secs

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB E Maximum DB E

Searched:

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Ada27058 Human 574
Ad689736 Nucleotid
Abk87174 CDNA enco
Aad27059 Mouse 574
Ad56629 Human LRR
Ad56629 Human LRR
Ad56197 Human LRR
Ad78510 Tumour-as
Ac738510 Tumour-as
Ac738510 Tumour-as
Ac738510 Tumour-as
Ad73851 Fibrotic
Aa87175 DNA encod
Aa84254 Human ful
Ad126162 Human cDN
Ad130831 Full leng
Ad130831 Full leng
Ad126160 Human cDN
Ad130831 Full leng
Ad126160 Human cDN
Ad126162 Human cDN
Ad26162 Human cDN
Ad26162 Human cDN
Ad3089 Enterococ
Ab98884 Enterococ
Ad900392 Lactcobaci
         Abx76333 Lung canc
Abb80503 Ovarian c
Adn38723 Cancer/an
Aad56198 Human LRR
Aby89349 Human NOV
Abb87175 cDNA enco
Adb97513 Feline 5T
Adb97452 DNA encod
Aaa27058 Human 574
Aaf89736 Nucleotid
Abx87174 cDNA enco
Aaa27059 Mouse 574
Aad5199 Human LRR
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                                                                                                                                                            AAA27059
AAD56199
ACC51052
ACC51052
AABX76332
AAD56197
AAD56200
ADN38721
ADN03961
ADN25444
ACC3626
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ADB97452
AAA27058
AAF89736
ABK87174
            ABX76333
ADB80503
ADN38723
AAD56198
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CHIR ) CHIRON CORP
WO2003057926-A1.
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ADK11641;
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249,339 Million cell updates/sec

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re greater than or equal to the score of the result being printed,
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    nucleic search, using frame_plus_p2n model

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                                                                                               The invention relates to a method of inhibiting a cancerous phenotype of a cell comprises contacting a cancerous mammalian cell with an agent for inhibition of DKF2566I133 activity. The methods are useful for treating cancer. e.g. breast cancer. This sequence represents a gene product which is differentially expressed in breast cancer cells. The sequence can be used in the method of the invention.
                      Inhibiting a cancerous phenotype of a cell, useful for treating breast cancer comprises contacting a cancerous mammalian cell with an agent for inhibition of DKFZp5661133 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burczynski ME, Twine NC, Slonim DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; expression profile; solid tumour; peripheral blood mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                                                                       Sequence 246 BP; 77 A; 49 C; 59 G; 61 T; 0 U; 0 Other;
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                                                                         Claim 30; SEQ ID NO 47; 257pp; English
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23-JAN-2004; 2004US-0538246P.
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WPI; 2003-577534/54
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unsupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the apopulation of patients who have the solid tumour, and where the cap oppulation of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, and the second class of patients has a second clinical outcome. Also described are: a system comprising (i) a memory or a cutome including data that represent an expression profile of a patient who has a solid tumour, (ii) at least another storage medium including data that comparing the expression profile of the gene, (iii) a program capable of comparing the expression profile to the reference expression profile, and (iv) a processor capable of executing the capression profile, and (iv) a processor capable of executing the expression profile, and (iv) a processor capable of executing the capression profile, and (iv) a processor capable of executing the capression profile, and (iv) a processor capable of executing the capression profile outcomes of the patients who have the solid tumour correlate with clinical outcomes of the patients so and a nucleic acid or protein array comprising concentrated probes for solid tumour prognosis genes, where each of the patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as a second class of patients as a second class of patients as a second clumours. This sequence represents a solid tumours. This sequence represents a solid tumours and where the first class of patients as a second class of the inventor, and the second class of patients as a second class of the inventor. The method, system, and array are useful for prognosing and treating cutcome, and the sequence represents a solid tumours. This sequence represents a solid tumours in the proposition, but was obtained in electronic f
expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an
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be part of the coding sequence and does not encode any
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immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
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tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour diagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inoculated with a virus expression vector containing the human or murine 5T4 gene sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably CTL or an antibody response in a

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Sequence 901 BP; 178 A; 246 C; 212 G; 153 T; 0 U; 112 Other;

Matches: Conservative: Mismatches: Indels:

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Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores: Pred. No.:

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Gaps:

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BP.

ABT07721 standard; DNA; 927

14-NOV-2002 (first entry)

ABT07721;

CTGATAGGCGCCATCTTCCTACTGGTT 1 LeulleGlyAlallePheLeuLeuVal

US-10-774-176-15 (1-9) x AAA27060 (1-901)

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Length:

carcinomas but has a highly restricted expression pattern in normal adult

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Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the canine 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 78-79; 79pp; English
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P-PSDB; AAY94351.
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corresponding amino acids"
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/note= "given in the specification
be part of the coding sequence and
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be part of the coding sequence and
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/note= "given in the specification
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corresponding amino acids"
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corresponding amino acids"
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be part of the coding sequence and
corresponding amino acids"
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Gene; ds; breast cancer; breast cancer-associated gene sequence; drug development; pharmacogenetics; biosensor development. Breast cancer-associated gene sequence 29 (EOSB-) EOS BIOTECHNOLOGY INC 22 - FEB - 2011, 2011US - 0.2559289 - 0.9 - APR - 2011, 2011US - 0.0829472 - 0.9 - APR - 2011, 2001US - 0.285989 - 0.4 - MAY - 2011, 2001US - 0.294443P - 29 - MAY - 2001, 2001US - 0.294443P - 0.294444444P - 0.294444444P - 0.29444444P - 0.2944444P - 0.2944444P - 0.2944444P - 0.294444P - 0.294444P - 0.294444P - 0.294444P - 0.294444P - 0.29444P - 0.29444P - 0.29444P - 0.29444P - 0.2944P - 0.2944P - 0.2944P - 0.2944P - 0.2944P - 0.2944P - 0.294P - 0. 24-JAN-2001; 2001US-0263965P 24-JAN-2002; 2002WO-US002242 Afar D; Gish KC, WO200259377-A2 Unidentified 01-AUG-2002 Mack DH, 

Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids. WPI; 2002-583738/62. N-PSDB; ABJ05564.

Claim 9; Page 372; 414pp; English.

The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown

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in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07693 - ABT07761 represent the 69 breast cancer-associated gene sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lung cancer-associated polynucleotide, gene, ds, cytostatic, emphysema, antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion, precancerous lesion; bronchitis; chronic obstructive pulmonary disease, hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 927 BP; 187 A; 297 C; 240 G; 203 T; 0 U; 0 Other;
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Matches:
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Gaps:
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2001US-0339245P.
2001US-0350666P.
2001US-0334370P.
2002US-0372246P.
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P-PSDB; ABU56604.
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Best Local Similarity:
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Pred. No.:
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DB:
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in cased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by cancer in a patient and for treating a mammal having lung cancer by cancer in a patient and for treating a mammal having lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, intersitial pulmonary disease, fibrosis, bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences harvest in a patient and cancer, such as antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection; ds; gene.
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Mismatches:
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Matches:
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27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-0317544P.
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DB:
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RESULT 8
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The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, enhanced the monitoring tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the nucleic acids
                                         Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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Matches:
Conservative:
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2002US-0347349P.
2002US-0355250P.
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2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
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                                                                                                                                      Claim 10; Page 297; 332pp;
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P-PSDB; ADB80504
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10-JAN-2002;
08-FEB-2002;
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03-DEC-2001;
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HARRIER REAL FOR SON SON SERVICE STREET BERNELLE STREET BERNEL
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of apthological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; use of such antibodies for drug targeting, and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atherosclerosis, inflammatory diseases, autoimmune diseases, retinal meovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.
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LRRCAPS; cancer; gene therapy; ds.
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3, Zlotnik A;
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                             Gish KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 41; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuIleGlyAlaIlePheLeuLeuVal 9
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                                                                                                                                                                                                                                                                                                                                                             Ginsburg WM,
R, Watson SR,
                                               04-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-039789P.
22-JUL-2002; 2002US-0397795P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
                                                                                                                                                                                                                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human LRRCAPS related DNA #5.
2002US-0359077P.
2002US-0368809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD56198 standard; DNA; 973
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100.0%
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Murray R,
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P-PSDB; ADN38724.
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ПН,
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Mack
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01-MAY-2003

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2001US-0279036P.
2001US-0279934P.
2001US-0279995P.
2001US-0280802P.
2001US-0280802P.
2001US-0280900P.
2001US-0280900P.
2001US-028949P.
2001US-028946EP.
2001US-028946EP.
2001US-028946EP.
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2001US-0274194P.
2001US-027422P.
2001US-027432P.
2001US-0275235P.
2001US-0275235P.
2001US-0275579P.
2001US-0275579P.
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2001US-0277231P.
2001US-0277321P.
2001US-0277338P.
2001US-0277791P.
2001US-0277833P.
2001US-0278833P.
2001US-0278838P.
2001US-02788984P.
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2001US-0291099P.
2001US-0291240P.
2001US-0294485P.
2001US-0294889P.
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                                                                            08-MAR-2002; 2002WO-US007288
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                WO200272771-A2.
                                                                                                                                                       08-MAR-2001;
09-MAR-2001;
12-MAR-2001;
                                                                                                                                                                                                     13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
                                                                                                        08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
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14-NOV-2001;
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                                               19-SEP-2002
\chi_3\chi_3\chi_3
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent acitvity, where a difference between the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antinfertility; carebroprotective; gene therapy; NOVX; NOV; Ertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma, dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; anglogenesis; ds.
                                                                                                                                                                                                                                                                                  Identifying a candidate p53 pathway-modulating agent for treating cancer comprises contacting an assay system comprising a purified leucine rich repeat, capricious related polypeptide or nucleic acid with a test agent
                                                                                                                                                                                                        Ö
                                                                                                                                                                                                        'n
                                                                                                                                                                                                        Plowman GD, Funke RP, Lioubin MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 973 BP; 203 A; 308 C; 254 G; 208 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 74-75; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-774-176-15 (1-9) x AAD56198 (1-973)
                                                                                                        22-OCT-2001; 2001US-03387339.
15-FEB-2002; 2002US-0357600P.
01-MAR-2002; 2002US-0361196P.
                                                                           21-OCT-2002; 2002WO-US033540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV99349 standard; DNA; 1156
                                                                                                                                                                                                       Belvin M, Schleithoff L, P
Francis-Lang H, Friedman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NOV8a coding sequence.
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40.00
100.0%
100.0%
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                                                                                                                                                                        (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                   WPI; 2003-421410/39.
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Best Local Similarity:
Query Match:
                WO2003035831-A2
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2002US-0345705P 2002US-00093463

CURA-) CURAGEN CORP

Homo sapiens

ABV99349;

ABV99349 RESULT

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Score:

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The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is any unber from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating.

The NOVX coding sequences and proteins are useful for treating, cancer, neurodegenerative diseases, such as metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders associated with obesity, metabolic syndrome X or wasting disorders and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, call profileration, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of anticonic dispense.
Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burges CE, Liu X, Spytek KA, Gorman L, Spadernas SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
                                                                                                                                                                                                                                                           New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 114-115; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic or diagnostic methods
                                                                                                                                                                                                                                                                                                                                              disorders, and asthma.
                                                                                                                                                                                    WPI; 2002-732824/79.
                                                                                                                                                                                                               P-PSDB; ABP70071
                                                                                                                              Zhong M:
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Sequence 1156 BP; 228 A; 383 C; 303 G; 242 T; 0 U; 0 Other; Length: Matches: 121 40.00 100.0% 100.0% Alignment Scores:

982 CTGATAGGCGCTATTTTCCTCCTGGTT 1008

(first entry) 07-OCT-2002

CDNA encoding feline oncofoetal leucine-rich glycoprotein, 5T4.

Felis sp

Key

Conservative: Mismatches: Indels: 1 LeulleGlyAlallePheLeuLeuVal 9 US-10-774-176-15 (1-9) x ABV99349 (1-1156) Best Local Similarity: Percent Similarity Query Match:

셤

ABK87175 standard; cDNA; 1260 BP. ABK87175; RESULT 10 ABK87175 

Feline; cat; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; ss.

Location/Qualifiers 1. .1260 /\*tag= a

Major Histocompatibility Complex class I peptide epitope; MHC; 5T4 antigen; 5T4 epitope; polyepitope string; vaccine; T cell; cytostatic; cancer; feline; gene; ds.

Unidentified

1090 CTGATAGGTGCCATTTTCTTACTGGTT 1116

ADB97513 standard; DNA; 1260 BP

RESULT 11 ADB97513 04-DEC-2003 (first entry) Feline 5T4 antigen DNA.

ADB97513;

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The present invention relates to the isolation of canine and feline oncofoetal leucine-rich glycoproteins known as 574, and the concofoetal leucine-rich glycoproteins known as 574, and the polynucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell control infections, inflammantory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extractes of plasma, urine, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The solation process may form part of a diagnostic method e.g. the foetal cells may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus(es).

The present sequence encodes feline 574 protein
                                                                                                                                                                                                                                                                                                                                                        encoding the
                                                                                                                                                                                                                                                                                                                                                  Novel canine or feline 574 polypeptide and polynucleotides encodir polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
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Conservative:
Mismatches:
Indels:
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/product= "5T4 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 68; 68pp; English.
                                                                                                                                                                                                          (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                 Carroll M;
                                                                                                                                                                 13-NOV-2000; 2000WO-GB004317.
                                                                                                                          13-NOV-2001; 2001WO-GB005004
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                                        WO200238612-A2
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                                                                                 16-MAY-2002
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No
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DNA encoding feline 5T4 protein.

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The invention relates to a novel Major Histocompatibility Complex (WHC) class I peptide epitope of the 5T4 antigen. The invention further class I peptide epitope of the 5T4 antigen. The invention further and by provides a polyepitope string of the 5T4 epitope or a polyepitope string of the 5T4 epitope. A vector system capable of delivering the 5T4 epitope nucleic acid to a cell; a cell pulsed with the 5T4 epitope of the 5T4 epitope, its encoding nucleic acid, or the vector system; a vaccine comprising the above; a method for treating and/or preventing a disease in a subject by administering the vaccine; an agent capable of binding specifically to the 5T4 epitope and/its encoding nucleic acid; a method comprising detecting the presence of the 5T4 epitope or its encoding nucleic acid in a subject; and a T cell line or clone capable of specifically recognising the 5T4 epitope has cytostatic activity. The vaccine comprising the 5T4 epitope has cytostatic activity. The vaccine comprising the 5T4 epitope or its encoding nucleic acid and the vector system or cell is useful in the prevention and/or treatment of a disease, particularly cancer. The detection method is useful for diagnosing or monitoring the progression of a cancerous disease, and for detecting the presence of the 5T4 epitope or its nucleic acid. The T cell line or clone is useful in the manufacture of a medicament for treating and/or preventing a disease. This polynuclectide sequence represents the feline of 5T4 antigen coding DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                            major histocompatibility complex class I peptide epitopes from human tumor-associated antigen, useful for preventing and/or treating a
Location/Qualifiers
1. .1260
/*tag= a
/product= "Peline 5T4 antigen protein"
                                                                                                                                                                                                                                                                                                                                    Redchenko I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 67; 73pp; English.
                                                                                                                                                                                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, particularly cancer.
                                                                                                                                                                                                  13-FEB-2003; 2003WO-GB000670
                                                                                                                                                                                                                                                13-FEB-2002; 2002GB-00003419.
                                                                                                                                                                                                                                                                                                                                    Kingsman S,
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-637141/60.
                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ADB97520
                                                                                                            WO2003068816-A1
                                                                                                                                                          21-AUG-2003
                                                                                                                                                                                                                                                                                                                                      Carroll M,
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Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other; Length:
Matches:
Conservative:
Mismatches:
Indels: JS-10-774-176-15 (1-9) x ADB97513 (1-1260) 133 40.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: .. 02

1090 CTGATAGGTGCCATTTTCTTACTGGTT 1116 LeuileGlyAlailePheLeuLeuVal 9 ADB97452 standard; DNA; 1260 BP (first entry) 04-DEC-2003 ADB97452; RESULT 12 ADB97452

ઠ 유 AXXXXX.

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The invention relates to a Major Histocompatibility Complex (MHC) class II peptide epitope of the 5T4 antigen. The vaccine or T-cell line or clone has a cytostatic activity, as it is useful in manufacturing a medicament for preventing and/or treating a disease, particularly cancer. The methods are useful for detecting T-cells capable of specifically recognising a peptide epitope in conjunction with an MHC molecule, for diagnosing or monitoring the progression of a cancerous disease, or for detecting the presence of a peptide or nucleic acid using an agent. The MHC class II peptide epitope of the invention can be used in gene therapy coding for the feline 5T4 protein.
                              gene; ds; feline; Major Histocompatibility Complex class II; MHC;
epitope; 5T4 antigen; vaccine; T-cell; cytostatic; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                             New Major Histocompatibility Complex class II peptide epitope of 5T4, useful for manufacturing a medicament for diagnosing, preventing and/or treating a disease, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, TAA; tumour-associated antigen, anti-tumour; cytostatic;
immunostimulant; vaccine; carcinoma; colorectal cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1260 BP; 221 A; 451 C; 346 G; 241 T; 0 U; 1 Other;
                                                                                                                                                    /product= "Feline 5T4 antigen protein"
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 5T4 tumour-associated antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-774-176-15 (1-9) x ADB97452 (1-1260)
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                                                                                                   Location/Qualifiers
1. .1260
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 49; 63pp; English
                                                                                                                                                                                                                                                                                                                                         Kingsman S
                                                                                                                                                                                                                                                                                                         (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                              13-FEB-2003; 2003WO-GB000618.
                                                                                                                                                                                                                                                                           13-FEB-2002; 2002GB-00003420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA27058 standard; DNA; 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133
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                                                                                                                                                                                                                                                                                                                                       Carroll M, Harrop R,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-663795/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ADB97455
                                                                                                                                                                                    WO2003068815-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                  21-AUG-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA27058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
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Carroll MW, Ellard FM;

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manufacture of a medicament for the prevention and treatment of a disease condition. The Scr antibody is useful in the manufacture of a medicament for the prevention and treatment of a disease condition. The Scr antibody is useful in the manufacture of a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The Scr antibody is also useful for treatment to a disease including antibody is also useful for treatment inflammatory diseases including variable of the script and diseases, cancers, central nervous system diseases, cancers, central nervous system diseases, cardiovascular diseases, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, and other immune disorders. The present sequence encodes a 574 protein, which is used to produce Scr of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes the use of a single chain antibody (ScFv),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine; dog; oncofoetal leucine-rich glycoprotein; 5T4; tumour; cell proliferative disorder; infection; inflammatory condition; cancer immunotherapy; foetal cell; maternal blood; cytostatic; foetal abnormality; foetal sex determination; gene; 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding canine oncofoetal leucine-rich glycoprotein, 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuileGlyAlailePheLeuLeuVal 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 26, 118pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD BIOMEDICA UK LTD
                      /product= "5T4"
                                                                                                                                                                                           18-NOV-1999; 99WO-GB003859.
15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
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                                                                                                                                                    13-NOV-2000; 2000WO-GB004317
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                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB83839.
                                                                  WO200136486-A2
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                                                                                                             25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                        Myers KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
The present sequence encodes the human 5T4 tumour-associated antigen (TAA). The TAA 5T4 is a glycoprotein which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 5T4 antigen may therefore be useful in tumour fadagnosis, targeting and immunotherapy. Mice in which tumours had been induced were inculated with a virus expression vector containing the present sequence. The 5T4 antigen was shown to be effective at eliciting an immunotherapeutic anti-tumour response. Both the nucleic acid encoding the antigen and the antigen test can be used to elicit an immune response, preferably CTL or an antibody response in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor associated antigen, 5T4 capable of eliciting cytotoxic T-lymphocyte response useful in vaccinating against and in treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1263 BP; 230 A; 428 C; 349 G; 256 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1093 CTGATAGGCGCTATTTTCCTCCTGGTT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LeuileGlyAlailePheLeuLeuVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-774-176-15 (1-9) x AAA27058 (1-1263)
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1. .1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 78; 79pp; English.
                                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LTD
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99GB-00001739.
99GB-00017995.
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                                                                                                                                                                             99WO-GB003859
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                                                                                                                                                                                                                                                                                                                                                        Carroll MW, Myers KA;
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-387735/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                    40200029428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                               Homo sapiens.
                                                                                                                                                                             18-NOV-1999;
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                                                                                                                                                                                                                                                                 30-JUL-1999;
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1263 9 0 0 0 0

AAF89736

RESULT 14

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Ouery Match: DB:

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Canis sp.

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concocetal laucine-rich glycoproteins known as 514, and the polymucleotide sequences encoding them. The 574 proteins are expressed in a significant proportion of tumours. The sequences of the invention are useful in a pharmaceutical composition for the prevention and/or treatment of tumours or other diseases associated with cell proliferation, infections, and inflammatory conditions in animals, preferably dogs or cats. The compositions may also be used for cancer immunotherapy in these animals. The sequences of the invention may also be used in diagnostic kits for rapid, reliable, sensitive, and specific measurement and localisation of 574 in extracts of plasma, unite, tissues, and in cell culture media. Antibodies specific for the 574 protein are useful for isolating foetal cells from maternal blood. The colls may then be subject to biochemical or genetic sampling used for testing foetal abnormalities, or to determine the sex of the foetus (es). The present sequence encodes canine 574 protein
                                                                                                                                                                                                                                                                                                                                                                                                 Novel canine or feline 5T4 polypeptide and polynucleotides encoding the polypeptide, useful in preparation of vaccine for treating and/or preventing cancer in a subject, preferably a dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to the isolation of canine and feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1263 BP; 200 A; 469 C; 377 G; 217 T; 0 U; 0 Other;
                                                       /*tag= a
/product= "5T4 protein"
               Location/Qualifiers
1. .1263
                                                                                                                                                                                                                                                                 (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 67; 68pp; English.
                                                                                                                                                                                                                                                                                                         Carroll M;
                                                                                                                                                                                         13-NOV-2001; 2001WO-GB005004.
                                                                                                                                                                                                                            13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-557449/59.
P-PSDB; AAU98693.
                                                                                                                                                                                                                                                                                                         Drury N,
                                                                                                              WO200238612-A2
                                                                                                                                                   16-MAY-2002
                                                                                                                                                                                                                                                                                                         Myers K,
                   Key
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-774-176-15 (1-9) x ABK87174 (1-1263) 40.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: Score:

Alignment Scores: Pred. No.:

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Search completed: May 27, 2006, 10:38:29 Job time : 379.5 secs

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Perfect score:

Sequence:

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AC128294 Rattus no
AC106962 Rattus no
AC172561 Bos tauru
AL935256 Lactobaci
AC145041 Macropus
AC149958 Strongylo
                      AX822164 Sequence
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AX316086 Sequence
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BD249732 Polypepti
AX052012 Sequence
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CQ731678 Sequence
BD127282 Primer fo
CQ782724 Sequence
BD127283 Primer fo
CQ782726 Sequence
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AX061916 Sequence
AX061916 Sequence
AX061912 Sequence
AX961912 Sequence
AX961914 Sequence
AX961914 Sequence
AX961915 Homo sapi
BC088198 Mus muscu
AX961914 Sequence
AX961915 Homo sapi
AJ012160 Mus muscu
AX961917 Human DNA
AL121977 Human DNA
AC158516 Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
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Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 32642 12-SEP-2002;
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9
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Sequence 32642 from Patent WO02070737.
CQ687716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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MMU012160
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AC158516
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AC172361
AL935256
AC145041
AC149958
                                                             AX821533
AX821548
BD249731
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DD174290
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AF063939
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BC037161
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AB168308
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CQ782724
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Location/Qualifiers
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Homo sapiens
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Pred. No.:
  LOCUS
DEFINITION
ACCESSION
VERSUON
KEYWORDS
SOURCE
ORGANISM
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
CQ687716
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     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
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-MODEL=frame+pan.model.-DEV=xlh
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-DB=GenEmbl -QFWT=fastap -SUPFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DWITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_NIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSTZE=570 -MINLEN=0 -MAXLEN=200000000 -MOST=abss04
-USER=US10774176_@CGN 1 1 7524_@runat_26052016_091443_24987 -NCPU=6 -ICPU=3
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CQ920916 Sequence
BD249733 Polypepti
                                                                                                     (without alignments)
257.039 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                          May 27, 2006, 09:51:03; Search time 3358.6 Seconds
                                                                                                                                                                                                                                                                                                      12732272
                GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                          6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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0.5
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CQ920916
BD249733
                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
  MILES WILLIAM CARROLL,KEVIN ALAN MYERS
C12N15/09,A61K39/00,A61K48/00,A61P35/00,C07K7/06,C07K14/065,
C07K19/00,
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Polypeptide
Patent: WO 0029428-A 3 25-MAY-2000;
CARROLL MILES WILLIAM (GB); MYERS KEVIN ALAN (GB); OXFORD
BIOMEDICA LTD (GB)
Location/Qualifiers
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Location/Qualifiers
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/organism="Canis sp."
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Methods for prognosis and treatment of solid tumors
Methods for Drognosis and treatment of solid tumors
Methods (US) 2017097052-A 2116 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis sp. (dog)
JP 2002530060-A/3
17-SEP-2002
18-NOV-1999 JP 2000582415
18-NOV-1998 GB 9825303.2,27-JAN-1999 GB
UL-1999 GB 9917995.4
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Carroll,M.W. and Myers,K.A.

Polypeptide

Patent: JP 2002530060-A 3 17-SEP-2002;

OXFORD BIOMEDICA LTD
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JP 2002530060-A/3.
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DD161112 linear PAT 23-NOV-2005 Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids Encoding The Antigens, and Methods of Use.
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Padigaru, M., Shenoy, S.G., Pochart, P.F., Kekuda, R., Gusev, V.Y.,
Zhong, M., Jr.R.J.T., Casman, S.J., Li, L., Miller, C.B.,
Patturajan, M., Anderson, D.W., Malyankar, U.M., Voss, B.Z.,
Spaderna, S.K., Gorman, L., Spytek, K.A., Liu, X., Burgess, C.E.,
Boldog, F.L., Guo, X., Vernet, C.A.M., Gangolli, E.A., Tchernev, V.T.
and Zerhusen, B.D.
Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic Acids
Brooding The Antigens, and Methods of Use
Patent: JP 2005508604, A 23 07-APR-2005;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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60/332271,
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60/277239,
60/277791,
60/278152,
60/278999,
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60/276994,16-MAR-2001 U
60/276000,13-MAR-2001 U
60/275578,20-MAR-2001 U
60/277321,21-MAR-2001 U
60/277833,23-MAR-2001 U
                   Conservative:
Mismatches:
Indels:
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60/274281,08-MAR-2001
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60/291240,16-MAY-2001
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60/309198,03-DEC-2001
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60/279036,28-MAR-2001
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Homo sapiens

17 2005508604-A/23

07-APR-2005

08-MAR-2005 JP 2002571827

08-MAR-2001 US 60/29310
                                                                             Gaps:
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Homo sapiens (human)
Homo sapiens
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PF 08-MAR-2
PR 19-JUN-2
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Query Match:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Patent: BP 1160323-A 3 05-DEC-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Canis sp."
/mol_type="unassigned DNA"
/db_xref="taxon:9616"
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                                                                                                   660 CTGATAGGCGCCATCTTCCTACTGGTT 686
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   Gaps:
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                                                                               LeuileGlyAlailePheLeuLeuVal
                                       US-10-774-176-15 (1-9) x AX025013 (1-901)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Carroll, M.W. and Myers, K.A.
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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AX316088
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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1. 1260
/organism="Felis catus"
/mol_type="unassigned DNA"
/db_xref="taxon:9685"
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Matches:
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Mismatches:
     Mismatches:
Indels:
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers

    1260
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9685"

                                                                                                                        1090 CTGATAGGTGCCATTTTCTTACTGGTT 1116
                                                                                                                                                                                                  Sequence 1 from Patent W003068816.
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                                       Gaps:
                                                                    US-10-774-176-15 (1-9) x AX467373 (1-1260)
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     Best Local Similarity:
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AX821533
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
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corine a m vernet,esha a gangolli,velizar t tchernev,bryan d
14-NOV-2001 US 60/33272,14-NOV-2001 US 60/332172, PR 14-NOV-2001 US 60/335301, PR 18-OCT-2001 US 60/335301, PR 18-OCT-2001 US 60/335301, PR 60/3369,27-SEP-2001 US 60/325691,22-SEP-2001 US 60/325691,22-SEP-2001 US 60/318462,03-GAN-2002 US 60/318470, PR 60/318F2,001 US 60/3187185,08-MAR-2002 US 10/093463, PR 16-AUG-2001 US 60/317185,08-MAR-2002 US 10/093463, PR 16-AUG-2001 US 60/317185,08-MAR-2002 US 10/093463, PR 16-AUG-2001 US 60/312903
                                                                                                                                                    vladimir y gusev, mei zhong, raymond j taupier jr, stacie j
                                                                                                                                                                      casman, li li,
PI charles e miller, meera patturajan, david w anderson, uriel
malyankar,
                                                                                                                                                                                                                        edward z voss, steven k spaderna, linda gorman, kimberly PI
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

    .1260
    /organism="Felis sp."
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Patent: WO 0238612-A 3 16-MAY-2002;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 3 from Patent W00238612.
AX467373 GI:21900603
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PI vladimir)
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Best Local Similarity:
Query Match:
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CC
FH Key
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PI xia
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Percent Similarity:
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Pred. No.:
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Pred. No.:
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                           Euteleostomi;
                                                                                       Polypeptide
Patent: WO 0029428-A 1 25-MAY-2000;
CARROLL MILES WILLIAM (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
BIOMEDICA LTD (GB) ; MYERS KEVIN ALAN (GB) ; OXFORD
1. 1263
| /organism="Homo sapiens" / mol type="unassigned DNA" / db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W.,
Ellacd, F.M. and Myers, K.A.
            Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleoi
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Conservative:
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Matches:
Conservative:
Mismatches:
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/nofe="574"
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synthetic construct
other sequences; artificial sequences.
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Gaps:
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Sequence 14 from Patent WO0136486.
AX149553
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                                                                                Carroll, M.W. and Myers, K.A.
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Homo sapiens (human)
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AX316086
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AX149553
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PN JP 2002530060-A/1
PD 17-SEP-2002
PP 18-NOV-1999 JP 2000582415
PR 18-NOV-1999 GB 9917995.4
30-JUL-1999 GB 9917995.4
PI MILES WILLIAM CARROLL, KEVIN ALAN MYERS
PC C12N15/09, A61K39/00, A61K48/00, A61P35/00, C07K7/06, C07K14/065, PC C12N15/00, CC Polypeptide Location/Qualifiers
FH Key 1. 1263
FT source /organism='Homo sapiens (human)'.
                                                                                                                                                                                                                       PAT 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1263)
Carroll, M.W. and Myers, K.A.
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Patent: JP 2002530060-A 1 17-SEP-2002;
OXFORD BIOMEDICA LTD
OS Homo sapiens (human)
PN JP 2002530060-A/1
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                                                                                                                                    Indels:

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AX025011 GI:10184932
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                                                                                                                                                                                                                       1263
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JP 2002530060-A/1.
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Homo sapiens
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BD249731
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AX025011
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Search completed: May 27, 2006, 19:35:21 Job time : 3359.6 secs

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Canis sp.
Canis sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 16-JUL-2002
                                                                             Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                           Carroll, M.W. and Myers, K.A.

5t4 tumour-associated antigen for use in tumour immunotherapy
Patent: EP 1160323-A 1 05-DEC-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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Polypeptide
Patent: WO 0238612-A 1 16-MAY-2002;
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    1263
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 Sequence 1 from Patent EP1160323.
AX316086
AX316086.‡ GI:17899278
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Sequence 1 from Patent W00238612.
AX467371 GI:21900602
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                                                        Homo sapiens (human)
Homo sapiens
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